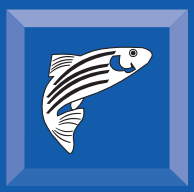
GSA

GENEtics

APRIL 2005





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9650 Rockville Pike
Bethesda, MD 20814-3998
Tel: (301) 634-7300
Fax: (301) 634-7079
Email:
society@genetics-gsa.org
www.genetics-gsa.org

From the President's desk:

The sequence of the human genome underscores the necessity for genetic analysis to define gene function and validates the importance of genomic and genetic approaches in model organisms for gene discovery. The GSA promotes genetic research in model organisms and its application to human genetics via our journal *Genetics*, supporting public education and congressional lobbying through the Joint Steering Committee for Public Policy (www.jscpp.org) and in its sponsorship of scientific meetings.

The GSA support of scientific meetings includes providing the crucial infrastructure, organization, administration, and financial foundation, as well as recognition for students and postdocs through the awards we sponsor. The society's sponsorship of model organisms meetings in *C. elegans*, Drosophila, Fungi, Yeast and Zebrafish has enabled those research communities to hold conferences that are particularly accessible to students and postdocs who are our future. The support of the GSA has been key in enabling these very successful meetings while permitting each of the model organism communities the independence to organize the meeting according to their needs. In recognition of the importance of genomics in our field, this year the GSA will support a new meeting of biocurators and database developers with the goal of bringing together developers of these bioinformatics tools for a variety of organisms. Your membership in the GSA entitles you to a reduced registration fee for all of these meetings.

The GSA will organize its own meeting "Genetic Analysis: Model Organisms to Human Biology," Jan. 5-7, 2006 in San Diego to draw together the entire constituency of our society and to promote interactions with our colleagues directly studying human disease. This timely meeting will feature recent advances in genetics arising from model organism research and highlight their significance for human disease. An outstanding lineup of speakers is being assembled (http://www.gsa-modelorganisms.org/), and it promises to be an exciting meeting.

Publication of the journal *Genetics* has long been the main activity of our society. In 1916 *Genetics* got off to a flashy start by publishing Bridges' paper on the proof of the chromosomal theory of inheritance as its first paper in volume 1. The next nearly 90 years of *Genetics* saw the publication of some of the most seminal papers in our field. As part of our commitment to preserving this legacy, all issues of *Genetics* are available on line.

Continued on page 3

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Dear Abbot:

Teaching the basics of mitosis and meiosis to the undergraduates has become a big chore. This is the birds and the bees, but you'd think I was lecturing on accounting or the names of rocks! Can you share any tips for helping my students become interested and curious about these key genetic processes?

Mystified in Minnesota

Dear Mystified,

I had the same problem! My monkish colleagues were more interested in the latest diocesan gossip than in what I discovered about inheritance of wrinkled pea seeds. And none of them read my paper on the subject! But, I hope you will persevere, because there's great satisfaction (and maybe eventual recognition) to be had if even only a few of them discover the exciting truths you're trying to tell them.

Because learning is enhanced when we connect what we want students to learn with their prior knowledge or experience (http://www.nap.edu/books/0309070368/html/), I devised the following strategy to teach mitosis and meiosis. I begin with a fairly detailed description of herpetology and timber rattlesnakes (*Crotalus horridus*, a species of pit viper) that is endangered (because of overcollecting by pet traders, loss of habitat and skin trade collection). They have low reproductive rates: females take about 7 years to become sexually mature, then breed only every 3 or 4 years. As for all pit vipers, timber rattlesnakes are viviparous.

One day, David Chiszar, a herpetologist at the University of Colorado, Boulder, noticed three newborn snakes in the cage of a female timber rattlesnake that he had raised from the time she was newborn. This female snake had never, to his knowledge, been with a male snake of any kind – and even if she had, this encounter would have occurred more than 10 years ago, when he first collected the snake. Two of the babies were dead, but one was alive. Curiously, all of them were male.

This mystery instantly piques the students' curiosity. I then tell them that by the end of the next two weeks, they will be able to explain where this baby snake came from, and why it is male and not female. To make things a bit more exciting, I offer bonus points to the first person who comes up with the correct explanation. (I have never had to award the bonus points until we get to the meiosis part of the lectures!)

We begin by talking about reproductive strategies that rely on mitosis. After learning the process of mitosis, we go back and ask whether the baby snake could have been produced by a mitotic form of reproduction. Clearly, the answer is "no" since the snake is male. Then the class learns how meiosis differs from mitosis and the answer emerges: an abnormal meiotic division produced a diploid egg, explaining the origin of the baby snake. After a discussion of parthenogenesis, we return to the question of why the baby snake is male. This question leads to discussions of sex determination, sex chromosomes, and gene expression…the next topics for my class. There are many examples of parthenogenesis that could be used as well. Google "Beltsville white" as a start!

