Kenro Kusumi, PhD

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3pm
SCOB 210

Associate Dean of Graduate Programs, CLAS

Professor, School of Life Sciences

Arizona State University

sbhse
school of biological and health systems engineering

Bio-Sketch

Kenro Kusumi is professor in the School of Life Sciences and associate dean of graduate programs in the College of Liberal Arts & Sciences. Kusumi received his BA from Harvard University and PhD from MIT, and he carried out postdoctoral training at the National Institute for Medical Research in London. Prior to coming to ASU, Kusumi taught at the University of Pennsylvania School of Medicine and the Children's Hospital of Philadelphia, where he served as director of pediatric orthopaedic basic research. At ASU, Kusumi has served as director of the Molecular & Cellular Biology interdisciplinary graduate program and interim associate director of graduate programs in the School of Life Sciences. Dr. Kusumi is a specialist in genomics, regenerative medicine, and developmental disorders. His laboratory has used next-generation genomic technologies to uncover the molecular profile of tail regeneration in the lizard, *Anolis carolinensis*, and he has previously identified genetic changes that lead to congenital scoliosis and vertebral malformations. Kusumi's research has been supported by the National Institutes of Health.

Abstract

Identifying the genetic toolkit for regeneration in vertebrates: Insights from comparative genomic analysis

Many vertebrates display the ability to regenerate appendages and complex tissues such as spinal cord, but classic models such as the mouse and chick have been unsuitable for regenerative studies since mammals and birds have very limited capacity. With the availability of whole genome sequences and functional genetic technologies for reptilian, amphibian, and teleost models, comparative studies of regeneration are now possible. Lizards, which are amniote vertebrates like humans, are able to lose and regenerate a functional tail with regrowth and patterning of spinal cord, cartilage, muscle, vasculature, and skin. Building on our annotation of the green anole genome, we analyzed the mRNA and microRNA transcriptomes during tail regeneration in the green anole lizard, *Anolis carolinensis*. Transcriptomic analysis revealed 326 differentially expressed genes, of which 302 have clear human orthologues, regulating wound and immune response, hormonal regulation, and musculoskeletal development. MicroRNA sequencing of lizard regenerating tail and associated tissues revealed both novel and known microRNA precursor families. By using a comparative systems biology approach, we are working to discover conserved gene regulatory networks for regeneration in vertebrates. Comparing our lizard transcriptomic data with manually curated, public RNA-seq and microarray data sets from anamniote models, including the salamander, *Xenopus* frog, and zebrafish, we have already identified common patterns of activation of the canonical Wnt and Wnt5-calcium signaling pathways. By combining evo-devo and genomic approaches, we are working to identify conserved and convergent gene regulatory networks that may impact on future regenerative medical therapies.