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The Genome Scientist

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Genome Sciences Welcomes Three New Faculty Members

Dr. Maitreya Dunham

Dr. Christine Queitsch

Dr. Jay Shendure

IN THIS ISSUE:

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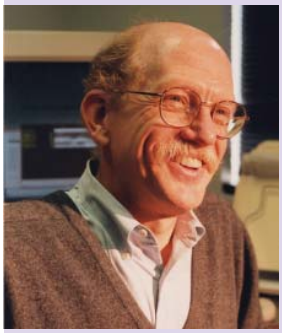
Notes From the Chair



Bob Waterston

Genome Sciences is an exciting place these days. Three new faculty members have joined us in the past year, and a fourth will arrive in December. Advances in technology are opening new avenues to attack problems with a scope and precision unimaginable even just a few years ago. Our new digs in the Foege Building are a delight. These factors combine to attract top notch graduate students and post-docs, who suffuse the place with energy and enthusiasm. Let me expand on each of these.

As you can read elsewhere in the newsletter, Jay Shendure and Christine Queitsch joined the department just over a year ago, with Jay bringing first-hand knowledge of the latest sequencing technologies, and Christine creating a local green revolution by bringing Arabidopsis to study fundamentals of phenotypic robustness in the face of genetic variation. Maitreya Dunham arrived this past summer, continuing the illustrious line of yeast scientists in the department. She is studying the role of structural rearrangements and other changes in adaptive evolution as yeast is shifted to new growth conditions. Jim Bruce will move soon from WSU to anchor our Proteomics Resource at the South Lake Union campus. Jim is devising methods to use mass-spectrometry to detail protein-protein interactions. With these additions, more than half our faculty will have joined since the formation of the Department, mixing their fresh perspective with our strong traditions and making the place amazingly vibrant and exciting.

New technologies are transforming how we do science. The new generation of DNA sequencing technologies, which Jay helped to bring about, are dropping the costs of DNA sequencing faster than the stock market, and the amount of data obtained in a single run is almost overwhelming. Jay, along with Debbie Nickerson, is developing methods to capture the functional regions of the human genome (or indeed any particular regions from any genome), thereby vastly decreasing the amount (and cost) of sequence that needs to be determined to identify a person's individual (rare) mutations. Success here will drop costs to a few thousand dollars per person, opening the way to broad resequencing of cases and controls. Josh Akey, working with Jay, Mike MacCoss and Stan Fields, is analyzing 35 or more different yeast isolates to examine the impact of DNA sequence variation comprehensively on mRNAs, proteins and metabolites, a tour de force simply unfathomable a few years ago. John Stamatoyannopoulos is applying this next-generation sequencing technology to identify DNaseI hypersensitive sites (regions of open chromatin) in genomes from yeast to human. The data are so rich that, in a collaboration with Stan Fields and Bill Noble, the individual binding sites of specific transcription factors are being identified across the yeast genome in a single experiment. Evan Eichler is at the forefront of efforts to develop methods to explore segmental duplications in the genome and their role in disease. In proteomics, Mike MacCoss and Bill Noble have devised methods that increase the efficacy of protein identification by 50% and are pursuing other strategies for still further improvements. Almost half the proteins in yeast grown under one condition can now be identified in a single experiment. All this is simply amazing!

The Foege Building now feels like home. We know who resides in what labs and can wander the building on autopilot and still end up in the right place. It is a lovely place to work, with bright, well-laid out labs, spacious common areas and wonderful views over the water and - on clear days - of the mountains. But even better, the layout of the building promotes interactions between labs, catalyzing new science. The collegiality of the Department has always been a strong point, but the Foege Building is raising it to another plane. Apparently the strong sense of community was a major factor in attracting our fantastic new faculty, and they have only enhanced it.

Of course the newer faculty, the building and the new technologies are only a part of the story. The Department thrives because of the talent and hard work of our students, post-doctoral fellows and staff. A couple projects are highlighted elsewhere in the Newsletter along with some selected publications from our students.
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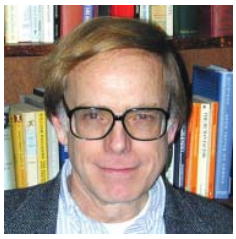
Faculty News & Honors

Olson Awarded Gruber Genetics Prize



Dr. Maynard Olson, Professor of Genome Sciences and of Medicine, has been awarded the 2007 Genetics Prize of the Gruber Foundation, becoming the third Genome Sciences faculty winner in the last 4 years to be awarded the Gruber prize. Dr. Olson's original concepts and technological and experimental innovations played a central role in laying the foundations for the Human Genome Project.