I find that this strategy – introducing a compelling puzzle that can only be solved by learning the course material – is routinely successful in motivating students to learn what I am teaching them. Good luck with your class!

And please, read my paper (http://www.mendelweb.org/).

The Abbot

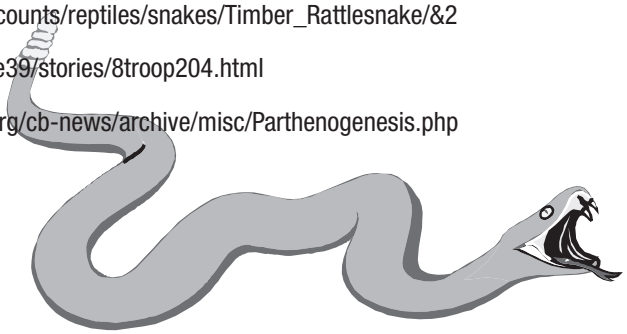
Useful web resources

Basic information about timber rattlesnakes:
http://herpcenter.ipfw.edu/index.htm?http://herpcenter.ipfw.edu/outreach/accounts/reptiles/snakes/Timber_Rattlesnake/&2

Information about David Chiszar: http://www.colorado.edu/Carillon/volume39/stories/8troop204.html

Description of the observation & scientific explanation: http://coloherp.org/cb-news/archive/misc/Parthenogenesis.php

Other instances of parthenogenesis:
snake: http://www.albinoburmese.com/parthenogenesis.pdf
turkey: http://www.genetics.org/cgi/reprint/56/4/727



Yanofsky Awarded National Medal of Science

President George W. Bush awards longtime GSA member and Past President (1970) Charles Yanofsky of Stanford University, CA, the National Medal of Science and Technology at a White House ceremony held on March 14, 2005. White House photo by Paul Morse

From the President's desk:

Continued from page 1

Why publish in *Genetics* now? *Genetics* provides what has become a rare opportunity to publish a complete story, with the supporting data in the publication rather than relegating it to the (sometimes ephemeral) supplemental material or simply referring to 'data not shown'. The editors who handle your papers are your peers: working research scientists who understand experimental analysis and are able to evaluate fairly reviewers' comments. Manuscripts accepted for publication are open at the journal web site within days of their acceptance, and the published version is freely available three months after publication. GSA members enjoy substantially reduced publication charges for the journal.

The GSA is composed of a diverse group of experimental scientists using a range of organisms to address a breadth of biological questions in a variety of research and educational settings. Consistent with the role that women have long played in making ground-breaking discoveries in genetics (witness the female Nobel Laureates in genetics), the GSA is proud that women comprise a sizable proportion of our society. Women are not only represented on the board of directors, but four of the past six society presidents have been women. This representation is reassuring and significant given recent speculations about the innate abilities of women in science and math and the media's captivation with this issue. As geneticists it is important for us to speak to the ability of women and other under-represented groups to excel in science and math.

I look forward to communicating with you this year through this letter, to reading your papers in *Genetics*, and to interacting with you at the "Genetic Analysis: Model Organisms to Human Biology" meeting next January.

Terry Orr-Weaver

From the May Issue of *GENETICS*

by R. Scott Hawley

These upcoming articles caught our interest.

MSID: GENETICS/2004/030106

Title: Mutations of a redundant α-tubulin gene affect *C. elegans* early embryonic cleavage via MEI-1/katanin dependent and independent pathways

Authors: C. Lu, and P. E. Mains

The functional significance of variant tubulin genes has been a matter of considerable interest in several organisms. Although the two α-tubulin genes (TBA-1 and TBA-2) of *C. elegans* are redundant with respect to viability, they can be distinguished by their differential requirement in a katanin mutant. Their results suggest that TBA-2 is preferred over TBA-1 by katanin. The authors also report two gain of function mutations in TBA-2 that rescue the lethality caused by mutations in katanin. Thus, while the *C. elegans* embryo expresses redundant α-tubulins, they have subtle functional specializations.

MSID: GENETICS/2004/039727

Title: Identification of zebrafish insertional mutants with defects in visual system development and function

Authors: J. M. Gross, B. D. Perkins, A. Amsterdam, A. Egana, T. Darland, J. I. Matsui, S. Sciascia, N. Hopkins, and J. E. Dowling

Gross and colleagues report the results of a large-scale retroviral insertional mutagenesis screen that resulted in the recovery of 315 new mutants. A screen for visual system defects within a subset of this collection of mutants revealed 40 genes whose wild-type products are required for eye development or visual system function. These mutants are carefully characterized in terms of the developmental, structural or behavioral defect, and offer an impressive resource for the study of eye development and function.

