



## David Kingsley

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

### CONTACT INFORMATION

- **Alternate Contact**

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### Bio

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#### 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, (2008-2023)
- Associate Chairman, Department of Developmental Biology, (2012-2023)

#### 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)
- GSA Medal for outstanding research in Genetics, Genetic Society of America (2017)

#### PROFESSIONAL EDUCATION

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

#### PATENTS

- David Kingsley. "United States Patent 7,122,328 Gene involved in mineral deposition and uses thereof", Oct 17, 2006

## LINKS

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

## Research & Scholarship

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### CURRENT RESEARCH AND SCHOLARLY INTERESTS

Wild species show spectacular differences in morphology, physiology, behavior, disease susceptibility, and lifespan. Although many organisms have now been sequenced, we still know relatively little about the specific DNA sequence changes that underlie key species-specific traits. My laboratory uses a combination of genetic and genomic approaches to identify the detailed molecular mechanisms that control evolutionary change in vertebrates, with a focus on 5 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 genes have changed to produce interesting evolutionary differences 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, can you predict the genes and mutations that 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 stickleback fish, mice, and humans.

Stickleback fish have recently diversified in thousands of new postglacial environments, offering an unusually powerful system for mapping the molecular basis of vertebrate evolution. My lab pioneered the development of many new genetic and genomic resources for sticklebacks, including crosses between divergent populations, genetic mapping of traits, comparative genome sequencing, and testing the molecular basis of evolutionary differences using transgenic and CRISPR methods. Our studies have revealed the molecular mechanisms that control repeated evolution of armor plate patterning, pelvic reduction, and spine and skin color changes in nature. We find that big evolutionary changes are controlled by regulatory changes in key developmental control genes. Although inactivating mutations in such genes are deleterious or lethal, evolution can preserve viability and increase fitness of wild populations by tweaking the expression of key control genes in particular tissues. Interestingly, the same genes are used repeatedly when similar phenotypes evolve in different populations, revealing a surprising commonality to the molecular mechanisms controlling evolutionary change in diverse organisms.

Mice are also a powerful system for studying traits and diseases in mammals, and for testing the phenotypic effects of particular sequence changes that have occurred in other species. Our genetic studies in mice have identified fundamental signaling pathways that control formation and patterning of cartilage, bone, and joints, and have revealed the regulatory sequences that control expression of many key genes during development and tissue injury. We also use genome editing in mice to model sequence changes that underlie common traits in other species, including some of the most prevalent pigmentation, height, and arthritis traits found in humans.

The genes and mechanisms that we have identified in fish and mice 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. To further study the genomic changes that underlie key evolutionary traits and diseases in humans, we are developing innovative new genetic approaches to compare gene expression and developmental differences between human and chimpanzee cells in vitro, and to map the specific genomic regions controlling these differences using targeted modification and recombination between primate chromosomes. 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 computationally and experimentally, providing new insights into both human origins and human medicine.

## Teaching

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### COURSES

#### 2025-26

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

#### 2024-25

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

#### 2023-24

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

#### 2022-23

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

### STANFORD ADVISEES

#### Doctoral Dissertation Reader (AC)

James Hemker, Andrea Navarrete Vargas

#### Doctoral Dissertation Advisor (AC)

Bohdana-Myroslava Briantseva, Francesca Cohn, Jack Hsu, Austin Katzer

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

## Publications

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### PUBLICATIONS

- **Ancient developmental genes underlie evolutionary novelties in walking fish.** *Current biology : CB*  
Herbert, A. L., Allard, C. A., McCoy, M. J., Wucherpfennig, J. I., Krueger, S. P., Chen, H. I., Gourlay, A. N., Jackson, K. D., Abbo, L. A., Bennett, S. H., Sears, J. D., Rhyne, A. L., Bellono, et al  
2024
- **Whole-genome Comparisons Identify Repeated Regulatory Changes Underlying Convergent Appendage Evolution in Diverse Fish Lineages.** *Molecular biology and evolution*  
Chen, H. I., Turakhia, Y., Bejerano, G., Kingsley, D. M.  
2023; 40 (9)
- **Evolution of stickleback spines through independent cis-regulatory changes at HOXDB.** *Nature ecology & evolution*  
Wucherpfennig, J. I., Howes, T. R., Au, J. N., Au, E. H., Roberts Kingman, G. A., Brady, S. D., Herbert, A. L., Reimchen, T. E., Bell, M. A., Lowe, C. B., Dalziel, A. C., Kingsley, D. M.

