Genetics Society of America

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From the President's desk:

The Urbilateria Book Project

Genetics is thriving as never before, spawning in recent years sub-disciplines such as genomics, bioinformatics, evo-devo, systems biology, and more. If genetics were a business, there would be much talk about its growing market share both in basic science, its traditional realm, and increasingly throughout the world of medicine (with significant upside potential). The ageless questions – how genomes evolved on Earth, how genotype programs phenotype, what makes each of us human but unique, how genetic knowledge can better our lives – suddenly seem less daunting, more like practical tasks. Unsurprisingly, some of the brightest young minds on the planet are striving to join this remarkable enterprise in what promises to be among its greatest years.

The Genetics Society of America should be at the forefront of all these developments. Genetic advances continue to unify all biological sciences, and a forum is needed to provide wise counsel, to nurture the careers of young geneticists, to communicate with the public, and to improve education, so more individuals can bring a true understanding of the biological world to today's issues. There are several steps the GSA must take to provide this needed leadership.

First, we must reach out and welcome every person who works to understand how genomes operate. We not only *want* a diverse membership, we *need* one. Splintering may succeed within ecosystems, but a tropical rainforest of genetics will not advance the future of our science, which is striving for unification. Most of the time we will continue to revel in our favorite realms, but we need a Genetics Society capable of overseeing the full scope of genetic science placing it all in its proper perspective. This will only be possible in the long run if we attract the best practitioners of every major approach to genetics, traditional and non-traditional alike.

Second, we must actively promote unification. Our field is still divided by organism, each with its own gene names, genome project, database project, resource centers and annual meeting. Recognizing the value of these organism-based approaches, the GSA focused many years ago on supporting each separate group. But the genome sequencing projects laid bare the unity of genetics, and it is now time to return to a unified genetic vision. Previous efforts to bring the model systems together were hampered by insufficient knowledge, as well as the formidable technical (and sociological) barriers of nomenclature, parochial annotation, etc. We must continue to support and enhance the biennial Model Organisms to Human Biology Meeting as one

Continued on page 19

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Dear Abbot:

I'm disturbed by the stereotypes of scientists and science that permeate our society today. Scientists are thought of as white men in white coats with hair á la Albert Einstein, doing something nasty to mice or frogs. Students use words like "mix chemicals" and "blow stuff up" to describe what scientists do. Science itself is thought to be a potentially dangerous exercise in malignant curiosity. How can I help my students understand what science really is and who does it?

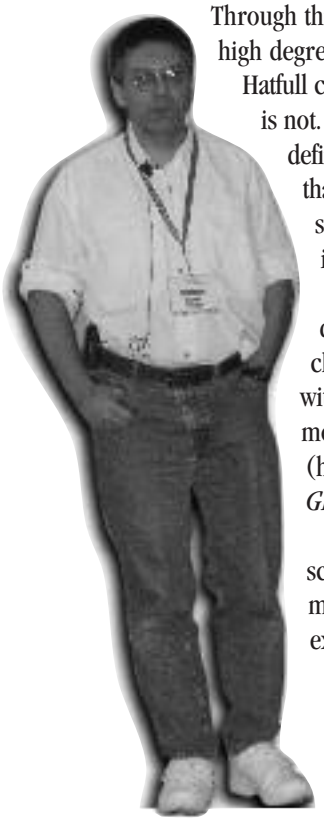
Refuses to be Stereotyped

Dear Refuses:

I wished I had done what Graham Hatfull is doing to demystify scientists and science. My pea plants would have lent themselves quite well to his approach.

Hatfull presented his exciting solution to the challenge of attracting the next generation of geneticists during the Education Luncheon at the 2008 *GENETIC Analysis: Molecular Organisms to Human Biology* Meeting in San Diego. (See pages 10 and 11 for more MOHB Meeting highlights.) Hatfull, an HHMI "Million Dollar Professor" and chair of the Department of Biological Sciences at the University of Pittsburgh, argued persuasively that students best learn what science is and who does it by becoming scientists themselves.

Since 2002, Hatfull has been making high school students and undergraduates into scientists with a research project focused on mycobacteriophages. The students discover a mycobacteriophage by plating dirt on a lawn of *Mycobacterium smegmatis* cells. Given the large number and extraordinary diversity of viruses in the environment, each phage is likely to be genetically unique. Consequently, students get to discover a new organism and name it. Pretty much anything goes in the name category: "Pipefish," "Bxz1," "Corndog," "Rosebush," "Halo," and "Omega" are examples. They purify the phage and view it by scanning electron microscopy to examine its morphology. Finally, they generate a library of fragments of its genome and determine the DNA sequence of the clones, assemble the genome sequence, then annotate the sequence. The truly dedicated students go on to perform some comparative genomic analysis. Through this work, high school and college undergraduates have discovered many novel genes, and revealed the high degree of mosaicism in mycobacteriophage genomes.



Graham Hatfull at the MOHB Educational Roundtable and Lunch.

Hatfull claims that including students in authentic research is the best way to teach them what science is, and what it is not. In addition, because they learn that even *they* can do original science and make novel discoveries, their definition of who scientists are and what they look like becomes broader and more accurate. He recommends that similar approaches should be taken by other scientists. Successful projects provide multiple, frequent successes, right from the start of the project. These projects generate a sense of personal ownership, investing the student in the project's success and developing confidence and self-esteem.

Hatfull's approach to teaching what science is by providing students with opportunities for genuine discovery is remarkable, but not unique. For example, Utpal Banerjee, Ph.D., also an HHMI professor and chair of the Molecular, Cell, and Developmental Biology Department at UCLA, pursues a similar approach with his course at UCLA in which students isolate and map mutations that affect Drosophila eye morphology. Results of his students' research are curated on the Drosophilia Genome website (http://flybase.bio.indiana.edu/), and have led to several publications, most recently in GSA's journal, *GENETICS* (Genetics 177:689-697, 2007).

Perhaps the answer to the question of how to help your students understand the nature and process of science and who scientists are is to consider how you, too, could welcome students into authentic, meaningful research experiences. In fact, to shatter stereotypes we should all consider making such an experience possible for every student.

The Abbot
Robin Wright
University of Minnesota, St. Paul

New Members Welcomed to GSA Board

Trudi M. Schüpbach
President

Four new members took their seats on the GSA Board of Directors January 1. Congratulations and welcome to Vice President Fred Winston, Harvard Medical School (president-elect for 2009), and newly-elected Board members Sally A. Camper, University of Michigan Medical School; Charles H. Langley, University of California, Davis; and Susan T. Lovett, Brandeis University, Waltham, MA. They will serve three year terms.

Trudi M. Schüpbach, Princeton University, (Vice-President, 2007) stepped into the President's position for 2008, and Allan C. Spradling, Carnegie Institution, Baltimore, MD, will continue to provide his counsel as the Past President.

Fred Winston
Vice-President

Sally A. Camper
Board Member

Susan T. Lovett
Board Member

Charles H. Langley
Board Member

Stepping down from the Board this year, and deserving thanks for their years of service are: Barry Ganetzky, University of Wisconsin–Madison, who served as president in 2006, and Directors Susan K. Dutcher, Washington University School of Medicine; Stanley Fields, University of Washington, Seattle; and Geraldine Seydoux, Johns Hopkins University School of Medicine, Baltimore, MD.

The GSA also wishes to thank the Nominating Committee including Chair Carol Gross, (University of California, San Francisco), and Terry Magnuson, (University of North Carolina, Chapel Hill), Terry Orr-Weaver, (Whitehead Institute-MIT, Cambridge, MA), and James Haber (Brandeis University, Waltham, MA).