Horwitz Receives NIH Pioneer Award

Dr. Marshall Horwitz, Professor of Pathology and of Medicine, Adjunct Professor of Genome Sciences, has received a 2007 NIH Director's Pioneer Award, one of only 12 awards given that year. Dr. Horwitz will use his Pioneer Award funding to chart cell lineages by tracking mutations in order to better understand how stem cells contribute to development and cancer.

Green Selected as UW Inventor of the Year

Dr. Philip Green, Professor of Genome Sciences, has received the Fourth Annual Inventor of the Year Award. The award honors a UW faculty researcher who exemplifies the philosophy of technology transfer by taking their inventions from the lab to industrial applications. Dr. Green was also recently awarded an honorary doctorate from the University of North Carolina.

Dr. Green's software has made the sequencing of the three billion pairs in the human genome possible and represents the most important technical advance in DNA sequencing of the 1990s.

Jarvik Selected as Head of UW Medical Genetics

Dr. Gail Jarvik, Professor of Medicine and of Genome Sciences, was selected in 2007 to lead the Department of Medicine's Division of Medical Genetics as the Arno G. Motulsky Endowed Professor of Medicine. Dr. Jarvik is a distinguished investigator of the genetics of complex disease.

Byers Receives March of Dimes Award

Dr. Peter Byers, Professor of Medicine and of Pathology, Adjunct Professor of Genome Sciences, has received the March of Dimes / Colonel Harland Sanders Award, given annually to an individual whose lifetime body of research, education, or clinical service has made a significant contribution to the genetic sciences. Dr. Byers' primary clinical and research specialty is inherited connective tissue disorders.

Felsenstein Awarded Darwin-Wallace Medal

Dr. Joseph Felsenstein, Professor of Genome Sciences and of Biology, has been awarded a 2008 Darwin-Wallace Medal for major advances in evolutionary biology since 1958. The award is presented every 50 years and commemorates the 150th anniversary of the reading of the joint Darwin-Wallace paper "On the Tendency of Species to form Varieties; and on the Perpetuation of Varieties and Species by Natural Means of Selection" at the Linnean Society of London in 1858. Dr. Felsenstein's research interests include evolution and population genetics.

The Genome Scientist layout: Brian Giebel

questions / comments: bgiebel@u.washington.edu

Faculty News & Honors

Thompson Elected to National Academy of Sciences

Dr. Elizabeth Thompson, Professor of Statistics and Adjunct Professor of Genome Sciences, has been elected to the National Academy of Sciences. Election to the Academy is considered one of the highest honors that can be accorded a U.S. scientist.

Dr. Thompson's research interest is in the development of methods for inference from genetic data, and particularly from data observed on large and complex pedigree structures.

News & Notes

2008 Symposium The Personal Genome: Implications for Medicine

This year's symposium included a community panel discussion, "The Personal Genome: Consequences for Society". The panel discussion was moderated by Dr. Maynard Olson, Professor of Genome Sciences and of Medicine, and a pioneer in human genome discoveries. Speakers included George Church, Professor of Genetics at Harvard Medical School and Director of the Center for Computational Genetics; Bill Gates III, Microsoft; Eric Lander, founder of The Broad Institute; and Leona Peltonen of The Wellcome Trust Sanger Institute.

Symposium speakers included :

Dr. George Church, Harvard University
"Interpretable, Affordable Personal Genomics"

Dr. David Haussler, UC Santa Cruz
"Using Genomes to Explore How We Became Human"

Dr. Eric Lander, Broad Institute
"Beyond the Human Genome Project"

Dr. Richard Lifton, Yale University
"Human Hypertension: From Rare Diseases to Common Pathways and New Therapeutics"