2022

- **Genetic studies of human-chimpanzee divergence using stem cell fusions.** *Proceedings of the National Academy of Sciences of the United States of America*  
Song, J. H., Grant, R. L., Behrens, V. C., Kucka, M., Roberts Kingman, G. A., Soltys, V., Chan, Y. F., Kingsley, D. M.  
1800; 118 (51)
- **DNA fragility in the parallel evolution of pelvic reduction in stickleback fish.** *Science (New York, N.Y.)*  
Xie, K. T., Wang, G., Thompson, A. C., Wucherpfennig, J. I., Reimchen, T. E., MacColl, A. D., Schluter, D., Bell, M. A., Vasquez, K. M., Kingsley, D. M.  
2019; 363 (6422): 81–84
- **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. n., Cao, J. n., Doxey, A. C., Kiapour, A. M., Schoor, M. n., Kingsley, D. M.  
2017; 49 (8): 1202–10
- **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
- **Human-specific loss of regulatory DNA and the evolution of human-specific traits** *NATURE*  
McLean, C. Y., Reno, P. L., Pollen, A. A., Bassan, A. I., Capellini, T. D., Guenther, C., Indjeian, V. B., Lim, X., Menke, D. B., Schaar, B. T., Wenger, A. M., Bejerano, G., Kingsley, et al  
2011; 471 (7337): 216–219
- **Genetic mechanisms of axial patterning in *Apeltes quadracus*.** *Evolution letters*  
Herbert, A. L., Lee, D., McCoy, M. J., Behrens, V. C., Wucherpfennig, J. I., Kingsley, D. M.  
2024; 8 (6): 893–901
- **Genomic Sequence of the Threespine Stickleback Iridovirus (TSIV) from Wild *Gasterosteus aculeatus* in Stormy Lake, Alaska.** *Viruses*  
Yoxsimer, A. M., Offenberg, E. G., Katzer, A. W., Bell, M. A., Massengill, R. L., Kingsley, D. M.  
2024; 16 (11)
- **Evolution of novel sensory organs in fish with legs.** *Current biology : CB*  
Allard, C. A., Herbert, A. L., Krueger, S. P., Liang, Q., Walsh, B. L., Rhyne, A. L., Gourlay, A. N., Seminara, A., Baldwin, M. W., Kingsley, D. M., Bellono, N. W.  
2024
- **Genetic mechanisms of axial patterning in *Apeltes quadracus*** *EVOLUTION LETTERS*  
Herbert, A. L., Lee, D., McCoy, M. J., Behrens, V. C., Wucherpfennig, J., Kingsley, D. M.  
2024
- **Fine-scale contemporary recombination variation and its fitness consequences in adaptively diverging stickleback fish.** *Nature ecology & evolution*  
Venu, V., Harjunmaa, E., Dreau, A., Brady, S., Absher, D., Kingsley, D. M., Jones, F. C.  
2024
- **Boundary stacking interactions enable cross-TAD enhancer-promoter communication during limb development.** *Nature genetics*  
Hung, T. C., Kingsley, D. M., Boettiger, A. N.  
2024