2008 GSA Award Recipients Announced

The Genetics Society of America is pleased to announce the 2008 recipients of its annual awards. The award winners are:

- **The Thomas Hunt Morgan Medal** for lifetime contributions in the field of genetics:
  Michael Ashburner
  Cambridge University, UK

- **The GSA Medal** for outstanding contributions to the field of genetics in the last 15 years:
  Susan Lindquist
  Whitehead Institute/MIT and HHMI, Cambridge, MA

- **The George W. Beadle Award** for outstanding contributions to the community of genetics researchers:
  Mark Johnston
  Washington University School of Medicine, St. Louis, MO

- **The GSA Award for Excellence in Education** in recognition of significant and sustained impact on genetics education:
  Scott Hawley
  Stowers Institute for Medical Research, Kansas City, MO

- **The Novitsky Prize** given in honor of an extraordinary level of creativity and intellectual ingenuity in solving significant problems in genetics research:
  Thomas J. Silhavy
  Princeton University, NJ

For additional information about the GSA award recipients, visit the GSA website at http://www.genetics-gsa.org/, and look for biographies of the recipients in the March issue of *GENETICS*.

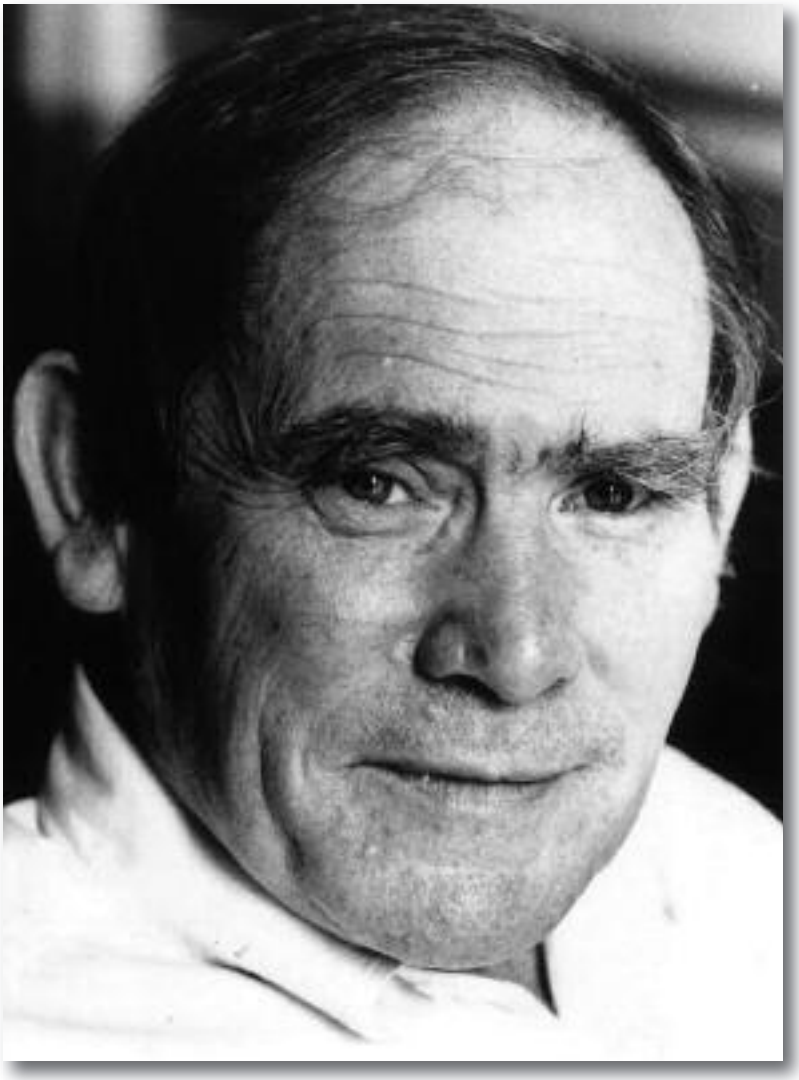
IN 1974, AFTER 7 YEARS OF WORK,

Sydney Brenner *wrote an extensive paper*

on The Genetics of *C. elegans* –

a paper destined to found an entire field of research.

The journal that allowed Brenner
to say everything he wanted to?



http://www.genetics.org/

A companion paper by Sulston and Brenner described a chemical analysis of the DNA of *C. elegans* that formed the basis of what was to follow once cloning and sequencing of DNA were invented: the first determination of the complete DNA sequence of a metazoan organism.

Beginning with the first paper published in the journal in 1916 — Calvin Bridges' proof that chromosomes are the carriers of heredity—some of the most important papers in the field have been published in *GENETICS*. From Muller and McClintock to Horvitz and Hartwell, the leaders of the field have chosen to publish some of their best work in *GENETICS*.

GENETICS is still the journal of choice for genetic analysis. The review of your paper will be managed by an associate editor who is your peer, who understands your science and knows its significance. You can tell your full story, because there are no arbitrary page limits. And with our open-access philosophy, your paper will be freely available within weeks of its acceptance.

Join your colleagues and send your best work to *GENETICS*. Even if your paper doesn't spawn an entire new field, it is likely to achieve maximum impact in the journal of The Genetics Society of America.

Annual Fly Meeting Set for San Diego

by Susan Celniker, Lawrence Berkeley National Laboratory, Berkeley, CA

The 49th Annual Drosophila Research Conference will be held **April 2-6, 2008** at the Town & Country Resort and Convention Center in San Diego, California. Please note the following important dates:

February 21, 2008: Deadline for Early Conference Registration. Fees increase after this date.

March 1, 2008: Deadline for Hotel Reservations.

Antonio Garcia-Bellido of the Universidad Autónoma de Madrid, Spain, will present the historical address. A student of the noted British entomologist Sir Vincent Wigglesworth, Garcia-Bellido started his studies of cell heredity and determination as a postdoctoral fellow with Ernest Hadorn at the University of Zurich, and subsequently at Cal Tech with future Nobel Laureate (1996) Ed Lewis.

Plenary talks will cover microRNAs, brain activity and function, viral infection, evolution of traits, neural and basic development, stem cells, and ongoing analysis of the 12 fly genomes. Speakers and their topics include:

- **David Bilder** (University of California, Berkeley), Trafficking and polarity in the control of Drosophila growth;
- **Dietmar Schmucker** (Harvard Medical School), Ig-receptor diversity in insect immunity and neuronal wiring;
- **Sara Cherry** (University of Pennsylvania Medical School), Pathways of anti-viral immunity;
- **Artyom Kopp** (University of California, Davis), Cross-regulation of HOX and sex determination genes in development and evolution;
- **Nicole Francis** (Harvard), Inheritance of Polycomb proteins through DNA replication in vitro;
- **Stephen Cohen** (Singapore), microRNA functions;
- **David Anderson** (Caltech), Modeling emotional behavior in Drosophila;
- **Rachel Wilson** (Harvard Medical School), Using electrophysiology and genetics to dissect neural circuit function;
- **Mark Biggin** (Lawrence Berkeley National Laboratory), Quantitative analysis of the transcription network controlling early embryo patterning;
- **Manolis Kellis** (MIT), Regulatory genomics in Drosophila species;
- **Pat Simpson** (University of Cambridge), Two or four bristles: evolution of regulation of the *achaete-scute* genes; and
- **Allan Spradling** (Carnegie Institution, Baltimore, MD), Regulating oogenesis: from stem cells to steroids.

Additional highlights include The Larry Sandler Memorial Lecture; workshops on topics covering the role of gases in development, monoamines, the zygotic transition, chromosome pairing and trans-sensing, the extracellular matrix, immunity, RNA control of development, ModENCODE undergraduate education and more. Prizes for outstanding poster presentations will be awarded.

Program Chairs are Nancy Bonini, University of Pennsylvania/HHMI, Philadelphia; Susan Celniker, Lawrence Berkeley National Laboratory, Berkeley, CA; Brian Oliver, NIDDK, Bethesda, MD; and John Tamkun, University of California, Santa Cruz.

For more information on the meeting, visit the GSA website: http://www.drosophila-conf.org/genetics/gsa/dros/dros2008/

Coming in April: New Website for *GENETICS* Journal

The *GENETICS* Journal website is being modernized. Why the change? To make articles easier to find and to read, and to highlight and emphasize the Journal's content. Excellent content is too often masked by clunky web interfaces; difficulty searching for papers results in an unpleasant online experience. A website should function as a conduit to effortlessly link scientists with the knowledge they seek.