MSID: GENETICS/2004/036343

Title: Synthetic lethality of retinoblastoma mutant cells in the Drosophila eye by mutation of a novel peptidyl prolyl isomerase gene

Authors: K. A. Edgar, M. Belvin, A. L. Parks, K. Whittaker, M. B. Mahoney, M. Nicoll, C. C. Park, C. G. Winter, F. Chen, K. Lickteig, F. Ahmad, H. Esengil, M. V. Lorenzi, A. Norton, B. A. Rupnow, L. Shayesteh, M. Tabios, L. M. Young, P. M. Carroll, C. Kopczynski, G. D. Plowman, L. S. Friedman, and H. L. Francis-Lang

Mutations in the retinoblastoma gene (*Rb*), common among human tumors, promote cell division by abrogating the G1 cell cycle checkpoint. To identify proteins required for viability of Rb mutant cells, which are potential targets for cancer therapy, Edgar et al performed an elegant screen for mutants that are synthetically lethal with mutations in *Rb*. They report the identification of a mutation in a peptidyl prolyl isomerase gene that selectively eliminates Rb- cells without affecting the viability of Rb+ neighbors.

MSID: GENETICS/2004/034538

Title: The Ku protein complex is involved in length regulation of Drosophila telomeres

Authors: L. Melnikova, H. Biessmann, and P. Georgiev

It is ironic that telomeres of Drosophila, which were the first to be discovered (by Muller and Herskowitz in 1954), turn out to be the exception to the rule. Substantial work by Mary Lou Pardue and others have shown that Drosophila telomeres are comprised of the telomere-specific retrotransposons, HeT-A and TART, and that chromosome ends can be elongated either by terminal attachment of these retrotransposons or by terminal gene conversion. Melnikova et al. show that a decrease in Ku70 or Ku80 gene dosage causes a sharp increase of the frequency of HeT-A and TART attachments to a broken chromosome end, and of terminal DNA elongation by gene conversion. These results suggest a critical role of the end-binding complex Ku in the accessibility and length regulation of Drosophila telomeres.

An Innovative Educational Technology for Genetics Problem Solving:

The Genetics Cognitive Tutor

Be the first to pilot some teaching software in your genetics course! A team of geneticists and cognitive scientists at Carnegie Mellon University may have the right software tool for you. CMU is developing an innovative "Genetics Cognitive Tutor" to support student problem solving and help make genetics more accessible to students. A cognitive tutor is an interactive computer program based on a computational cognitive model that follows a student's individual problem-solving path and provides just the help that is needed for the student to achieve a successful solution.

With funding from the National Science Foundation, U. S. Department of Education and the Howard Hughes Medical Institute, CMU is developing 15 Genetics Cognitive Tutor units in these areas:

- Mendelian Transmission
- Pedigree Analysis
- Recombination and Gene Mapping
- Gene Regulation
- Population Genetics

The problem-solving activities are designed to develop students' domain knowledge, quantitative reasoning skills, and scientific reasoning skills.

Piloting Opportunity

The Genetics Cognitive Tutor units have been piloted and evaluated with hundreds of students at several colleges and universities over the past two years. CMU is seeking to expand the piloting opportunity to a limited number of colleges and universities. Participants in the pilot will select cognitive tutor units that align with the content of their course and will make the units available to students as in-class or homework activities. Evaluation as pre- and post-tests or performance on exams is required.

Visit out website http://www.cs.cmu.edu/~genetics to learn more about the Genetics Cognitive Tutor project and cognitive tutors more generally.

If you are interested in trying Genetics Cognitive Tutor units in your course, have questions, or would like more information, send an email to lk01@andrew.cmu.edu. Please do this ASAP, because the participant list will be finalized in early June.

The Genetics Cognitive Tutor Research Team

Elizabeth Jones
Professor and Head
Biological Sciences

Albert Corbett
Associate Research Professor
Human-Computer Interaction

Linda Kauffman
Teaching Professor
Biological Sciences

Ben MacLaren
Senior Research Programmer
Human-Computer Interaction

Researchers Swarm to Drosophila Meeting

More than 1500 researchers and students from 29 countries and the U.S. converged on San Diego for the 46th Annual Drosophila Research Conference, March 30 – April 5, 2005. The attendees participated in the four-day meeting that included an opening session featuring 1995 Nobel Laureate Christiane Nusslein-Volhard as the keynote speaker, two plenary sessions, 16 concurrent slide talk sessions, nine workshop sessions, and over 800 posters.