- **The genetic basis of novel trait gain in walking fish.** *bioRxiv : the preprint server for biology*  
Herbert, A. L., Allard, C. A., McCoy, M. J., Wucherpfennig, J. I., Krueger, S. P., Chen, H. I., Gourlay, A. N., Jackson, K. D., Abbo, L. A., Bennett, S. H., Sears, J. D., Rhyne, A. L., Bellono, et al  
2023
- **Sea robins** *CURRENT BIOLOGY*  
Allard, C. A. H., Herbert, A. L., Kingsley, D. M., Bellono, N. W.  
2023; 33 (13): R704-R706
- **Sea robins.** *Current biology : CB*  
Allard, C. A., Herbert, A. L., Kingsley, D. M., Bellono, N. W.  
2023; 33 (13): R704-R706
- **Genomic changes underlying repeated niche shifts in an adaptive radiation.** *Evolution; international journal of organic evolution*  
Marques, D. A., Jones, F. C., Palma, F. D., Kingsley, D. M., Reimchen, T. E.  
2022
- **Characterization of mouse Bmp5 regulatory injury element in zebrafish wound models.** *Bone*  
Heller, I. S., Guenther, C. A., Meireles, A. M., Talbot, W. S., Kingsley, D. M.  
2021: 116263
- **Longer or shorter spines: Reciprocal trait evolution in stickleback via triallelic regulatory changes in Stanniocalcin2a.** *Proceedings of the National Academy of Sciences of the United States of America*  
Roberts Kingman, G. A., Lee, D., Jones, F. C., Desmet, D., Bell, M. A., Kingsley, D. M.  
2021; 118 (31)
- **Predicting future from past: The genomic basis of recurrent and rapid stickleback evolution.** *Science advances*  
Roberts Kingman, G. A., Vyas, D. N., Jones, F. C., Brady, S. D., Chen, H. I., Reid, K., Milhaven, M., Bertino, T. S., Aguirre, W. E., Heins, D. C., von Hippel, F. A., Park, P. J., Kirch, et al  
2021; 7 (25)
- **Fitness maps to a large-effect locus in introduced stickleback populations.** *Proceedings of the National Academy of Sciences of the United States of America*  
Schluter, D. n., Marchinko, K. B., Arnegard, M. E., Zhang, H. n., Brady, S. D., Jones, F. C., Bell, M. A., Kingsley, D. M.  
2021; 118 (3)
- **Assembly of the threespine stickleback Y chromosome reveals convergent signatures of sex chromosome evolution.** *Genome biology*  
Peichel, C. L., McCann, S. R., Ross, J. A., Naftaly, A. F., Urton, J. R., Cech, J. N., Grimwood, J. n., Schmutz, J. n., Myers, R. M., Kingsley, D. M., White, M. A.  
2020; 21 (1): 177
- **Predictive covariation among trophic, isotopic, and genomic traits is consistent with intrapopulation diversifying selection** *EVOLUTIONARY ECOLOGY RESEARCH*  
Reimchen, T. E., Frey, S., Brady, S. D., Kingsley, D. M.  
2019; 20 (2): 231–45
- **DNA fragility in the parallel evolution of pelvic reduction in stickleback fish** *SCIENCE*  
Xie, K. T., Wang, G., Thompson, A. C., Wucherpfennig, J. I., Reimchen, T. E., MacColl, A. D. C., Schluter, D., Bell, M. A., Vasquez, K. M., Kingsley, D. M.  
2019; 363 (6422): 81-+
- **Efficient CRISPR-Cas9 editing of major evolutionary loci in sticklebacks** *EVOLUTIONARY ECOLOGY RESEARCH*  
Wucherpfennig, J., Miller, C. T., Kingsley, D. M.  
2019; 20 (1)
- **Efficient CRISPR-Cas9 editing of major evolutionary loci in sticklebacks.** *Evolutionary ecology research*  
Wucherpfennig, J. I., Miller, C. T., Kingsley, D. M.  
2019; 20 (1): 107-132
- **A novel enhancer near the Pitx1 gene influences development and evolution of pelvic appendages in vertebrates.** *eLife*  
Thompson, A. C., Capellini, T. D., Guenther, C. A., Chan, Y. F., Infante, C. R., Menke, D. B., Kingsley, D. M.