The website's updated, clean design will provide increased readability and easier usability, and reflect the modern science that is presented in *GENETICS*, while maintaining *GENETICS*' long-standing reputation for quality. Reader-friendly features will include a list of most-read and most-accessed articles; a citation map showing links between a paper and cited articles; a straightforward electronic table of contents and alerts page; and easier ways to search and browse articles. Plus, the online Journal's aesthetic will mirror that of the recently redesigned print journal and GSA website – creating a cohesive view of the Society and its publications.

Since last summer, a committee of Senior Editors chaired by Suzanne Sandmeyer (UC, Irvine) has worked with *GENETICS* Editor-in-Chief Beth Jones and Managing Editor Tracey DePellegrin Connelly to modernize the online gateway to our Journal. The group implemented the project with Elizabeth Kairys Design (San Francisco) and HighWire Press (Stanford). Check out our beautiful new site this April!

Molly Przeworski: The Accidental Geneticist

by Phyllis Edelman, GENEtics, Managing Editor

It is not surprising that Molly Przeworski chose to pursue a career in academia. Both her parents are academics, so maybe it's a heritable trait. But Przeworski is an evolutionary geneticist in the University of Chicago's Department of Ecology and Evolution, and her parents are in the social sciences. By Przeworski's own admission, she became a geneticist "by accident." Like many accident victims, she "was really shocked" when Beverly Emanuel, Professor of Pediatrics and Genetics at Children's Hospital of Philadelphia, and chair of the selection committee for the 2007 Rosalind Franklin Young Investigators Award, called to tell her that she had just won the prestigious $75,000 award from the Peter and Patricia Gruber Foundation. The award, presented every three years, is given to a young woman geneticist one to three years into an independent faculty-level position. Przeworski is the second recipient of this award; Amy Pasquinelli, UCSD, was the first recipient in 2004.

An Evolving Career Path

Przeworski's pathway to evolutionary genetics evolved over time. Unlike many of her geneticist colleagues who claim an interest in science since childhood, Przeworski didn't even think about a career in science, let alone genetics, until college, and then only after considerable arm-twisting.

An only child, Pzeworski and her parents moved to France when she was four, and she was educated there until heading off to college at Princeton. Fluent in French and able to speak some Spanish and German, Przeworski's interests leaned toward the humanities. At Princeton, Przeworski started out as a philosophy major, but "the philosophy department is very analytic so there were requirements in logic. I took those courses and I liked them, so I took more and ended up taking math classes," and eventually switched her major to that subject.

Princeton Professor Simon Levin, a mathematical biologist "was very encouraging to people with quantitative backgrounds in math and physics to get us to consider graduate school in biology. It took me a year to come around, but ultimately I decided to go to graduate school in biology," Przeworski noted.

With little background in biology, Przeworski claims the only graduate program willing to risk accepting her was the one in the Department of Ecology and Evolution at the University of Chicago. The Department, she says, "has a tradition of taking in quantitative students and then teaching them biology."

Although not entirely certain about what she was getting into, population genetics was logical for Przeworski to pursue because it's been "a quantitative field since its inception. It's part of the nature of the subject – it uses tools of probability and statistics." But even though population genetics was the logical place for Przeworski, she still had some doubts. "I spent a couple of years catching up on the science and a year or two asking myself whether or not I enjoyed it. It was very interesting, and by the time I figured out how I felt, I was about to receive my PhD, so I decided to keep going. It really was very accidental; not at all directed," she said.

Przeworski's decision to "keep going" in the field was supported by departmental professors and fellow graduate students who "were incredibly motivating and kept the bar high," which were "pivotal aspects" for her. Her two closest friends in graduate school were GSA member Peter Andolfatto, now at UCSD, and Jeff Wall, UCSF, both prominent population geneticists. In addition, Przeworski noted that the Department "has this nice tradition of letting graduate students write papers on their own, which we did. Faculty members gave us feedback, but they do not put their names on papers, which really gave us the freedom to work on our own."

From Graduate Student to Teacher

Although Przeworksi is now teaching in the department that awarded her Ph.D. degree, the leap from graduate student to assistant professor wasn't automatic. She taught human evolution and population genetics to biology majors at Brown University for a year and a

half before moving back to the University of Chicago two years ago. One of her responsibilities now is to teach a required "core" undergraduate course, "Ancestry, Genetics, and Medicine," which she says is "an attempt to introduce students to concepts in population genetics, race and ancestry and their potential relevance to medicine." The objectives are twofold: 1) "to get students to start thinking about the sociological and ethical issues" affecting genetics and 2) "to get students interested in science." Przeworski thinks the course has achieved some success in fulfilling both objectives, and as she gains more experience as a teacher she expects it will become even more fulfilling for her students and herself.

Lab work

Przeworski finds the University of Chicago to be "a wonderful working environment." In addition to teaching, she "has a dry lab that I run jointly with (GSA member) Jonathan Pritchard and Matthew Stephens. Both of them are leading population and statistical geneticists and it's an incredibly stimulating environment to work in."

"With very rare exceptions we generate data; almost always we collaborate with experimentalists whenever data analysis is involved. Most of what I do is either modeling or data analysis," she adds.

Przeworski is interested in the "big picture." She is trying to answer questions like, "How do species form?" and "What can we learn about the importance of natural selection in shaping patterns of genetic variation?"

"Most of my work focuses on the importance of natural selection, in part because I am specifically interested in human evolution. Hopefully the models and data analysis approaches can be easily generalized and relevant to other species, as I also work with nonhuman primates – chimpanzees in particular. However, the models and theories should also be applicable to Drosophila or whatever model organism people are interested in."

Przeworski is currently working in a couple of areas. "One of them is trying to understand which regions of the genome are involved in evolutionary adaptation, like linguistic or cognitive abilities, or in some cases it might be susceptibility to disease. Given data collected in humans we can learn something about evolutionary history of a particular genetic region or of the genome in general."

"...I am specifically interested in human evolution..."

"Until very recently, population genetics was primarily driven by observations in Drosophila. When I received my Ph.D. in 2000, there was some human data, but the bulk of the models were inspired by work in Drosophila and that's where all the interesting questions were. But it shifted toward humans because there's (grant) money available in that area and now we have a lot more data on humans. It's natural to ask questions about the organisms for which you have the data, but the major questions are very portable, so learning from a Drosophila or yeast perspective can carry over to humans."

Grateful for Award

Although initially shocked about receiving the 2007 Rosalind Franklin Young Investigators Award, Przeworski said she is "extremely flattered" to receive this prize. Her lab is currently working on "understanding recombination in humans." Although she has some NIH funding, "there are a couple of higher risk, high reward projects that I'd like to do, which I was reluctant to do with the grant money I have." The Rosalind Franklin Award will enable Przeworski to pursue those riskier projects.

Unfortunately for Przeworski, the fires in Los Angeles and San Diego prevented her from arriving in San Diego in time to receive the award at the 57th Annual Meeting of the American Society of Human Genetics in October. She was unable to publicly acknowledge her thanks to the Peter and Patricia Gruber Foundation and to the women on the Selection Committee, from both the GSA and ASHG, including chair Beverly S. Emanuel, (Children's Hospital of Philadelphia), and Marian Carlson (Columbia University), Judith Kimble (University of Wisconsin), Mary-Claire King (University of Washington), Amy E. Pasquinelli, (University of California, San Diego), Leena Peltonen-Palotie, (University of Helsinki), and Janet Rowley, (University of Chicago).

"I want to thank the women of the Committee for this award. As incredibly successful scientists, they are role models, which have been extremely helpful to me in thinking about my career," Przeworski noted.

Continued on page 18

Thank You

The Genetics Society of America would like to thank all members who donated to the Society with their 2008 dues renewal. We greatly appreciate these 80 members who made a significant donation to the Society:

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Stephan G. Zweifel, Carleton College, Northfield, MN

These donations help the Society support travel grants and educational opportunities for graduate students and postdoctoral fellows at all GSA-sponsored model organism meetings.

Please join your colleagues in lending your support to the next generation of geneticists.