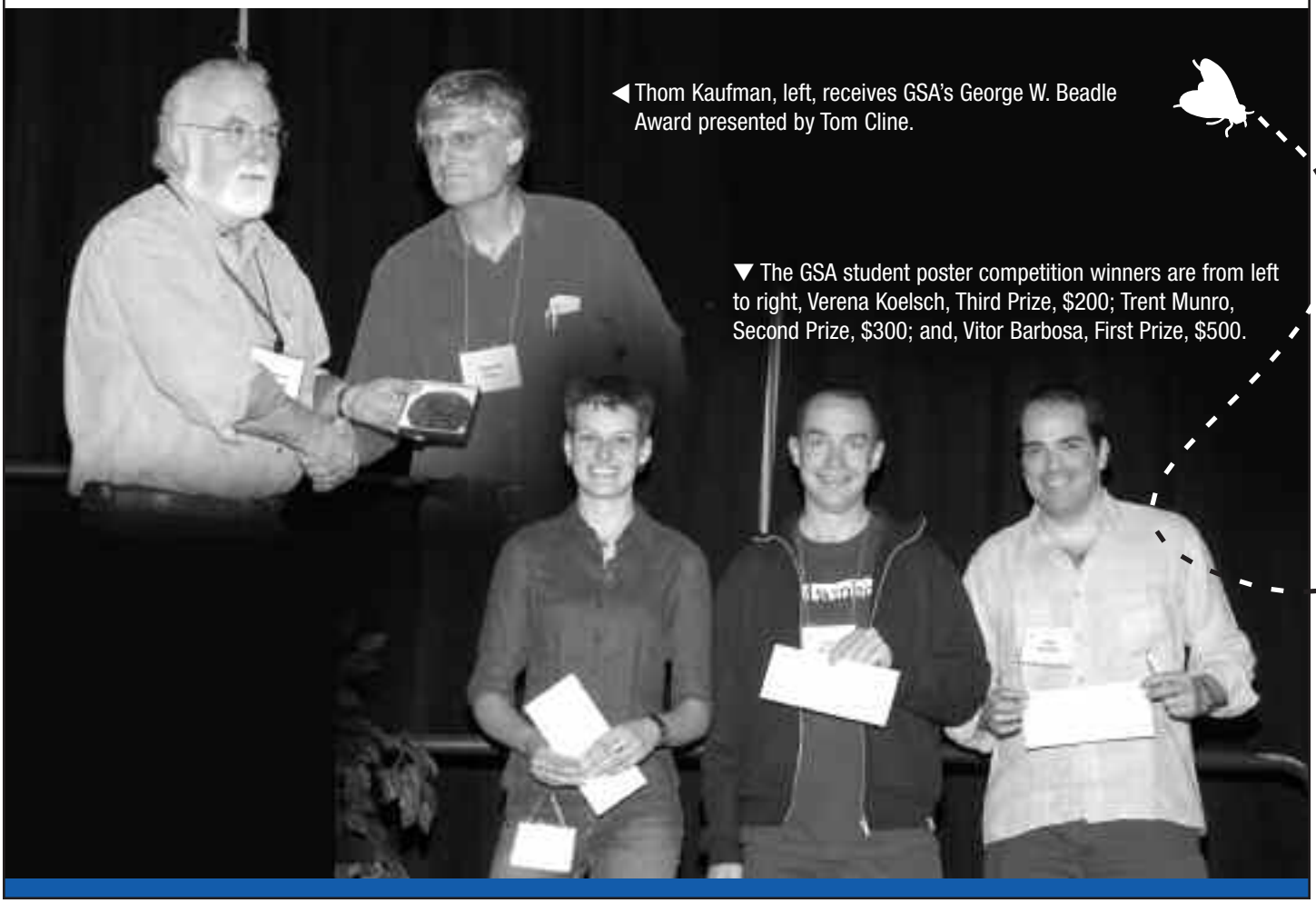
Nusslein-Volhard spoke on her Nobel Prize winning studies of the genetics of embryonic segmentation in Drosophilia. Also featured at this session was Elissa Hallem, Yale University, New Haven, CT, the 2005 Larry Sandler Memorial Lecturer whose winning thesis, carried out in the lab of John Carlson, was "The Molecular Basis of Odor Coding in the Antenna."

At the first plenary session, Tom Cline, University of California, Berkeley, presented Thom Kaufman, Indiana University, Bloomington, with the George W. Beadle Award of the GSA, for outstanding contributions to the community of geneticists. Winners in the GSA-sponsored student poster competition are: first prize, $500, Vitor Barbosa from the Skirball Institute at New York University; second prize, $300, Trent Munro from the Gurdon Institute, University of Cambridge, United Kingdom; and third prize, $200, Verena Koelsch from the Institute of Genetics, University of Cologne, Germany.

