Stanford

David Kingsley

Rudy J. and Daphne Donohue Munzer Professor in the School of Medicine

Developmental Biology

CONTACT INFORMATION

- **Alternate Contact**

  Lisa Palermo - Administrative assistant

  Email lpalermo@stanford.edu

  Tel 650 725-7658

Bio

ACADEMIC APPOINTMENTS

- Professor, Developmental Biology
- Member, Bio-X
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Director, NIH Center of Excellence in Genomic Science at Stanford: The Genomic Basis of Vertebrate Diversity, (2007-2012)
- Co-Director, Genetics and Developmental Biology Training Grant, (2008- present)
- Associate Chairman, Department of Developmental Biology, (2012- present)

HONORS AND AWARDS

- Scholar in Biomedical Research, Lucille P. Markey Foundation (1989 to 1996)
- Investigator, Howard Hughes Medical Institute (1997 to present)
- Fellow, American Academy of Arts and Sciences (2005)
- Conklin Medal for outstanding research in Developmental Biology, Society for Developmental Biology (2009)
- Member, National Academy of Sciences (2011)

5 OF 6

PROFESSIONAL EDUCATION

- B.S., Yale , Biology (1981)
- Ph.D., MIT , Biology (1986)
- Postdoc, National Cancer Institute - Frederick , Mouse genetics (1987)

LINKS

- KingsleyLab Web Site: http://kingsley.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Naturally occurring species show spectacular differences in morphology, physiology, lifestyle, and behavior. They also differ in disease susceptibility and life span. Although the genomes of many organisms have now been completely sequenced, we still know relatively little about the specific DNA sequence changes that underlie interesting species-specific traits. My laboratory is using a combination of genetic and genomic approaches to identify the detailed molecular mechanisms that control evolutionary change in vertebrates, with a focus on five fundamental questions:

1. Are new evolutionary traits controlled by countless genetic differences of small effect, or by a few genetic changes with large effects?

2. What specific genes have changed to produce interesting evolutionary differences seen in nature?

3. What kinds of mutations have occurred in these genes (e.g., dominant or recessive, coding or regulatory, preexisting or de novo)?

4. How predictable is evolution? If you know how evolution has occurred in one population, is it possible to predict the genes and mutations that also underlie the same trait in different populations?

5. How has evolution produced the unique characteristics of humans?

We study these questions using a variety of methods in mice, sticklebacks, and people.

Mice are often the best system available for asking detailed mechanistic questions in mammals, or testing the phenotypic effects of particular sequence changes seen in other species. We have used classical genetics in mice to identify fundamental pathways that control formation and patterning of cartilage, bone, and joints. We also make extensive use of mice identifying the regulatory mechanisms that lay out expression of key developmental control genes, with the ultimate aim of identifying how vertebrate morphology itself is encoded in the genome.

Sticklebacks offer an unusually powerful system for studying the molecular basis of evolutionary change in naturally occurring species. Our lab has pioneered the development of a large number of new genetic and genomic resources for the fish, and has worked with Hudson Alpha Institute and the Broad Institute to develop a high-quality whole genome sequence assembly for sticklebacks. Using these new tools, we have now successfully identified both the molecular mechanisms that control repeated evolution of armor plate patterning, pelvic reduction, and spine and skin color changes in nature. Our studies show that big evolutionary changes can be controlled by single chromosome regions. The big changes are controlled by alterations in major developmental control genes (key signaling molecules and transcription factors). Although null mutations in these genes are typically deleterious or lethal, sticklebacks have made regulatory alterations in these genes that produce large morphological effects in particular tissues, while preserving overall viability. Interestingly, the same genes are used repeatedly when similar phenotypes evolve in different populations, revealing a surprising commonality to the molecular mechanisms that control rapid evolutionary change in diverse organisms.

Although many of our studies have begun in mice or sticklebacks, the genes and mechanisms that we have also turn out to control major differences in human morphology, hair color, arthritis susceptibility, and incidence of major psychiatric diseases in billions of people around the world. Building on this work, we have now begun a variety of projects to identify other mechanisms responsible for key evolutionary traits and diseases in humans. Although we are still far from knowing the detailed molecular basis of most human traits, we are optimistic that many aspects of this problem can now be studied both computationally and experimentally, and will provide new insights into both human origins and human medicine.

Teaching

COURSES

2018-19

- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2016-17

- Development and Disease Mechanisms: DBIO 201 (Aut)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

2015-16

- Development and Disease Mechanisms: DBIO 201 (Aut)
- Genetics and Developmental Biology Training Camp: DBIO 200, GENE 200 (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Leslie Koyama, Gerald Tiu, John Vaughen

Postdoctoral Faculty Sponsor

Amy Herbert

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Developmental Biology (Phd Program)
- Neurosciences (Phd Program)

Publications

PUBLICATIONS

- **Characterization of a Human-Specific Tandem Repeat Associated with Bipolar Disorder and Schizophrenia.** *American journal of human genetics*
  Song, J. H., Lowe, C. B., Kingsley, D. M.
  2018
- **Ancient selection for derived alleles at a GDF5 enhancer influencing human growth and osteoarthritis risk.** *Nature genetics*
  Capellini, T. D., Chen, H., Cao, J., Doxey, A. C., Kiapour, A. M., Schoor, M., Kingsley, D. M.
  2017; 49 (8): 1202–10
- **Evolving New Skeletal Traits by cis-Regulatory Changes in Bone Morphogenetic Proteins.** *Cell*
  Indjeian, V. B., Kingman, G. A., Jones, F. C., Guenther, C. A., Grimwood, J., Schmutz, J., Myers, R. M., Kingsley, D. M.
  2016; 164 (1-2): 45-56
- **A molecular basis for classic blond hair color in Europeans.** *Nature genetics*
  Guenther, C. A., Tasic, B., Luo, L., Bedell, M. A., Kingsley, D. M.
  2014; 46 (7): 748-752
- **The genomic basis of adaptive evolution in threespine sticklebacks.** *Nature*
  Jones, F. C., Grabherr, M. G., Chan, Y. F., Russell, P., Mauceli, E., Johnson, J., Swofford, R., Pirun, M., Zody, M. C., White, S., Birney, E., Searle, S., Schmutz, et al
  2012; 484 (7392): 55-61