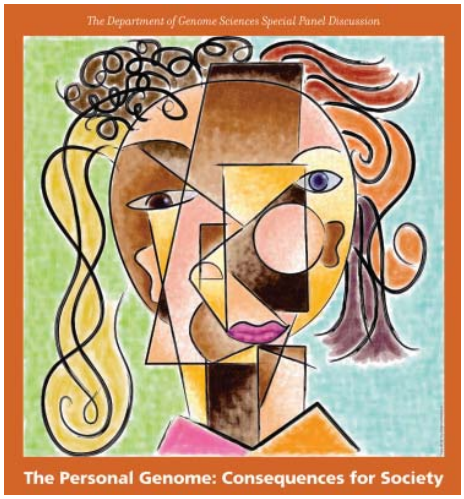
Dr. Leena Peltonen, Wellcome Trust Sanger Institute
"Drafting Genome Wide Profiles of Our Diseases"

Dr. Nancy Wexler, Columbia University
"When Personal is Really Personal"

UW Launches Northwest Institute of Genetic Medicine

The University of Washington has received a $5.3 million grant from the state of Washington's Life Sciences Discovery Fund to support the translation of human genetic research into clinical medicine. The Northwest Institute of Genetic Medicine will be a collaborative effort between researchers at the UW, Seattle Children's Hospital Research Institute, Group Health, and local biotech companies. It will facilitate the design, development and execution of translational genetic studies that bridge the gap between basic science research and clinical studies.

The institute will be led by Dr. Gail Jarvik, Professor of Medicine and Genome Sciences. The leadership team also includes Genome Sciences faculty members Dr. Deborah Nickerson, Dr. Michael Bamshad, and Dr. Bruce Weir, among other distinguished UW researchers.



News & Notes

Notes from the Chair,

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The wide variety of journals represented is impressive, reflecting the diversity of work occurring in the department. Our post-doctoral fellows have been very successful in obtaining outside funding, particularly the K99/R00 transition awards, where in the past three years, three fellows have received these highly competitive awards. Our students and fellows have been gratifyingly successful in landing top jobs upon the completion of their training here.

Of course these highlights only scratch the surface. Among other notable events, our 2008 Spring Symposium on the personal genome drew top speakers from around the country. The night before the symposium, we hosted a public forum on the personal genome in which a panel that included Bill Gates, Eric Lander, George Church and Leena Peltonnen fielded questions from the audience and shared their views of the opportunities and challenges ahead. Our faculty continue to garner recognition for their accomplishments, and funding continues strong. Debbie Nickerson and Gail Jarvik led a group that successfully competed for a Washington State Life Sciences Discovery Fund award, which supports the translation of human genetic research into clinical practice. The Proteomics Resource, also facilitated by state funding, is catalyzing cutting edge developments in mass-spectrometry analysis of proteins as well as fostering its application to biologically important projects across the campus. Carol Sibley, with support from the Gates Foundation, is developing a worldwide database to track malaria variants and the efficacy of therapies. The list goes on (and on …).

Yet we hope the best is yet to come. These past few weeks have made us more aware than ever that we are dependent on the whole to prosper. But barring disaster on the national and world scenes, we have much to look forward to in the coming year.

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Featured Alumnus

Edward Ramos, Ph.D.

After earning his Ph.D. in 2006, former Genome Sciences graduate student Ed Ramos began a public policy fellowship with the NHGRI, working in the office of Senator Barack Obama. Dr. Ramos has recently accepted a new position at the NIH Intramural Center for Genomics and Health Disparities and was willing to take time from his busy schedule to answer a few questions.

What aspects of your graduate training did you find most helpful for your current position?
PhD training reinforces the skills necessary to solve difficult problems. I have been fortunate to be able to transition these skills to a different forum and apply my training to a variety of complex policy issues. Being able to approach a problem from multiple angles has its utility in and outside of the laboratory.

Do you have any advice for graduate students or those considering graduate school?
It is important to maintain lines of communication between yourself and your advisor. Consistently dialoguing with your advisor helps limit surprises by keeping everyone on the same page. I would also point out that it's sometimes difficult to commiserate with those that are not sharing (or have not shared) in the graduate school experience. Therefore, maintaining a relationship with your peers (i.e., fellow grad students) and developing a support system is also very valuable.

New Faculty Members

Maitreya Dunham, Assistant Professor

Maitreya Dunham, Ph.D., came to Genome Sciences from Princeton University where she had been a Lewis-Sigler Fellow. Dr. Dunham comments, "Genome Sciences is about as perfect a fit for me as I could imagine. I have a lot of overlapping research interests with the other faculty, including yeast genetics, evolution, and technology development." She notes as well that the department attracts very good graduate students and postdocs, and the departmental environment encourages collaboration.