The meeting was also home to the Ecdysone Workshop held annually in conjunction with the Drosophila conference and the FlyBase Demo that was open for the entire meeting for tutorials and discussions.

For the full meeting program with abstracts, see the GSA Web site at Past Meetings at http://genetics.faseb.org/genetics/g-gsa/past_meetings.shtml.

In 2006 GSA will sponsor the 47th Annual Drosophila Research Conference, March 29-April 2, at the Hilton Americas in Houston, Texas.



◀ Thom Kaufman, left, receives GSA's George W. Beadle Award presented by Tom Cline.

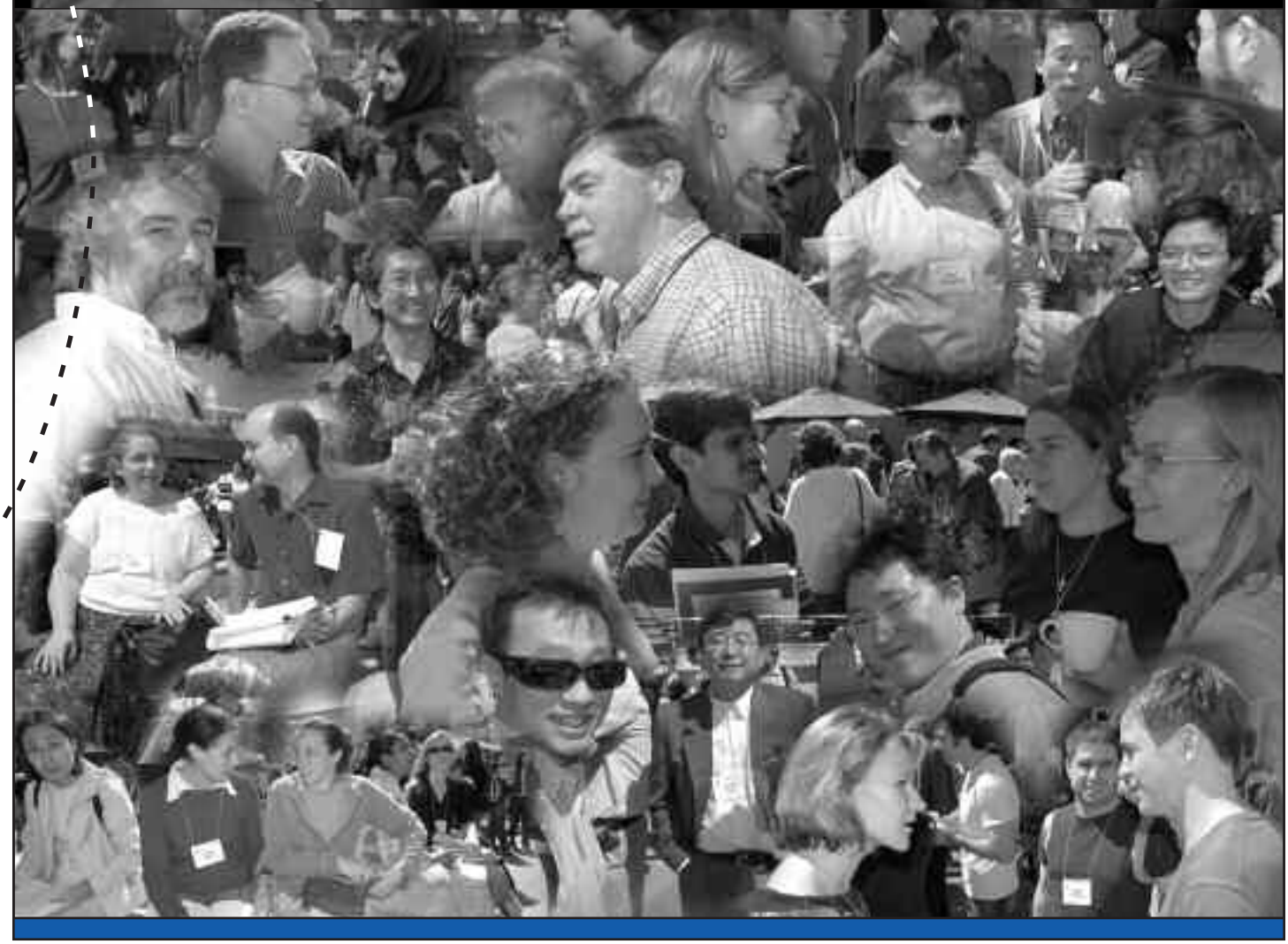
▼ The GSA student poster competition winners are from left to right, Verena Koelsch, Third Prize, $200; Trent Munro, Second Prize, $300; and, Vitor Barbosa, First Prize, $500.