2018; 7

- **A novel enhancer near the Pitx1 gene influences development and evolution of pelvic appendages in vertebrates** *ELIFE*  
Thompson, A. C., Capellini, T. D., Guenther, C. A., Chan, Y., Infante, C. R., Menke, D. B., Kingsley, D. M.  
2018; 7
- **Characterization of a Human-Specific Tandem Repeat Associated with Bipolar Disorder and Schizophrenia** *AMERICAN JOURNAL OF HUMAN GENETICS*  
Song, J. H. T., Lowe, C. B., Kingsley, D. M.  
2018; 103 (3): 421-430
- **Detecting differential copy number variation between groups of samples.** *Genome research*  
Lowe, C. B., Sanchez-Luege, N. n., Howes, T. R., Brady, S. D., Daugherty, R. R., Jones, F. C., Bell, M. A., Kingsley, D. M.  
2018; 28 (2): 256-65
- **Experimental evidence for rapid genomic adaptation to a new niche in an adaptive radiation.** *Nature ecology & evolution*  
Marques, D. A., Jones, F. C., Di Palma, F. n., Kingsley, D. M., Reimchen, T. E.  
2018; 2 (7): 1128-38
- **Genomic dissection of conserved transcriptional regulation in intestinal epithelial cells.** *PLoS biology*  
Lickwar, C. R., Camp, J. G., Weiser, M., Cocchiario, J. L., Kingsley, D. M., Furey, T. S., Sheikh, S. Z., Rawls, J. F.  
2017; 15 (8): e2002054
- **Convergent evolution of SWS2 opsin facilitates adaptive radiation of threespine stickleback into different light environments** *PLOS BIOLOGY*  
Marques, D. A., Taylor, J. S., Jones, F. C., Di Palma, F., Kingsley, D. M., Reimchen, T. E.  
2017; 15 (4)
- **Dorsal spine evolution in threespine sticklebacks via a splicing change in MSX2A.** *BMC biology*  
Howes, T. R., Summers, B. R., Kingsley, D. M.  
2017; 15 (1): 115
- **Genetic Coupling of Female Mate Choice with Polygenic Ecological Divergence Facilitates Stickleback Speciation.** *Current biology : CB*  
Bay, R. A., Arnegard, M. E., Conte, G. L., Best, J. n., Bedford, N. L., McCann, S. R., Dubin, M. E., Chan, Y. F., Jones, F. C., Kingsley, D. M., Schluter, D. n., Peichel, C. L.  
2017; 27 (21): 3344-49.e4
- **Beautiful Piles of Bones: An Interview with 2017 Genetics Society of America Medal Recipient David M. Kingsley.** *Genetics*  
Kingsley, D. M.  
2017; 207 (4): 1221-22
- **An Unexpectedly Complex Architecture for Skin Pigmentation in Africans.** *Cell*  
Martin, A. R., Lin, M. n., Granka, J. M., Myrick, J. W., Liu, X. n., Sockell, A. n., Atkinson, E. G., Werely, C. J., Möller, M. n., Sandhu, M. S., Kingsley, D. M., Hoal, E. G., Liu, et al  
2017; 171 (6): 1340-53.e14
- **Heads, Shoulders, Elbows, Knees, and Toes: Modular Gdf5 Enhancers Control Different Joints in the Vertebrate Skeleton** *PLOS GENETICS*  
Chen, H., Capellini, T. D., Schoor, M., Mortlock, D. P., Reddi, A. H., Kingsley, D. M.  
2016; 12 (11)
- **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
- **Extent of QTL Reuse During Repeated Phenotypic Divergence of Sympatric Threespine Stickleback** *GENETICS*  
Conte, G. L., Arnegard, M. E., Best, J., Chan, Y. F., Jones, F. C., Kingsley, D. M., Schluter, D., Peichel, C. L.  
2015; 201 (3): 1189-U730
- **A distinct regulatory region of the Bmp5 locus activates gene expression following adult bone fracture or soft tissue injury.** *Bone*  
Guenther, C. A., Wang, Z., Li, E., Tran, M. C., Logan, C. Y., Nusse, R., Pantalena-Filho, L., Yang, G. P., Kingsley, D. M.  
2015; 77: 31-41