Contributions can be made by check, to "Genetics Society of America" with "donation" in the memo and mailed to:

Genetics Society of America
9650 Rockville Pike
Bethesda, MD 20814-3998
Attn: Elaine Strass, Executive Director

Eight DeLill Nasser Awards Given for 2008

Four graduate students and four postdoctoral fellows are the recipients of the 2008 DeLill Nasser Awards for Professional Development in Genetics. Thanks to a generous gift from the Burroughs Welcome Fund in 2007 and donations from GSA members, the GSA was able to distribute more than $10,000 in travel grants this year.

The DeLill Nasser Awards honor the memory of and recognize the critical role that DeLill Nasser, a GSA member and Program Director for Eukaryotic Genetics at the National Science Foundation, played in advancing the science of genetics. Since its inception in 2001, approximately $27,000 in travel grants have been awarded to 25 young researchers to enable them to attend national and international meetings or enroll in laboratory courses.

The eight award recipients and how they plan to use their grant are:

• **Gilles R. Hickson** is a postdoctoral fellow at the **University of California, San Francisco**, working in Pat O'Farrell's lab. Using Drosophila as a model organism, Gilles is dissecting molecular mechanisms controlling cytokinesis. He used his award to attend the "Mechanics and Control of Cytokinesis" meeting in Edinburgh, Scotland, January 9-12, 2008.

• **Yen-Ping Hsueh**, a graduate student who is working in Joe Heitman's lab at **Duke University**, is doing research on the genetic and molecular control of mating type and cell fate transitions in the human fungal pathogen, *Cryptococcus neoformans*. Yen-Ping used her award to broaden her horizons at the GSA-sponsored meeting, *GENETIC ANALYSIS: Model Organisms to Human Biology* meeting, January 5-8, 2008, in San Diego, California.

• **Roshan A. Jain**, a graduate student working in Elizabeth Gavis' lab at **Princeton University**, is about to begin his postdoctoral research. He is looking forward to researching neural circuitry in zebrafish. Jain will be using his award to attend the "Zebrafish Development and Genetics" course at Woods Hole Marine Biological Laboratory in Massachusetts, August 10-24, 2008.

• **Chanhee Kang** is a graduate student at the **University of Texas Southwestern Medical Center** working with Leon Avery. Chanhee is researching the mechanisms that trigger anti-hunger (food) signaling in *Caenorhabditis elegans*. He used his award to attend the GSA-sponsored meeting, *GENETIC ANALYSIS: Model Organisms to Human Biology*, January 5-8, 2008, in San Diego, California.

• **Amanda M. Larracuente** is a graduate student at **Cornell University** in Ithaca, NY, working in Andy Clark's lab. Amanda's research focuses on the evolution of the Y chromosome of *D. pseudoobscura*. She will use her award to attend the 49th Annual Drosophila Research Conference, sponsored by GSA, in San Diego, April 2-6, 2008.

• **Kate O'Connor-Giles**, is a postdoctoral fellow working in Barry Ganetzky's lab at the **University of Wisconsin-Madison**. She is studying synaptic growth and plasticity using the larval neuromuscular junction (NMJ) of Drosophila as a model system. In order to learn about emerging technologies in light microscopy and fluorescent molecular probes, Kate will attend the "Imaging Structure & Function in the Nervous System" course at Cold Spring Harbor Laboratory, July 22-August 11, 2008.

• **Mara Schvarzstein** is a postdoctoral fellow in Anne Villeneuve's lab at **Stanford University School of Medicine**. Her goal is to investigate mechanisms that ensure successful chromosome inheritance during meiosis. To help her reach this goal, Mara will use her award to attend the Gordon Meiosis Conference in New London, NH, June 8-13, 2008.

• **Sarit Smolikov**, a postdoctoral fellow in Monica Colaiacovo's lab at **Harvard Medical School**, studies the structure and function of the synaptonemal complex in *C. elegans*, and in particular the mechanisms underlying chromosome segregation in meiosis. Sarit will use her award to attend the Gordon Meiosis Conference in New London, NH, June 8-13, 2008.

Congratulations to these colleagues!


Gilles R. Hickson


Yen-Ping Hsueh


Roshan A. Jain


Chanhee Kang


Amanda M. Larracuente


Kate O'Connor-Giles


Mara Schvarzstein


Sarit Smolikov

MOHB Participants Storm into San Diego

by Susan Dutcher, Washington University School of Medicine, St. Louis, MO

The rain in San Diego did not dampen either the quality of or the enthusiastic response to the genetics research presented at the 2nd *Genetic Analysis: Model Organisms to Human Biology* meeting, January 5-8, 2008. More than 300 participants from around the world heard great presentations from established and emerging leaders in genetics, and saw once again how analysis of yeasts, worms, flies and bacteria leads to a deeper understanding of human physiology and pathophysiology.

The size of the meeting permitted graduate students and postdoctoral fellows to mingle with Nobel Laureates and renowned speakers. The keynote addresses by Nobel Laureates Andy Fire (Stanford) and Richard Axel (Columbia University), and Francis Collins (NHGRI) set a high standard. Fire's discovery of RNA interference and gene silencing is an inspiring example of how seemingly esoteric discoveries in basic science lead to new discoveries about gene regulation, and potentially to new therapeutic tools. Axel described the wiring of the brain for olfaction, noting that epithelial cells of the nose express only one of the more than 1000 olfactory receptor genes. He suggested the novel idea that this is due to a type of transvection, where a limited number of enhancers act in *trans* to recruit and activate one of the ~1000 olfactory receptor genes. In an inspiring after-dinner talk, Francis Collins described how the next generation sequencing methods will soon provide thousands of human genome sequences and reveal the rich variation of our species. In addition, Collins described his lab's efforts to develop drugs to treat children with progeria (premature aging) due to a defect in splicing of the mRNA encoding the nuclear membrane protein laminB. Remarkably, this splicing defect is also seen in "normal" aging brains.

Complex traits that impact human health – atherosclerosis, obesity, diabetes – are of great concern and Trudy MacKay (NC State) presented her elegant work to develop tools and methods to understand quantitative traits in Drosophila. Daniel Promislow (U of Georgia) described how man's best friend can be a model organism for the study of aging. It is clear that the determinants of aging are complex, including autophagy (Malene Hansen, UCSF), protein homeostatis and ubiqination (Andrew Dillin, Salk Institute), cilia (Peter Swoboda, Karolinska Institute), and caloric restriction (Leonard Guarente, MIT).

Epigenetics was prominently featured. The search for DNA sequences conferring X chromosome dosage compensation, and the role of the protein complex responsible for it was beautifully illustrated by Barbara Meyers, (UC-Berkeley). Rudy Jaenisch (MIT) presented his recent results on the use of embryonic stem cells derived from adult cells to cure sickle cell anemia in mice.

Genomic tools continue to advance our ability to carry out genetic analysis. Alan Bradley (Sanger Center) and Hugo Bellen (UTSW) described new technologies for transposon mutagenesis in mice and flies that are enabling the construction of the complete set of gene knockouts for these organisms. Steve Scherer (UToronto) and Mike Snyder (Yale) suggested that DNA sequence copy number variation may account for a significant fraction of human disease. Michele Calos (Stanford University) increased our optimism for gene therapy with her description of bacteriophage vectors that promise to provide a safe method of gene delivery to a small number of sites in the genome.

The lineages of transcriptional pathways in development are being dissected in *C. elegans* by John Murray (University of Washington), who showed the lineage of expression of 46 genes. Cori Bargmann's (Rockefeller University) description of her lab's identification of an oxygen sensor in *C. elegans* showed us that forward genetics can still be productive, and through her studies of cocaine addicted flies, Ulricke Heberlein (UCSF) is informing the basis of addictions. And the genomics revolution has extended geneticists' reach, as illustrated by Gene Robinson's (University of Illinois) application of genomic analysis for understanding social behavior in the honeybee.