▼ 2005 Organizing Committee member, Kavita Arora, University of California, Irvine, addressing the participants.

◀ 2005 Organizing Committee member, Frank Laski, University of California, Los Angeles addressing participants.

2005 Organizing Committee ▶ member, Rahul Warrior, University of California, Irvine, listens to a speaker.

Photos courtesy of Gates Photography, San Diego, CA.



Fungal Meeting Highlights

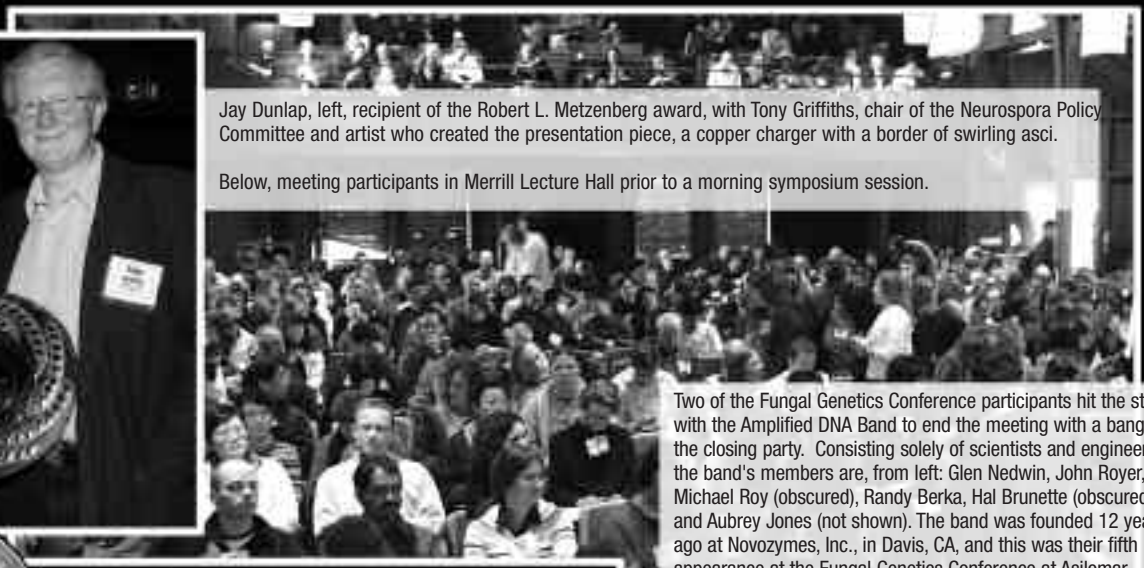
by Marc J. Orbach

Research on over 160 fungi species was featured at the 23rd Fungal Genetics Conference attended by 750 researchers from 30 countries. This biennial meeting held on March 15-20, 2005 at Asilomar, CA, included four plenary sessions covering, Genomes and Evolution, Fungal Interactions, Cell Biology and Development, and Signaling and Gene Regulation, as well as 22 concurrent sessions and over 600 poster presentations. Many reports focused on the impact the dramatic expansion of fungal genome data has had on our understanding of fungal biology issues ranging from evolution and population biology to proteomics, industrial mycology and basic fungal cell metabolism. Also included was a session on using this information in teaching, particularly at the undergraduate level.

The meeting concluded with a banquet featuring the presentation of awards. The GSA's Thomas Hunt Morgan award for lifetime achievement was given to one of the founding members of the fungal community: longtime GSA member and former GSA President (1990) Robert L. Metzenberg, University of California, Los Angeles, (formerly of UW-Madison). Former GSA President (1977) David Perkins, Stanford University, CA, the 1994 Morgan award recipient, presented the award to Metzenberg. Also unveiled at the banquet was a new award for contributions in the field of Neurospora genetics, which was named in honor of Robert Metzenberg. Jay Dunlap of Dartmouth University, NH, was the first recipient of this award.

Awards were followed by a lecture by Joan Bennett, Tulane University, New Orleans, LA, who humorously described her personal view of the history of fungal molecular genetics, which emphasized the impact of the Asilomar meeting and other such meetings on advances in fungal biology. She credited the current expansion in fungal research partly to the dramatic increase in fungal genomics.

For the full meeting program with abstracts, see the Web site at the Fungal Genetics Stock Center at http://www.fgsc.net/asil2005/asil2005.htm.



Jay Dunlap, left, recipient of the Robert L. Metzenberg award, with Tony Griffiths, chair of the Neurospora Policy Committee and artist who created the presentation piece, a copper charger with a border of swirling asci.

Below, meeting participants in Merrill Lecture Hall prior to a morning symposium session.