- **A recurrent regulatory change underlying altered expression and Wnt response of the stickleback armor plates gene EDA** *ELIFE*  
O'Brown, N. M., Summers, B. R., Jones, F. C., Brady, S. D., Kingsley, D. M.  
2015; 4
- **Mesenchymal cells. Defining a mesenchymal progenitor niche at single-cell resolution.** *Science*  
Kumar, M. E., Bogard, P. E., Espinoza, F. H., Menke, D. B., Kingsley, D. M., Krasnow, M. A.  
2014; 346 (6211)
- **The phosphate exporter xpr1b is required for differentiation of tissue-resident macrophages.** *Cell reports*  
Meireles, A. M., Shiau, C. E., Guenther, C. A., Sidik, H., Kingsley, D. M., Talbot, W. S.  
2014; 8 (6): 1659-1667
- **Evolved tooth gain in sticklebacks is associated with a cis-regulatory allele of Bmp6.** *Proceedings of the National Academy of Sciences of the United States of America*  
Cleves, P. A., Ellis, N. A., Jimenez, M. T., Nunez, S. M., Schluter, D., Kingsley, D. M., Miller, C. T.  
2014; 111 (38): 13912-13917
- **Genetics of ecological divergence during speciation.** *Nature*  
Arnegard, M. E., Mcgee, M. D., Matthews, B., Marchinko, K. B., Conte, G. L., Kabir, S., Bedford, N., Bergek, S., Chan, Y. F., Jones, F. C., Kingsley, D. M., Peichel, C. L., Schluter, et al  
2014; 511 (7509): 307-311
- **Efficient Imputation of Missing Markers in Low-Coverage Genotyping-by-Sequencing Data from Multiparental Crosses** *GENETICS*  
Miller, C. T., Glazer, A. M., Summers, B. R., Blackman, B. K., Norman, A. R., Shapiro, M. D., Cole, B. L., Peichel, C. L., Schluter, D., Kingsley, D. M.  
2014; 197 (1): 405-?
- **A recurrent regulatory change underlying altered expression and Wnt response of the stickleback armor plates gene EDA.** *eLife*  
O'Brown, N. M., Summers, B. R., Jones, F. C., Brady, S. D., Kingsley, D. M.  
2014; 4
- **Phylogeography and adaptation genetics of stickleback from the Haida Gwaii archipelago revealed using genome-wide single nucleotide polymorphism genotyping** *MOLECULAR ECOLOGY*  
Deagle, B. E., Jones, F. C., Absher, D. M., Kingsley, D. M., Reimchen, T. E.  
2013; 22 (7): 1917-1932
- **Pitx1 broadly associates with limb enhancers and is enriched on hindlimb cis-regulatory elements** *DEVELOPMENTAL BIOLOGY*  
Infante, C. R., Park, S., Mihala, A. G., Kingsley, D. M., Menke, D. B.  
2013; 374 (1): 234-244
- **A penile spine/vibrissa enhancer sequence is missing in modern and extinct humans but is retained in multiple primates with penile spines and sensory vibrissae.** *PloS one*  
Reno, P. L., McLean, C. Y., Hines, J. E., Capellini, T. D., Bejerano, G., Kingsley, D. M.  
2013; 8 (12)
- **A "Forward Genomics" Approach Links Genotype to Phenotype using Independent Phenotypic Losses among Related Species** *CELL REPORTS*  
Hiller, M., Schaar, B. T., Indjeian, V. B., Kingsley, D. M., Hagey, L. R., Bejerano, G.  
2012; 2 (4): 817-823
- **Genetic Architecture of Variation in the Lateral Line Sensory System of Threespine Sticklebacks** *G3-GENES GENOMES GENETICS*  
Wark, A. R., Mills, M. G., Dang, L., Chan, Y. F., Jones, F. C., Brady, S. D., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., Kingsley, D. M., Peichel, C. L.  
2012; 2 (9): 1047-1056
- **GENETIC SIGNATURE OF ADAPTIVE PEAK SHIFT IN THREESPINE STICKLEBACK** *EVOLUTION*  
Rogers, S. M., Tamkee, P., Summers, B., Balabhadra, S., Marks, M., Kingsley, D. M., Schluter, D.  
2012; 66 (8): 2439-2450
- **Population genomics of parallel phenotypic evolution in stickleback across stream-lake ecological transitions** *PROCEEDINGS OF THE ROYAL SOCIETY B-BIOLOGICAL SCIENCES*  
Deagle, B. E., Jones, F. C., Chan, Y. F., Absher, D. M., Kingsley, D. M., Reimchen, T. E.