Dr. Dunham's research interests include how genomes evolve, using yeast as a model system. This ranges from characterizing the mutations that occur over 3 months of evolution in a controlled laboratory environment to looking for signs of divergence between species of yeast. She is also interested in how hybrids may evolve in special ways. These insights will teach us more about the wiring of a cell, and what parts of the system are most important for regulation and adaptation.

Maitreya has moved to Seattle with her husband, software engineer Mark Huang.

Jay Shendure, Assistant Professor

Jay Shendure, M.D., Ph.D., came to Genome Sciences from Harvard University where he had been a postdoctoral fellow in the lab of Dr. George Church. Dr. Shendure notes he was drawn to the department by the "amazing concentration of investigators who've individually and collectively had a huge impact on genomics (and are continuing to). It's also a very collegial and collaborative department. I feel incredibly lucky to have landed here."

The Shendure Lab is broadly interested in developing new experimental and computational tools that allow one to interrogate biological systems in new ways or at very high throughput. They are especially focused on trying to exploit potential synergies between massively parallel methods for DNA synthesis and DNA sequencing.

Jay's spouse, Dr. Alexandra Molnar is a UW faculty member and primary care physician at the International Medicine Clinic at Harborview Medical Center. Their daughter, Ariya Marion Shendure, was born on April 8, 2008.

New Faculty Members

Christine Queitsch, Assistant Professor

Christine Queitsch, Ph.D, came to Genome Sciences from the FAS Center for Systems Biology at Harvard where she had been a Bauer Fellow. Dr. Queitsch comments, "coming to Genome Sciences was love at first sight. My group members and I are very excited to be here. We are learning tremendously from our colleagues, and thanks to their generous support and encouragement we have started to explore new research avenues already."

Dr. Queitsch aims to identify and characterize molecular mechanisms that govern phenotypic robustness, repress developmental noise, and rapidly generate selectable phenotypic variation, particularly when such variation arises in response to environmental change. Among the many possible mechanisms, the lab focuses on three separate but interconnected ones: cryptic genetic variation; genetic variation affecting developmental noise; and fast evolving tandem repeat copy number polymorphisms. All three mechanisms drastically increase phenotypic variation and affect natural selection in laboratory settings, yet their global relevance for shaping phenotype and evolutionary trajectories in natural populations is unclear.

Christine's spouse, Dr. Adeyinka Adedipe, is a UW faculty member and an Emergency Medicine physician at the UW Medical Center. The couple has two sons, 18-year-old Konstantin and 1-year-old Anton.

Notes from the Chair,

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Our new faculty are off to a fast start, with promise of more for the future.

We will be recruiting for two more faculty this coming year, with the applications already pouring in. The technological advances bring exciting new possibilities that we are racing to exploit. Of course, we face strong competition from other fine institutions, with more and more places recognizing the potential of genome sciences and investing in it.

Support Our Research

Your donations help ensure that our faculty, students, and staff have the equipment, facilities, and training they need to continue our leading edge research.

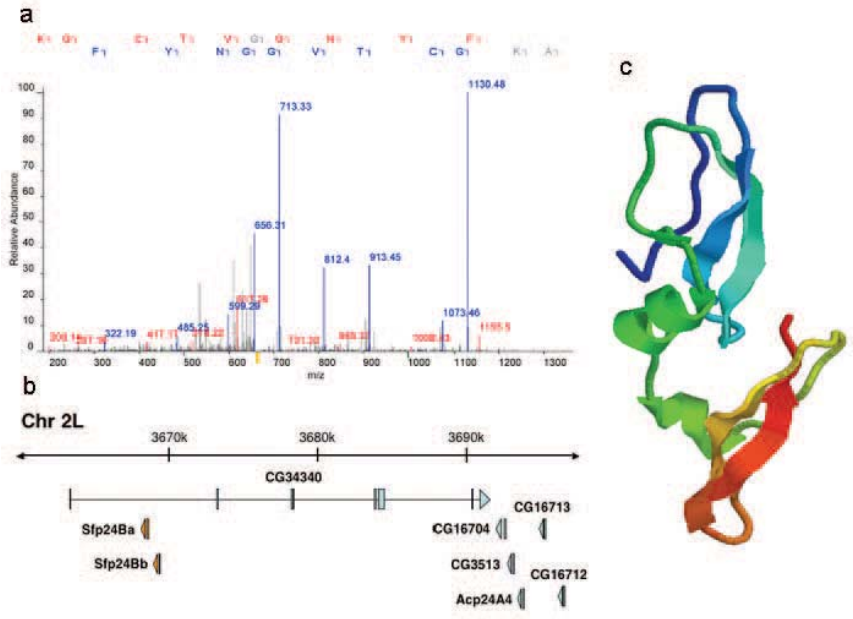
Please support our research by making a donation online at www.gs.washington.edu.