Chromosome mechanics and maintenance in the genetics of cancer was prominently featured at the meeting. Terry Orr-Weaver (MIT) described what her lab has learned about the roles of the Rb, myc, and ef2a oncogenes and tumor suppressors in chromosome replication in Drosophila. Tom Petes (North Carolina) presented evidence for a role for mitotic gene conversion in the genome instability that is a hallmark of cancer cells. Johannes Walter (Harvard) explained DNA cross-link repair mechanisms. Judith Yanowitz's (Carnegie Institution) description of an autosomal gene that affects homologous chromosome pairing in *C. elegans* was very exciting. Finally, Pat Hunt (Washington State) gave us pause when she told us that polycarbonate plastic, which is ubiquitous in our surroundings, contains estrogen mimics that have significant adverse effects on mice that can be passed on to their grandchildren! Matthew Gentry (UCSD) described the link between carbohydrate metabolism via the phosphatase laforin and neuronal disease revealed by his comparative genomic analysis. Nels Elde (Fred Hutchinson Cancer Center, Seattle) described an arms race between cells and a virus involving protein kinase R that is a beautiful example of pathogen and host interactions.

Continued on page 14
Pictoral review on page 11

At MOHB...

Andrew Z. Fire, Stanford University School of Medicine delivering his keynote presentation.

Richard Axel, HHMI, Columbia College of Physicians and Surgeons, NYC, and 2004 Nobel Laureate giving his keynote address on Monday evening.

Francis Collins, National Human Genome Institute, National Institutes of Health, delivering the final keynote address, Tuesday evening.

Daniel Promislow, right, University of Georgia with postdoc and graduate students at the Mentor Luncheon on Tuesday.

GSA Board Member Mike Snyder, left, Yale University, New Haven, CT, with students at the Mentor Luncheon.

Past President Allan Spradling, left, Carnegie Institution, HHMI, Baltimore, MD, at the Mentor Luncheon with students on Tuesday.

GSA Board Treasurer Trudy Mackay, right, North Carolina State University, Raleigh, during the mentor luncheon.

Robert Herman, University of Minnesota, thanking his peers for the 2007 GSA George W. Beadle Award

R. Scott Hawley, Stowers Institute, Kansas City, MO, receiving the 2008 GSA Award for Excellence in Education.

Thomas Silhavy, Princeton University, first recipient of The Novitski Prize

Mark Johnston, Washington University, St. Louis, MO, thanking audience for the 2008 George S. Beadle Award.

Elizabeth Jones accepting the 2007 GSA Award for Excellence in Education and thanking her peers.

Dean Dawson, OMRF, Oklahoma City and Terry Orr-Weaver, GSA Past President, 2005, Whitehead Institute/MIT, Cambridge, MA during a rare break in the proceedings.

Fred Winston, Harvard Medical School, and GSA Vice President, at Education Session.

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From the February Issue of *GENETICS*

by R. Scott Hawley, Stowers Institute of Medical Research, Kansas City, MO and Andrew G. Clark, Cornell University, Ithaca, NY

Neuropathology in Drosophila mutants with increased seizure susceptibility

Authors: Tim Fergestad, Lisa Olson, Khelan P. Patel, Rosie Miller, Michael J. Palladino and Barry Ganetzky

Seizure-prone mutants of Drosophila have proven to be an important experimental model of epilepsy. This article describes the use of these mutants to investigate how genetic predisposition to seizures affects the long-term viability of neurons. They found that seizure-prone mutants have shortened life spans and premature neurodegeneration, indicating that the affected proteins play a neuroprotective role. They also show that proper cellular metabolism is required to maintain normal neuronal activity and viability.

Caenorhabditis elegans* ABC$_{RNAi}$ transporters interact genetically with *rde-2* and *mut-7

Authors: Prema Sundaram, Wang Han, Nancy Cohen, Benjamin Echalier, John Albin and Lisa Timmons

This article adds a surprising twist to a bewildering story emerging from transposon-related studies of Argonaute proteins, repeat-associated RNAs, and RNAi. These authors previously surprised us with their observation that some mutants of *Caenorhabditis elegans* with nonfunctional ABC transporters are defective in RNAi. Here they report another surprise – in addition to influencing RNAi, these same ABC transporter genes are required for silencing of parasitic mobile elements. Could it be that ABC transporters add an environmental factor to this story, or do they protect chromosomes from environmental assault? Stay tuned.

Multiple pathways influence mitochondrial inheritance in budding yeast

Authors: Rebecca L. Frederick, Koji Okamoto and Janet M. Shaw

Mitochondrial inheritance is tightly coupled with yeast bud emergence, ensuring that mothers pass their mitochondria on to their daughters. These authors describe multiple, independent pathways that facilitate organelle distribution during yeast budding. Despite the tight physical association of mitochondria and endoplasmic reticulum (ER), coordinated inheritance of these two organelles is not required to ensure each bud receives both mitochondria and ER.

DAF-16-dependent suppression of immunity during reproduction in *Caenorhabditis elegans*

Authors: Sachiko Miyata, Jakob Begun, Emily R. Troemel and Frederick M. Ausubel

How do animals balance the demands of different energy-intensive activities, such as pathogen defense and reproduction? These authors address this intriguing question by demonstrating that sterile mutants of the nematode *Caenorhabditis elegans* have increased resistance to pathogens, dependent on the evolutionarily conserved DAF-16 FOXO transcription factor. Because the timing of DAF-16 activation in sterile animals coincides with embryonic development in wild-type animals, the authors propose that a reproduction-dependent signal from developing embryos normally turns down DAF-16 activity, thus trading immunity for reproduction.

Microarray analysis of replicate populations selected against a wing-shape correlation in *Drosophila melanogaster*

Authors: Kenneth E. Weber, Ralph J. Greenspan, David R. Chicoine, Katia Fiorentino, Mary H. Thomas and Theresa L. Knight

How complex are complex traits? These authors address this question by profiling gene expression in wings of flies subjected to bidirectional selection on the phenotypic correlation between two wing dimensions. Replicated experiments on one population identified 29 loci with consistent, significant association with the trait. Additional experiments with a geographically distant population identified almost completely different loci associated with the trait, confirming recent evidence that a surprisingly large number of genes can affect wing shape.

Population biology of cytoplasmic incompatibility: Maintenance and spread of Cardinium symbionts in a parasitic wasp

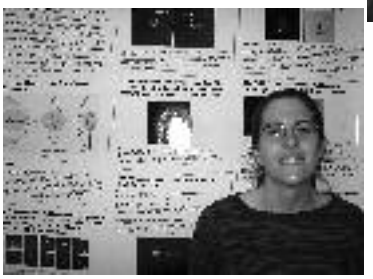
Authors: Steve J. Perlman, Suzanne E. Kelly and Martha S. Hunter

A common cause of incompatibility in insects occurs when uninfected females mate with Wolbachia-infected males, resulting in death of all or most of their offspring. The authors study how the recently discovered incompatibility microbe Cardinium spreads through infected wasp populations. They find that virtually all hosts in a population are infected and the infection is faithfully transmitted from mothers to their offspring. The low fecundity of infected females still poses a mystery: How does the infection initially spread in the population?

Three Students Receive Poster Awards

Congratulations to three poster presenters at the MOHB meeting who received a $300 award plus a five-set volume of the GSA DVD, "Conversations in Genetics." The three award recipients are:

• Joshua J. Bayes, graduate student, Fred Hutchinson Cancer Research Center, Seattle, for his poster, "Cytological characterization of a hybrid sterility gene in Drosophila." Joshua is working in Dr. Harmit Malik's lab at FHCRC.



• Stacie E. Hughes, Postdoctoral fellow, Stowers Institute, Kansas City, for her poster, "Heterochromatic threads connect oscillating achiasmate chromosomes during meiosis in Drosophila oocytes." Stacie is working with Scott Hawley.

• Chanhee Kang, graduate student, UT Southwestern, Dallas, for his poster, "Anti-hunger (Food) signaling in *Caenorhabditis elegans*." Kang is working with Leon Avery.

Kang also received a DeLill Nasser Award for Professional Development in Genetics to attend this meeting.

MOHB in San Diego

Continued from page 10

The meeting made it clear that many of the interesting questions discussed at the MOHB, from sensory biology to aging to gene control, will be well served by using a wide spectrum of organisms and approaches.

