potential source for regenerating tail muscle, and we have isolated cells from Anolis with the morphological features, molecular profile, and differentiation capacity matching murine satellite cells. We have created the web portal, AnolisGenome.org, as an Anolis biology and genomics community resource.

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Program/Abstract # 372
Degeneration–regeneration dynamics in the zebrafish lateral line nerve
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Wallerian degeneration (WD) is a classical example of axonal degeneration, which occurs when an axon is cut. The part of the axon that is disconnected from the cell body disassembles in a characteristic and orderly way. In vertebrates, this part of the axon can continue to conduct action potentials for a day or two when it is electrically stimulated, but it then quickly degenerates. WD can occur in both the peripheral and central nervous systems. In this work we characterize the dynamics of nerve degeneration–regeneration of zebrafish posterior lateral line (PLL), after axotomy. The method uses focused laser power on a 2-photon microscope, which allows us to induce very accurate and precise injuries, without harming nearby cells. After injury, we employ time lapse confocal microscopy to monitor the behavior of recovering neurons or their neighbors at high-resolution in vivo. We determined that a percentage of innervated sensory cells die after being denervated, but most remain and the formation of new cells during regeneration is unaffected by the absence of the nerve. In contrast, the absence of sensory targets causes abnormal behavior in the regenerate axon, as erratic paths are followed during the time sensory cells are absent. Once these cells differentiate, the axon is able to reinnervate them. Our results show that there is a relationship of dependency between sensory receptor cell and sensory neuron in the lateral line system of zebrafish. Future work will be aimed at identifying the molecules involved in this dependency.

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Program/Abstract # 373
The role of matrix metalloproteinases in the repair of the Xenopus laevis pronephric kidney
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The kidney is necessary for maintenance of vertebrate homeostasis, thus the ability to repair acute damage to nephric structures is critical for survival. Previous work examining the effects of chemically-induced nephrotoxicity has been described in several adult vertebrates including fish, dogs and rats. However, the complexity as well as the inaccessibility of these organs makes it difficult to examine the repair response of the renal system after mechanical damage. In contrast, amphibian pronephroi (embryonic kidneys) are accessible, have relatively simple architecture, and have previously proven to be amenable to surgical manipulation. Since the inductive processes that give rise to amphibian pronephroi are very similar to those that give rise to adult mammalian kidneys, it is useful to study the process of renal repair in this simpler system. For these reasons, our lab is currently investigating the repair response in the pronephros following partial removal of pronephric tubules. Previously, we have found that partially excised pronephroi are replaced by organized tissue that morphologically resemble pronephric tubules, and that these ‘restored’ structures express differentiated-kidney markers. Currently we are examining the involvement of matrix metalloproteinases (MMPs) during renal repair. Since, mechanical injury induced via partial nephrectomy of pronephric tubules creates a similar condition to those seen in kidneys experiencing infections, kidney stones and tumors, the information acquired during this research may be applicable to therapeutic alternatives in the treatment of many causes of human renal dysfunction.

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Program/Abstract # 375
Finding the ancestral wound healing response
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The study of wound closure is important for the advancement of medicinal applications in surgical scar healing, as well as initiation of tissue regeneration. Research on wound closure has primarily focused on vertebrate models, although the process is found throughout all animal groups. Non-vertebrate models provide efficient cost-effective tools for examining the general properties necessary for wound repair and regeneration, generating novel targets for clinically translatable studies of vertebrates. Non-vertebrate models can also provide evolutionary insight and help fill the gaps between animals that exhibit extraordinary regenerative capabilities and those with more limited capabilities. We chose to address the process of wound closure in the basal cnidian, Nemastostella vectensis, because it readily regenerates in lab, has a sequenced genome, and its phylogenetic position gives direct insight into bilaterian evolution. In this study we preformed the first cnidian microarray screen to look for genes activated after injury. We then used multiple techniques, including: in situ hybridization, quantitative PCR, and immunohistochemistry to determine the cellular and molecular mechanisms involved in Nemastostella wound healing. Nemastostella’s wound healing response exhibits conserved molecular mechanisms such as apoptosis and MAPK signaling, while perturbation of MAPK signaling inhibits wound closure and confirms functional conservation of wound healing mechanisms. This study shows that the process of wound closure in metazoans is well conserved between basal cnidarians and vertebrates and provides a new model for medicinal applications.

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Program/Abstract # 376
Flotillin2 inhibits the activity of an epidermal wound response sensor
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Development coordinates gene regulatory processes throughout both the initiation of growth and tissue regeneration. During injury cells quickly react to activate repair systems. Drosophila’s epidermal monolayer provides an excellent system to study the genetic and developmental function of genes that control the wound healing process. We have cloned the enhancers of several wound response genes and generated wound-dependent reporters that provide a visible read-out of transcriptional activation. Results from a genetic screen of deletions that alter the activity of wound response reporters identified Flotillin2 (FLO2), a well-conserved gene that encodes a membrane-associated protein.