Research Highlights

Male-Female Conflict in Reproductive Strategies

While reproduction is usually thought of as a cooperative process between males and females, many studies have shown that the sexes are actually in conflict over different aspects of mating. This conflict brings up a number of questions. How often should mating occur? If a female mates with multiple males, whose sperm should she use to fertilize her eggs? How can a male stop a female from remating in order to prevent this "sperm competition"? To study these questions, graduate student Geoff Findlay and his mentor, Associate Professor Willie Swanson, have turned to the fruit fly model system, *Drosophila melanogaster*. Along with sperm, male flies transfer dozens of seminal fluid proteins to females during copulation, and these proteins cause dramatic changes in female behavior and physiology. Working in collaboration with Assistant Professor Michael MacCoss, Findlay and Swanson developed a new method to detect those seminal proteins that males transfer to females during mating. The key to their approach? A technique called mass spectrometry, which allows proteins of all shapes and sizes to be detected without any knowledge ahead of time about what is being searched for. "When labs have studied this question in the past, researchers had to have a specific protein in mind that they wanted to look for in the mated female," explained Findlay. "Using the cutting-edge technology in the MacCoss lab, we've been able to use just a few experiments to find 138 proteins that females receive during mating."

The results from these experiments, which were published in the July 2008 issue of *PLoS Biology*, revealed a complex picture of the molecules that are crucial to male reproductive success. By comparing the sequences of the seminal proteins in *Drosophila melanogaster* with their sequences in other species of flies, the group showed that seminal proteins have evolved many changes in a short period of time, suggesting that males are continuously evolving to improve their reproductive success. Furthermore, the genes encoding these proteins tend to be located in small clusters throughout the genome. The researchers also took advantage of the sequenced genome of the fruit fly to identify 19 new reproductive genes in the genome that no one had previously identified. The next step will be to determine the functions of some of the newly identified proteins encoded by these genes. "Does a seminal protein cause a female to lay eggs? To stop mating with other males? Or to do something else entirely?" asked Findlay. To address these questions, Findlay, Swanson and MacCoss are using a combination of genetic, proteomic and evolutionary approaches, highlighting the diversity of techniques and collaborative efforts of Genome Sciences.



Picture caption: a) Example of a mass spectrum that identifies a new seminal fluid protein, Sfp24Ba. b) Map of the genomic region containing Sfp24Ba. Located next to it is another new gene, Sfp24Ba, and a previously known seminal protein, Acp24A4. c) The predicted three-dimensional structure of seminal fluid protein 24Ba.

Research Highlights

Improving the Dynamic Range of Proteomics Measurements without Increasing the Analysis Time

Mass spectrometry is an analytical technique used to identify a compound by measuring its mass. It has become the workhorse procedure in the field of proteomics, the large-scale study of proteins. A common problem faced in mass spectrometry is the identification of all the components in a complex mixture. Despite the advances in a type of instrument known as ion trap mass spectrometers, their ability to detect low-abundance ions is often masked by high-abundance ions that elute at the same time. In proteomics, this translates to the inability to detect low-abundance peptides because of interfering signals from the most abundant peptides in the mixture. Because researchers generally are keenly interested in proteins present at low abundance, current solutions to the problem usually involve simplifying the mixture biochemically or separating it into multiple fractions prior to analysis in the mass spectrometer. However, these solutions are inherently slow and can increase the analysis time of the original mixture by 12-fold or more.