A comprehensive description of Graham Hatfull's (Pitt) inspiring talk at the educators' lunch organized by GSA Education Committee Chair Robin Wright (Univ. of Minnesota) can be found on page 2 of this newsletter. Many of the students in attendance enjoyed meeting some of their senior colleagues at the mentors' lunch. And we learned about amazing next generation sequencing techniques and equipment at a lunch sponsored by Applied Biosystems, Illumina, Inc., and Roche.

In addition, several GSA awards were presented at the meeting, including the 2007 and 2008 George W. Beadle awards to Bob Herman (University of Minnesota) and Mark Johnston (Washington University, St. Louis, MO); the 2007 and 2008 GSA Award for Excellence in Education to Beth Jones (Carnegie Mellon) and Scott Hawley (Stowers Institute); and the 2008 Novitski Prize to Tom Silhavy (Princeton).

Based on the results of the meeting survey, and on comments heard (and overheard) during the meeting, it was another resounding success. Attendees appreciated the meeting's broad scope (an increasingly rare conference commodity) and enjoyed the opportunity to interact with a diverse group of colleagues. The GSA plans to continue to promote the unification of genetics: Planning of the 2010 GSA MOHB meeting is already underway by a committee chaired by GSA Vice President Fred Winston. Watch this newsletter (and your e-mailbox) for further information, and **plan to join us in 2010 for the 3rd *GSA Model Organisms to Human Biology* meeting**.

1 Joshua Bayes, left, and Mary Gehring, Fred Hutchinson Cancer Research Center, Seattle, WA, discussing posters. **2** Pinky Kain, left, NCBS, TIFR, Bangalore, India and Tariq Maqbool, INSERM, Clermont Ferrand, France, viewing posters. **3** L to R: Kathryn A. Hedges, Humboldt State University, Arcata, CA discussing her poster with Rhonda Hyde, Massachusetts General Hospital, Charleston. **4** L to R: Taosheng Huang, University of California, Irvine, and Zhiyan Liu, Harvard University/MEEI, Boston, MA, watching Donghui Yang-Zhou, Harvard Medical School/MEEI, Boston, MA as she pins up her poster. **5** Yen-Ping Hsueh, Duke University, Durham, NC, DeLill Nasser Award Recipient and MOHB Poster Award Recipient talking with Dan Barbash, Cornell University, Ithaca, NY, at the poster session.

Worming your Way into WormBase

by Paul Sternberg, California Institute of Technology, Pasadena

Ontology and Curation of Phenotypes in WormBase

Genotype is useless without phenotype. Accurate and accessible phenotype information is an essential resource for all geneticists, and it is a highly desired item for model-organism database users. Over a year ago, WormBase implemented a variety of phenotype annotation changes to facilitate curation and the search for genes associated (or not) with particular phenotypes. WormBase developed a phenotype ontology, a structured vocabulary for phenotypes that is organized hierarchically, based on relationships between phenotype terms. The phenotype ontology currently consists of over 1500 terms that are now being used to curate mutant phenotypes. WormBase also features a sophisticated browser to view its different ontologies (phenotype, gene, cell) and the association of the terms to genes or alleles.

WormMart

WormMart (http://www.wormbase.org/biomart/martview) is the WormBase implementation of BioMart. This tool provides easy, interactive access to data *en masse*, enabling the user to retrieve sequences and genome annotations using a variety of filters to constrain results. Filters include such parameters as genomic location and the presence or absence of specific annotations. Data can be displayed in a variety of formats, including HTML, text, FASTA, and even Microsoft Excel.

Nematode Genomes in WormBase

With the sequencing of several nematode species in various stages of completion, WormBase is working on incorporating these sequence data and providing tools like genome browsers and blast servers for searching this data. WormBase also provides comparative data such as, protein clusters, predicted orthologs and genome alignments. The *C. briggsae* sequence was the first non-*elegans* sequence data to be completely incorporated into WormBase; we are currently curating *C. briggsae* gene models based on experimental evidence and community feedback. Genome browsing is also available for *C. briggsae, Brugia malayi* and *C. remanei* (preliminary analysis), including gene model predictions, protein and EST alignments and nucleotide-level alignments to the *C. elegans* sequence. And BLAST servers are available for the protein data sets of *C. briggsa*e and for preliminary protein data-sets of *C. remanei* and *B. malayi*. WormBase plans to incorporate other nematode genome sequences and their annotations as they become available, including *C. japonica, C. brenneri, P. pacificus* and *H. bacteriophora*.

WormBook

WormBook, is a first of a kind: an open-access book/journal that is a companion to WormBase. WormBook (www.wormbook.org) now has over 140 original, peer-reviewed chapters provided by the *C. elegans* community, including a 'WormMethods' section. All chapters are now indexed in PubMed.

Textpresso: The New Generation Search Engine

Textpresso (www.textpresso.org), the literature search engine for WormBase, makes it possible to deal with the growing avalanche of publications. It enables searches of over 9,400 full-text papers for individual sentences, words, or phrases of interest within sentences, and by categories such as 'gene' or 'human disease,' so, you can find sentences that mention any worm gene and any human disease. The new Textpresso interface also allows filtering of results by additional criteria. Textpresso will soon have scanned all pre-electronic papers related to *C. elegans*. The *Drosophila* version of Textpresso is now live from FlyBase (www.textpresso.org/fly) and indexes over 20,000 papers about *Drosophila*. Check out Textpresso at WormBase; we predict you'll soon be using it regularly.

The WormBase Virtual Machine

Some people want to browse WormBase off-line, or integrate their own data into the database, or carry out a local query, or build a WormBase mirror site. You can now do all this because WormBase has developed software packages for downloading and running WormBase locally on any computer. Be the first on your block to get it!

dictyBase: New Features and Functionality

by Petra Fey, Eric Just and Pascale Gaudet, Northwestern University, Chicago, IL, on behalf of dictyBase

The eukaryote *Dictyostelium discoideum* has its own database: dictyBase! *Dictyostelium* is a soil amoeba that feeds on bacteria, and when its food supply is exhausted, *D. discoideum* develops into a multi-cellular fruiting body containing spores that are able to survive in those unfavorable conditions. dictyBase presents genomic and biological information (www.dictybase.org), that is updated daily (for an overview see Figure 1).

Data

In addition to the genome sequence, the complete body of *Dictyostelium* literature, gene ontology annotations, and results of genome expression profiling experiments, several new data types have been recently integrated into the database, including tRNAs and other non-coding RNAs. The pseudogene display has been improved and they now appear without introns and without a protein translation. To display *D. discoideum* biochemical pathways, dictyBase now hosts dictyCyc, created with the Pathway Tools software developed by P. Karp and colleagues at SRI International (www.BioCyc.org). One can browse or access the pathways from the relevant gene pages. See how it works by going to the pages for the *pgkA* and *fumH* genes.

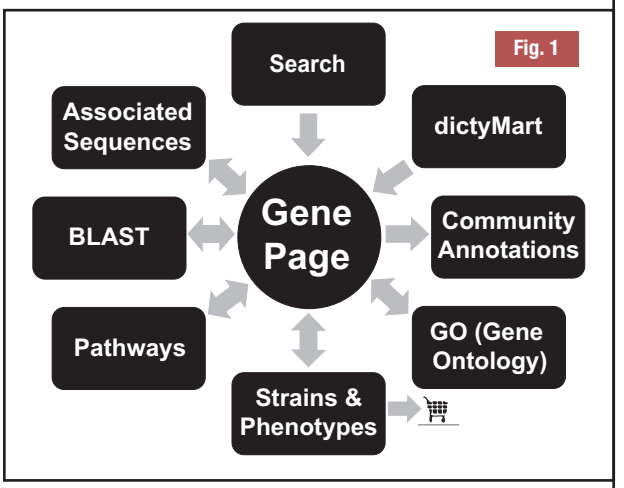


Fig. 1. A simple overview of basic data and functions linked to and/or from the Gene Page at dictyBase.

Information Retrieval

The search tool has been expanded to include numerous database fields, including gene names, synonyms and gene product names, sequence IDs, gene ontology terms, colleagues, authors, phenotypes, strains, plasmids, and all general (non-database) dictyBase web pages. A powerful tool, dictyMart, created with the open source software Biomart (www.biomart.org), allows complex queries such as the retrieval of gene sets annotated with a specific gene ontology term.