Two of the Fungal Genetics Conference participants hit the stage with the Amplified DNA Band to end the meeting with a bang at the closing party. Consisting solely of scientists and engineers, the band's members are, from left: Glen Nedwin, John Royer, Michael Roy (obscured), Randy Berka, Hal Brunette (obscured) and Aubrey Jones (not shown). The band was founded 12 years ago at Novozymes, Inc., in Davis, CA, and this was their fifth appearance at the Fungal Genetics Conference at Asilomar.

Robert Metzenberg, left, Joan Bennett and Dave Perkin's celebrate Bob's award of the GSA Thomas Hunt Morgan Medal for 2005 at the 23rd Fungal Genetics Conference at Asilomar.

Photos by Matthew Sachs

A Dozen Fly Genomes *compiled by William Gelbart, Doug Smith and Thom Kaufman*

This is a special time for Drosophila geneticists: The sequencing of 12 different Drosophila species is well underway, thanks to four separate National Human Genome Research Institute (NHGRI) funded initiatives. These sequences should be available within the next few months. Projects that have already produced traces and/or assembled sequences are:

D. melanogaster:

- Euchromatic Arms (Sequenced to finished quality by the Berkeley Drosophila Genome Project: http://www.fruitfly.org/)
- Heterochromatin (Draft assembly produced by the Drosophila Heterochromatin Genome Project: http://www.dhgp.org/)

D. pseudoobscura:

WGS assembly produced by the Baylor Human Genome Sequencing Center: http://www.hgsc.bcm.tmc.edu/)

D. simulans* and *D. yakuba:

WGS assembly produced by the Washington University Genome Sequencing Center (http://genome.wustl.edu/)

D. erecta, D. ananassae, D. virilis, D. mojavensis:

WGS assemblies produced by Agencourt Bioscience Corp. (http://www.agencourt.com/company/experience/nhgri/)

D. willistoni:

Traces deposited by the J. Craig Venter Institute; WGS assembly will appear shortly (see http://www.venterinstitute.org/).

Projects that are in their early stages are:

D. grimshawi:

WGS assembly to be carried out by Agencourt Biosciences Corp.

D. sechellia and D. persimilis:

WGS assembly to be carried out by the Broad Institute (see http://www.broad.mit.edu/info.html).

Rationales for these projects (except *melanogaster* and *pseudoobscura*), may be found in community whitepapers at http://flybase.net/.data/docs/CommunityWhitePapers/. They include: (1) using comparative sequence analysis to improve the annotations of *D. melanogaster*, (2) understanding genome evolution, (3) describing variation at a genome scale, and (4) investigating differences between recently diverged species that produce interfertile hybrids.

The sequencing centers, FlyBase and members of the community are collaborating to assemble, align and annotate these genome sequences, which can be accessed at FlyBase (http://flybase.bio.indiana.edu/), the AAA page (http://rana.lbl.gov/drosophila/multipleflies.html), the UCSC genome browser (http://genome.ucsc.edu/cgi-bin/hgGateway), and the UC Davis sim-yak project (http://www.dpgp.org/sim_yak/index.html). All of the genome assemblies and annotations will be deposited in GenBank and fully integrated into FlyBase and other resources. Watch FlyBase and *GENEtics* for further announcements about these efforts.

How authors can help database curators: be clear, be specific, be consistent

by Paul W. Sternberg

We all recognize that accessibility of information is crucial to our research. Those of us fortunate enough to be blessed with model organism databases (MODs) for our favorite organisms, such as The *Saccaromyces* Genome Database (SGD), Flybase, Mouse Genome Database (MGD), Rat Genome Database (RGD), The Arabidopsis Information Resources (TAIR), WormBase, The Zebrafish Model Organism Database, (ZFIN), etc., we are grateful daily. Yet, no matter which database we use, we all want more information.

How does the information get into these MODs? Much data comes from large-scale projects because such data is usually in some standard format that is relatively easy for the database curators to upload. But it is the more detailed data we covet. For example, in *C. elegans*, RNAi experiments performed by individual researchers are typically more carefully done than the large-scale screens. Yet it is the large-scale data sets that get into WormBase first. Why? Time is one reason. It can take from 10 minutes to an hour for an expert curator to deal with an individual RNAi experiment because the information about DNA sequences used, conditions and phenotypes are often buried in different sections of a paper. This "curation" process would be helped if researchers completed on-line forms describing their experiments in a standard format but in practice this simply does not get done systematically.