To improve the dynamic range and peak capacity when analyzing complex mixtures, Dr. Michael MacCoss and Jesse Canterbury installed a device known as high-field asymmetric waveform ion mobility spectrometry (FAIMS) to the front of a commercial bench-top ion trap mass spectrometer. A FAIMS device separates ions based on their shape by changing their gas-phase mobilities as they flow between two electrodes at atmospheric pressure using a high-voltage asymmetric RF waveform and an adjustable compensation voltage. This device can separate co-eluting peptides using different compensation voltages, leading to their successful identification.

Jesse Canterbury

Although FAIMS has been around for a few years, MacCoss and Canterbury are the first to apply it in a proteomics context on an ion trap mass spectrometer. They achieved >8-fold increase in the number of molecular species that could be separated and >5-fold increase in the dynamic range when analyzing a complex mixture, without the need to perform simplification or chromatographic separation steps prior to analysis on the mass spectrometer. Thus, the addition of FAIMS to a bench-top mass spectrometer increased the throughput by a factor of 12.

Canterbury JD, *et al.* (2008). Assessing the dynamic range and peak capacity of nanoflow LC-FAIMS-MS on an ion trap mass spectrometer for proteomics. *Analytical Chemistry* (Epub ahead of print).

Graduate Student News

Congratulations to 2007 - 2008 Graduates!

Laura Certain (Ph.D. in Genome Sciences)
"Genetic profiling of drug resistance in *Plasmodium falciparum*"

Karen Chisholm (Ph.D. in Genome Sciences)
"Genetic backgrounds susceptible to genomic deletions: Alu-mediated mutations of BRCA1 as a model"

Nathan Clark (Ph.D. in Genome Sciences)
"The adaptive evolution of reproductive proteins from abalone and primates: studies of positive selection, populations, and protein structure"

Kiran Dhillon (Ph.D. in Genetics)
"Analysis of in vivo functions of the Werner syndrome protein"

Ilona Holcomb (Ph.D. in Molecular Biotechnology)
"Genomic profiling of prostate cancer within and beyond the primary tumor"

Chung-Ying Huang (Ph.D. in Genome Sciences)
"Targeting mechanisms of resistance to taxane-based chemotherapy"

Joanna Kelley (Ph.D. in Genome Sciences)
"Adaptive evolution: from genome-wide scans to biological significance"

Aaron Klammer (Ph.D. in Genome Sciences)
"Revealing the proteome: a machine learning approach to peptide identification"

Charla Lambert (Ph.D. in Genome Sciences)
"The population genetics of Duffy and Duffy-like loci in the human genome"

Tobias Mann (Ph.D. in Genome Sciences)
"A thermodynamic approach to PCR primer design"

Allyson McCormick (Ph.D. in Genetics)
"Modeling epilepsy in the nematode *Caenorhabditis elegans*"

James Ronald (Ph.D. in Genome Sciences)
"Analysis of naturally occurring cis-acting gene expression variation in the yeast *Saccharomyces cerevisiae*"

Chris Saunders (Ph.D. in Molecular Biotechnology)
"Insights from modeling protein evolution with context-dependent mutation and asymmetric amino acid selection"

Sara Selgrade (Ph.D. in Genome Sciences)
"*Pseudomonas aeruginosa* regulation of resistance to antimicrobial peptides"

David Spencer (Ph.D. in Genome Sciences)
"A conceptual framework for analyzing individual genome sequences"

Jonathan Ulmer (Ph.D. in Genetics)
"Analysis and studies of inhibition of the two divergent thymidine biosynthesis pathways in *Mycobacterium tuberculosis*"

Stephen Voght (Ph.D. in Genetics)
"Development and analysis of a *Drosophila* model of dietary sterol absorption"

Graduate Student News

2007 Incoming Class:

Renee George, University of Washington
Sayer Herin, University of Chicago
Andy Itsara, UW Medical Scientist Training Program
Ray Malfavon-Borja, California State Univ, San Marcos
Sarah Ng, University of Wisconsin
Alex Nord, Carleton College
Rupali Patwardhan, Indiana University
Caitlin Rippey, UW Medical Scientist Training Program
Daniel Skelly, University of Wisconsin
Cailyn Spurrell, University of California, Berkeley

2008 Incoming Class:

Keisha Carlson, Brown University
Katrina Claw, Arizona State University
Jarrett Egertson, University of California, Los Angeles
Leslie Emery, Alfred University
Jacob Kitzman, Massachusetts Institute of Technology
Matt Maurano, University of California, Berkeley
Melody Rynerson, Lewis & Clark College
Sean Schneider, University of Washington
Peter Sudmant, University of Waterloo
Ben Whiddon, UW Medical Scientist Training Program

Jiang Receives China National Award

Zhaoshi Jiang (pictured below) received the 2006 China National Award for Outstanding Overseas Students at an award ceremony at the Chinese Consulate General in San Francisco. This award was given to only 75 Chinese students in the United States, including 3 from the University of Washington.