Community Annotations

dictyBase now also has a versatile community annotation page, based on Wikimedia software, and linked from each gene page. Users can add information such as sequence updates, recent findings, or pictures by using 'Wiki' style editing. Please help us keep dictyBase up-to-date by contributing to "WikiDicty".

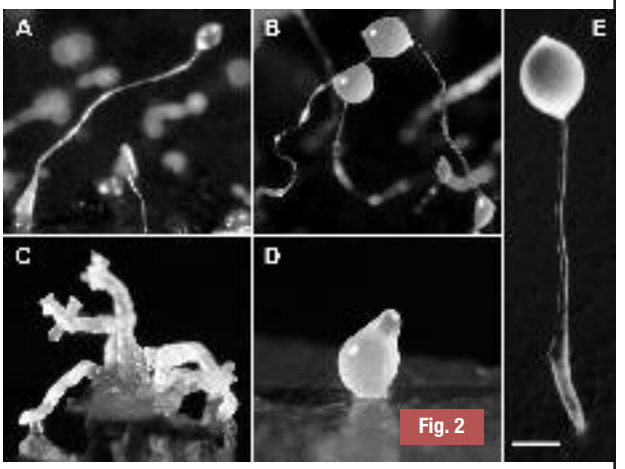


Fig. 2. Images of mutant strains of *D. discoideum* available from the wiki community annotation pages linked from each gene page. These pictures were contributed by D. L. Fuller and W. F. Loomis, UCSD, obtained in a large-scale screen for development mutants. All mutant strains are available to interested researchers. A. DG1074 (protein: RNA-binding region-containing), B. DG1113 (protein: C2 domain-containing), C. DG1040 (protein: CCR4-NOT1 complex subunit), D. DG1016 (protein: Rab GTPase). E. Wild type fruiting body (P. Fey and R. L. Chisholm, unpublished). Scale bar, 0.1 mm.

Strains and Phenotypes

Previously, phenotypes were directly linked to genes, but we recently updated our data model to more accurately reflect the fact that phenotypes are characteristics of strains rather than genes. Phenotypes are now associated with strains, which are linked to the gene(s) that is (are) responsible for them. Strains are entered into the database either from the literature, or when they are received by the Dicty Stock Center. All information about a strain, including phenotypes, can be found on the strain details page. The phenotypes are annotated using a controlled vocabulary organized in an ontology. Figure 2 shows some mutant phenotypes observed in *Dictyostelium*. For each strain, Stock Center availability is indicated, and researchers can order strains directly through dictyBase free of charge.

The Awesome Power of Chlamy

Susan K. Dutcher, Washington University School of Medicine, St. Louis, MO

Chlamydomonas reinhardtii, affectionately known as Chlamy, is a unicellular green alga that has long served as a model for several important cellular processes, including the biogenesis, function and inheritance of chloroplasts, cilia and basal body biogenesis and function, and nutrient sensing and utilization. With the combination of the *Chlamy* genome sequence and genetic tools that include insertional mutagenesis and RNA interference, it is possible to study an increasing spectrum of biological questions, such as human disease, pigment biosynthesis, cellular polarity and biofuels by using *Chlamydomonas*.

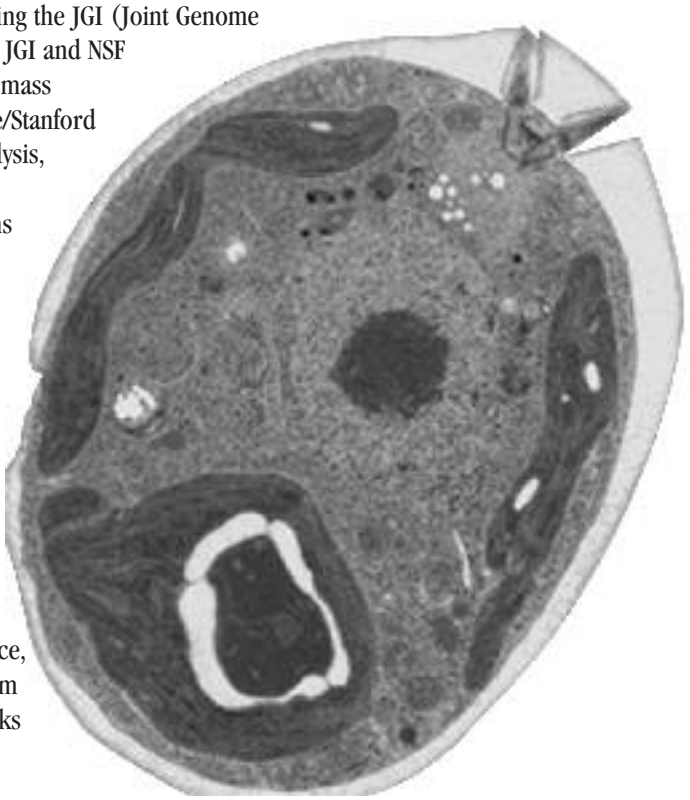
A Community Resource

The door to a community resource that provides a wide variety of services and information about *Chlamydomonas*, including the *Chlamydomonas* Genetics Center and ChlamyDB, can be opened at www.chlamy.org. The *Chlamydomonas* Genetics Center, funded by the National Science Foundation, serves as the central repository to receive, catalog, preserve and distribute wild-type and mutant cultures of *C. reinhardtii* and other *Chlamydomonas* species. It receives, catalogs, preserves and distributes over 1000 mutant and wild-type cultures of *Chlamy*. The Center also maintains and distributes molecular reagents that include genomic and cDNA clones of *Chlamydomonas* nuclear, chloroplast and mitochondrial genes, as well as cDNA libraries.

ChlamyDB and Links

ChlamyDB, available at http://www.chlamy.org/chlamydb.html was originally developed as part of the *Chlamydomonas* Genetics Center, and has evolved into a major resource that integrates databases of many different groups studying the organism. ChlamyDB, disseminates information to the international scientific community by providing descriptions of the culture collections, historical information and reference material on genetic loci and mutant alleles. It also provides an address directory and site for seeking information from members of the community, along with an extensive bibliography. These efforts are expected to expand under the direction of GSA member Elizabeth H. Harris, Duke University, Durham, NC.

ChlamyDB also provides seamless links to other databases, including the JGI (Joint Genome Institute) databases for searching genomic and EST databases (from JGI and NSF funding), to the flagellar proteome database that contains data from mass spectroscopy, to the microarrays that are available from the Carnegie/Stanford group. Because *Chlamydomonas* is used extensively for genetic analysis, ChlamyDB provides access to genetic and physical maps and links to marker sets in "mapping kits," and large sets of primer combinations for putative physical markers between the standard lab strains and a commonly used polymorphic (CC-1952) strain (Rymarquis et al., 2005).



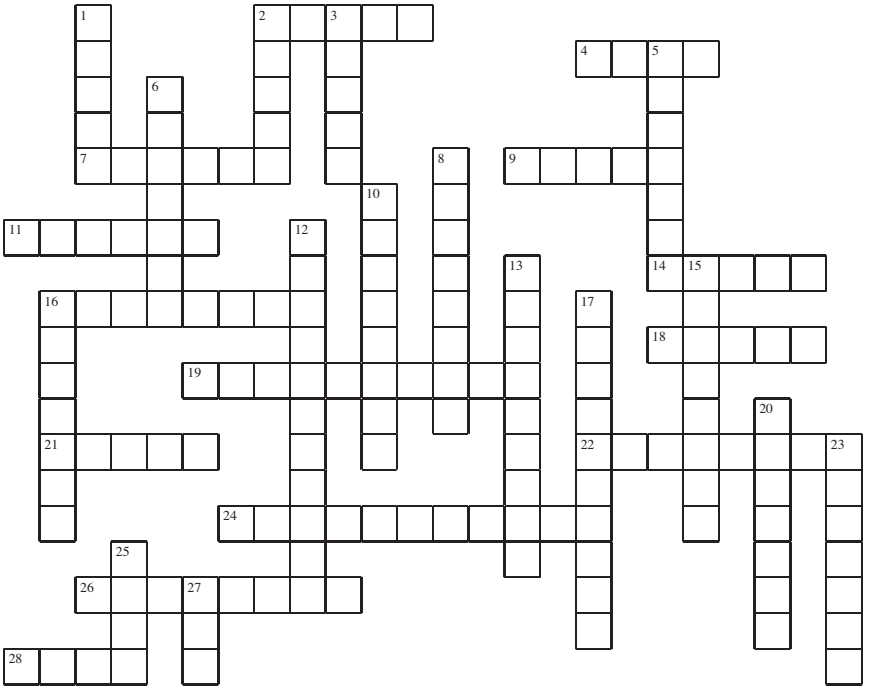
Other Resources

A valuable information resource that is in the works is "The Chlamydomonas Sourcebook, Second Edition," to be published by Academic Press in mid-2008. The three-volume Sourcebook will provide an introduction to *Chlamydomonas* and its laboratory use, with chapters on metabolism, photosynthesis, organelle biogenesis, cell motility, and behavior, written by *Chlamy* experts. And to complement and highlight the release of the Chlamy genome sequence, a special issue of the GSA journal, *GENETICS*, devoted to the organism is being planned. Look for it this summer. The future for Chlamy looks bright (green).