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- **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
- **A Genome-wide SNP Genotyping Array Reveals Patterns of Global and Repeated Species-Pair Divergence in Sticklebacks** *CURRENT BIOLOGY*  
Jones, F. C., Chan, Y. F., Schmutz, J., Grimwood, J., Brady, S. D., Southwick, A. M., Absher, D. M., Myers, R. M., Reimchen, T. E., Deagle, B. E., Schluter, D., Kingsley, D. M.  
2012; 22 (1): 83-90
- **Three Periods of Regulatory Innovation During Vertebrate Evolution** *SCIENCE*  
Lowe, C. B., Kellis, M., Siepel, A., Raney, B. J., Clamp, M., Salama, S. R., Kingsley, D. M., Lindblad-Toh, K., Haussler, D.  
2011; 333 (6045): 1019-1024
- **The genetic basis of divergent pigment patterns in juvenile threespine sticklebacks** *HEREDITY*  
Greenwood, A. K., Jones, F. C., Chan, Y. F., Brady, S. D., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., KINGSLEY, D. M., Peichel, C. L.  
2011; 107 (2): 155-166
- **The Progressive Ankylosis Protein Regulates Cementum Apposition and Extracellular Matrix Composition** *CELLS TISSUES ORGANS*  
Foster, B. L., Nagatomo, K. J., Bamashmous, S. O., Tompkins, K. A., Fong, H., Dunn, D., Chu, E. Y., Guenther, C., KINGSLEY, D. M., Rutherford, R. B., Somerman, M. J.  
2011; 194 (5): 382-405
- **Human-specific loss of an androgen receptor enhancer is associated with the loss of vibrissae and penile spines** *80th Annual Meeting of the American-Association-of-Physical-Anthropologists*  
Reno, P. L., McLean, C. Y., Pollen, A. A., Bejerano, G., Kingsley, D. M.  
WILEY-BLACKWELL.2011: 252-252
- **Synovial joint morphogenesis requires the chondrogenic action of Sox5 and Sox6 in growth plate and articular cartilage** *DEVELOPMENTAL BIOLOGY*  
Dy, P., Smits, P., Silvester, A., Penzo-Mendez, A., Dumitriu, B., Han, Y., de la Motte, C. A., Kingsley, D. M., Lefebvre, V.  
2010; 341 (2): 346-359
- **Adaptive Evolution of Pelvic Reduction in Sticklebacks by Recurrent Deletion of a Pitx1 Enhancer** *SCIENCE*  
Chan, Y. F., Marks, M. E., Jones, F. C., Villarreal, G., Shapiro, M. D., Brady, S. D., Southwick, A. M., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., Petrov, D., Jonsson, et al  
2010; 327 (5963): 302-305
- **Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10 000 Vertebrate Species** *JOURNAL OF HEREDITY*  
Haussler, D., O'Brien, S. J., Ryder, O. A., Barker, F. K., Clamp, M., Crawford, A. J., Hanner, R., Hanotte, O., Johnson, W. E., McGuire, J. A., Miller, W., Murphy, R. W., Murphy, et al  
2009; 100 (6): 659-674
- **A role for a neo-sex chromosome in stickleback speciation** *NATURE*  
Kitano, J., Ross, J. A., Mori, S., Kume, M., Jones, F. C., Chan, Y. F., Absher, D. M., Grimwood, J., Schmutz, J., Myers, R. M., Kingsley, D. M., Peichel, C. L.  
2009; 461 (7267): 1079-1083
- **The Genetic Architecture of Skeletal Convergence and Sex Determination in Ninespine Sticklebacks** *CURRENT BIOLOGY*  
Shapiro, M. D., Summers, B. R., Balabhadra, S., Aldenhoven, J. T., Miller, A. L., Cunningham, C. B., Bell, M. A., Kingsley, D. M.  
2009; 19 (13): 1140-1145
- **Muscle Contraction Is Necessary to Maintain Joint Progenitor Cell Fate** *DEVELOPMENTAL CELL*  
Kahn, J., Shwartz, Y., Blitz, E., Krief, S., Sharir, A., Breitel, D. A., Rattenbach, R., Relaix, F., Maire, P., Rountree, R. B., Kingsley, D. M., Zelzer, E.  
2009; 16 (5): 734-743
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