Zhaoshi's research in the Eichler Lab focuses on understanding the evolution of human segmental duplications.

Recent Student Funding Awards:

Katrina Claw – NSF fellowship
Nick Coley – NRSA individual fellowship
Diane Dickel – NRSA individual fellowship
Renee George – UW School of Medicine Hurd Fellowship
Zhaoshi Jiang – Rosetta fellowship
Jeff Kidd – NSF fellowship
Graham McVicker – NSERC fellowship, government of Canada
Sarah Ng – A-STAR fellowship, government of Singapore
Kevin Roach – NSF fellowship
Peter Sudmant – NSERC fellowship, government of Canada

Graduate Student News

Selected Publications and Conference Presentations:

Lisa Beutler:

Heusner CL, Beutler LR, Houser CR, Palmiter RD.Deletion of GAD67 in dopamine receptor-1 expressing cells causes specific motor deficits. Genesis. 2008 46:357-67.

Shameek Biswas:

Biswas S, Storey JD, Akey JM. Mapping gene expression quantitative trait loci by singular value decomposition and independent component analysis. BMC Bioinformatics. 2008 9:244.

Max Boeck:

Murray JI, Bao Z, Boyle TJ, Boeck ME, Mericle BL, Nicholas TJ, Zhao Z, Sandel MJ, Waterston RH.Automated analysis of embryonic gene expression with cellular resolution in C. elegans.Nat Methods. 2008 5:703-09.

Cindy Desmarais:

Reiner AP, Wurfel MM, Lange LA, Carlson CS, Nord AS, Carty CL, Rieder MJ, Desmarais C, Jenny NS, Iribarren C, Walston JD, Williams OD, Nickerson DA, Jarvik GP.Polymorphisms of the IL1-receptor antagonist gene (IL1RN) are associated with multiple markers of systemic inflammation. Arterioscler Thromb Vasc Biol. 2008 28:1407-12.

Diane Dickel:

Hanna GL, Veenstra-Vanderweele J, Cox NJ, Van Etten M, Fischer DJ, Himle JA, Bivens NC, Wu X, Roe CA, Hennessy KA, Dickel DE, Leventhal BL, Cook EH Jr.Evidence for a susceptibility locus on chromosome 10p15 in early-onset obsessive-compulsive disorder.Biol Psychiatry. 2007 62:856-62.

Dickel DE, Veenstra-VanderWeele J, Bivens NC, Wu X, Fischer DJ, Van Etten-Lee M, Himle JA, Leventhal BL, Cook EH Jr, Hanna GL.Association studies of serotonin system candidate genes in early-onset obsessive-compulsive disorder. Biol Psychiatry. 2007 61:322-9.

Sara Di Rienzi:

"Correlation of origins of replication and fragile genomic sites." 2008 Yeast Chromosome Structure, Replication and Segregation, Carefree, Arizona

"Comparative analysis of replication origins using the genome organization of pre- and post-whole genome duplication yeast species." 2007 Comparative Genomics of Eukaryotic Microorganisms: Eukaryotic Genome Evolution, Sant Feliu de Guixols, Spain

Geoff Findlay:

Clark, NL, Findlay GD, Yi X, MacCoss MJ, Swanson WJ. 2007. Duplication and selection on abalone sperm lysin in an allopatric population. Molecular Biology and Evolution 24: 2081-2090.

Findlay GD, Yi X, Maccoss MJ, Swanson WJ. Proteomics reveals novel Drosophila seminal fluid proteins transferred at mating.PLoS Biol. 2008 6:e178.