Yeast is the Beast

by Julie Park and The Saccharomyces Genome Database Project, Stanford University, CA

Sharpen your pencils and rise up to the challenge of the yeasties to solve this crossword puzzle. The answers? Check online at http://www.genetics-gsa.org/pages/newsletter.shtml.



ACROSS

2 Yeast mating type
4 Abbreviation for the compound 5- phospho - ribosyl - pyrophosphate
7 16 down's Protein _____
9 Yeast Kingdom
11 Constituent of yeast cell walls
14 Yeast cell form named after a comic strip character
16 Human protein homologous to yeast Taz1p
18 [PSI], e.g.
19 GO:0005813
21 Lab strain of yeast particularly suited for study of pseudohyphal growth
22 Yeast food?
24 Process commonly studied in the lab strain SK1
26 Mapmaker Robert _____
28 A popular yeast product

DOWN

1 Saccharomyces means "sugar fungus" in this language
2 Sentenac or Goffeau
3 The fission yeast S. _____
5 Yeast mutants that have little or no mitochondrial DNA
6 A pathological genus of yeasts
8 Non fermentable carbon source
10 Gene _____ (GO)
12 Localization site of Sgo1p
13 Latin translation of 28 across
15 Nobel prize winner for their work in yeast
16 Scientist _____ Toda
17 Drug resistance conferred by mutating CAN1
20 Number of nuclear chromosomes in budding yeast
23 Substrate of E.C. 1.1.1.1
25 Number of spores in an ascus
27 Better known moniker of Spt15p

CROSSWORD PUZZLE

Molly Przeworski: The Accidental Geneticist

Continued from page 7

The Importance of Role Models

Przworski noted that role models – both female and male – have been part of her support system throughout her education and career. Since women are still a minority in the field, she said there were many males in her support system, including her former colleagues Peter Andolfatto and Jeff Wall, but says that she was "lucky enough to have multiple sources of support." She encourages other female students to follow in her footsteps, saying that with each step along the way – from undergrad to graduate student, from graduate student to postdoctoral fellow, from postdoc to faculty member – the path became easier, and a strong support network helped to make it that way.

"I'm very lucky to have senior female faculty in my department who are incredibly supportive. I think my department is quite an unusual place because on every level of seniority it's about 50 percent female. That definitely has an impact on the atmosphere and it makes it a pleasant place to work," she added.

A self-described "city person," Przeworski likes to "go for walks, go to the movies, read novels, see friends and travel," when she isn't crunching data sets. And although she claims to be an accidental geneticist, it is no accident that she is fast becoming a leader in her field, and that she was chosen to be the recipient of the 2007 Rosalind Franklin Young Investigators Award.

JSC Debuts New Name:

The Coalition for the Life Sciences

The Joint Steering Committee for Public Policy (JSC) has changed its name to the Coalition for the Life Sciences (CLS), effective December 12, 2007. The new name better reflects the nature of the organization and its primary goals.

Since its inception in 1989, the JSC historically focused on responsible science policy and adequate funding for the National Institutes of Health and the National Science Foundation. In recent years, as its number of member societies has increased, the JSC expanded its interests to include science education, professional training, and the funding, management, and oversight of scientific work, especially by the federal government. The GSA has long been one of the member societies of the JSC and a stalwart supporter of its mission. Other member organizations include the American Society for Cell Biology, American Society for Clinical Investigation, Howard Hughes Medical Institute, Society for Neuroscience, and Science Service.

"After careful consideration, the JSC board agreed that the name Coalition for the Life Sciences more accurately reflects our composition and our goals," said Nobel Laureate Harold Varmus, Chair of the CLS, President and CEO of Memorial Sloan-Kettering Cancer Center, and former NIH Director.

The CLS remains committed to the highly successful and well-regarded programs started under the JSC, including the Congressional Biomedical Research Caucus, the Congressional Liaison Committee, and Capitol Hill Days.

From the President's desk:

Continued from page 1

way to highlight and promote research and researchers who join diverse systems in the service of genetics. (See pages 10-11 on the 2008 meeting.) But that is not enough: we must also seek and implement new initiatives.

The GSA should begin by taking a lesson from the *C. elegans* Wormbook (www.wormbook.org) a web-based information resource that is freely available under a common license. Each chapter is invited, peer-reviewed, and produced like a journal article, by experienced editors. The GSA should promote and support the creation of a *Coli*book, a Yeastbook, a Flybook, a Fishbook, a Mousebook, a Humanbook, and as many others as enthusiasm allows. As with the Wormbook, individual experts on each system, using their genome and ontology projects as resources, will put the pieces together, gene by gene, pathway by pathway and cell by cell. We must then convince the authors to cross-annotate their chapters. Each step in this plan will require contributions across the membership of our diverse society. Success will not be measured by the volume of data, or the amount of traffic, but by the quality of the unifying biological ideas and insights. As a result, it will become easier to compare the genomes, metabolomes, expression profiles, embryology, anatomy, histology, and physiological processes of our favored systems, revealing more clearly how they relate to us. Eventually, if we add enough model organisms, collect enough data, do enough experiments, we expect to be able to write the ultimate books: the LUCAbook and Urbilateriabook.

The GSA should be the society to lead us into this future of a biological science unified by genetics. I urge you to help me and our colleagues in the GSA formulate this vision and implement this unification of our field. Please send you comments and suggestions to <GSA2008@ciwemb.edu>.

I have enjoyed my year as GSA President and look forward to continuing to work with all of you in striving to fulfill the goals of the GSA.

Sincerely,
Allan Spradling
Past President (2007)

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Public Policy Update

Small Business Bill Could Further Restrict NIH Researcher Funds

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A bill designed to fuel the economy by expanding small business growth may have a devasting impact on the amount of academic research the National Institutes of Health (NIH) would be able to support. The bill, S. 1932, introduced by Senator Evan Bayh (D-IN) would double the contributions made by federal agencies, including NIH, to the Small Business Innovation Research (SBIR) and the Small Business Technology Transfer (STTR) programs.

While laudable in its intent, increasing the SBIR/STTR set-aside could decrease NIH funding of academic research. The Coalition for the Life Sciences (formerly the Joint Steering Committee for Public Policy) wrote to Senator Bayh, expressing its concern.

"The JSC believes that the SBIR/STTR programs are an important component of the NIH's mission to advance science to improve health and longevity, yet doubling the SBIR/STTR set-aside from its current 2.5% level to 5% would adversely affect the ability of the NIH to support other important components of its portfolio at a time when the agency's spending power is shrinking," Harold Varmus, chair of the CLS, wrote to Senator Bayh.

The SBIR/STTR programs will be renewed by Congress in 2008, in separate, yet-to-be-introduced legislation. The SBIR/STTR are substantial programs, and it's possible that S.1932 could become one of the many components of the SBIR/SSTR reauthorization bill. The CLS will continue to monitor this legislation.

To see a copy of the letter sent to Senator Bayh, please visit www.jscpp.org.