2007 Society of Molecular Biology and Evolution, Halifax, Canada

2007 American Genetics Association Annual Meeting on genome evolution, Bloomington, Indiana

2008 Society of Molecular Biology and Evolution, Barcelona, Spain

Greg Finney:

Hoopmann MR, Finney GL, MacCoss MJ. High-speed data reduction, feature detection, and MS/MS spectrum quality assessment of shotgun proteomics data sets using high-resolution mass spectrometry. Anal Chem. 2007 79: 5620-32.

Finney GL, Blackler AR, Hoopmann MR, Canterbury JD, Wu CC, MacCoss MJ. Label-free comparative analysis of proteomics mixtures using chromatographic alignment of high-resolution muLC-MS data. Anal Chem. 2008 80: 961-71.

Graduate Student News

Mike Hoopmann:

Hoopmann MR, Finney GL, MacCoss MJ. High-speed data reduction, feature detection, and MS/MS spectrum quality assessment of shotgun proteomics data sets using high-resolution mass spectrometry. Anal Chem. 2007 79: 5620-32.

Finney GL, Blackler AR, Hoopmann MR, Canterbury JD, Wu CC, MacCoss MJ. Label-free comparative analysis of proteomics mixtures using chromatographic alignment of high-resolution muLC-MS data. Anal Chem. 2008 80: 961-71.

"Improved peptide identification in complex mixtures by LC-MS using Fourier-transform mass spectrometry." 2007 American Society for Mass Spectrometry, Indianapolis

"Iterative MS/MS sampling of proteomics mixtures: Software and methodology to maximize sampling of detectable components in a mixture." 2008 American Society for Mass Spectrometry, Denver

Chung-Ying Huang:

Huang CY, Beer TM, Higano CS, True L, Vessella R, Lange P, Garzotto M, and Nelson PS. Molecular alterations in prostate carcinomas that associate with in vivo exposure to chemotherapy: identification of a cytoprotective mechanism involving growth differentiation factor 15. Clin Cancer Res 2007 13: 5825-5833.

Andy Itsara:

Mefford HC, Sharp AJ, Baker C, Itsara A, Jiang Z, et al. Recurrent rearrangements of chromosome 1q21.1 and variable pediatric phenotypes. N Engl J Med. 2008 Sep 10. [Epub ahead of print]

Zhaoshi Jiang:

Mefford HC, Sharp AJ, Baker C, Itsara A, Jiang Z, et al. Recurrent rearrangements of chromosome 1q21.1 and variable pediatric phenotypes. N Engl J Med. 2008 Sep 10. [Epub ahead of print]

Zody MC, Jiang Z, Fung HC, Antonacci F, Hillier LW, Cardone MF, Graves TA, Kidd JM, Cheng Z, Abouelleil A, Chen L, Wallis J, Glasscock J, Wilson RK, Reily AD, Duckworth J, Ventura M, Hardy J, Warren WC, Eichler EE. Evolutionary toggling of the MAPT 17q21.31 inversion region. Nat Genet. 2008 Aug 10. [Epub ahead of print]

Jiang Z, Hubley R, Smit A, Eichler EE. DupMasker- A tool for annotating the duplication architecture of primate genome sequences. Genome Res 2008 18:1362-8.

Kirsch S, Munch C, Jiang Z, Cheng Z, Chen L, Batz C, Eichler EE, Schempp W. Evolutionary dynamics of segmental duplications from human Y-chromosomal euchromatin/heterochromatin transition regions. Genome Res. 2008 18:1030-42.

Sharp AJ, Mefford HC, Li K, Baker C, Skinner C, Stevenson RE, Schroer RJ, Novara F, De Gregori M, Ciccone R, Broomer A, Casuga I, Wang Y, Xiao C, Barbacioru C, Gimelli G, Bernardina BD, Torniero C, Giorda R, Regan R, Murday V, Mansour S, Fichera M, Castiglia L, Failla P, Ventura M, Jiang Z, Cooper GM, Knight SJ, Romano C, Zuffardi O, Chen C, Schwartz CE, Eichler EE. A recurrent 15q13.3 microdeletion syndrome associated with mental retardation and seizures. Nat Genet. 2008 40 :322-8.

Jiang Z, Tang H, Ventura M, Cardone MF, She X, Pevzner PA, Eichler EE. ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution. Nat. Genet. 2007; 39:1361–1368.

"Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution." 2007 American Society of Human Genetics 57th Annual Meeting, San Diego

Jeff Kidd:

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