We could also assist curators by being more careful in including the relevant information about each experiment in our written papers (this can, and eventually will, be enforced by the journals!). For example, for DNA sequences, unique identification of a location in a genome requires a string of 30 or more nucleotides. Most databases tie information to the genome sequence, so genome coordinates are essential. Nucleotide sequences are also important for mutant sites: it can be very difficult to find Lys234, especially when the protein sequence prediction changes!

Standard nomenclatures for life-stages, anatomy, proteins, genes, phenotypes, cellular locations etc., also are very helpful. You can always use descriptors such as gene/allele/protein/phenotype to specify the entity to which you are referring (the sevenless protein, the sevenless phenotype, the sevenless gene). One can subvert the journals' requirement for brevity by packing this information into supplementary material if necessary. Our yeast colleagues' predeliction to include a strain table specifying strain, genotype, derivation and reference is to be emulated by those working with other organisms. The downside of putting this information into supplementary material is that it tends to get lost from the paper. But, it's not lost to the MOD curators, so please try to include as much of it as possible. The goal is to keep key information in the main text while maintaining brevity, but to include as much information as possible for posterity.

The bottom line: be clear, be specific, be consistent – be a MODel researcher! The curators, and future generations of colleagues will be grateful.

Elledge Receives GSA Medal

Jim Haber, Brandeis University, Walthan, MA, left, congratulates Steve Elledge, Harvard Medical School, Boston, MA, on receiving the GSA Medal for 2005, presented at a special event in his honor in Boston on January 26, 2005.

Public Policy Update

Continued from page 12

Grant Funding in Jeopardy? What You Can Do: Talk to Your Elected Officials

Support for funding increases to the NIH and NSF budgets depends on the engagement of biomedical scientists in the political process. Helping to educate lawmakers about basic research and science policy is the responsibility of the research community regardless of career level. The GSA is a founding member of the Joint Steering Committee (JSC) for Public Policy's Congressional Liaison Committee (CLC), which promotes the idea of scientific citizenship and assists scientists with their public policy efforts. The JSC has made it extremely easy for CLC members to write letters to their elected officials with their Online Advocacy Center at http://capwiz.com/jscpp/home/. Suggested text, which you can customize, is available on a variety of issues in a matter of minutes.

In addition, CLC members will be invited to participate in one of the JSC's upcoming Capitol Hill Days in which scientists meet with their elected officials on Capitol Hill. This year, the JSC will be hosting Capitol Hill Days on Wednesdays — June 15, July 27 and September 21. The JSC can also set up district meetings and/or lab visits with members of Congress during congressional district work periods when members travel back to their home districts to meet and discuss with constituents the issues that are of citizens' concern.

To deal with the growing funding crisis in biomedical research, GSA members are encouraged to join the CLC by visiting www.jscpp.org or by `contacting Matt Zonarich at mzonarich@jscpp.org or 301-347-9309. There is no cost associated with joining the CLC.

House Leadership to Allow Vote on Stem Cell Bill

The Stem Cell Research Enhancement Act of 2005, introduced in February by Representatives Mike Castle (R-DE) and Diana DeGette (D-CO), seeks to expand the number of stem cell lines that are eligible for federal funding. It proposes using embryos that were created by in vitro fertilization and otherwise would be discarded. Companion legislation was introduced in the Senate by Senators Arlen Specter (R-Pa) and Tom Harkin (D-IA).

Growing congressional and public support for federal funding of embryonic stem cell research has forced the House leadership to allow a vote on expanding embryonic stem cell research lines. The vote is expected before the July 4th recess.

Under the current federal policy, only research on those stem cell lines derived before August 9, 2001, are eligible for federal funding.

Genetic Nondiscrimination Legislation Closer to Congressional Passage

By a near unanimous vote in February, the Senate passed the Genetic Information Non-Discrimination Act. The legislation ensures the enactment of protections that would prevent insurers and employers from denying health coverage or job opportunities based on a person's genetic information. The bill also includes clear provisions for the use of genetic information for research. Companion legislation was introduced in the House by Representative Judy Biggert (R-IL). The White House supports this initiative but it faces strong opposition from special interest groups. Similar legislation passed the Senate in the last Congress, but languished in the House.

Congress to Fast Track NIH Reauthorization

Bipartisan legislation for the reauthorization of the NIH is expected to be ready for introduction in May or June, according to House Energy and Commerce Chair Joe Barton (R-TX). Reauthorization bills allow Congress to make structural and administrative changes to a government agency. The NIH was last authorized in 1993. Barton alluded to three areas he would like the bill to address. He stated his intention to give the NIH director more authority, streamline the NIH budget and institute a more transparent reporting system. Barton said "NIH's growth has resulted in an almost random collection of structures in which largely independent institutes and centers are tasked to advance research programs not in cooperation with one another but according to disease, organ systems or stage of life in which they specialize. It defies reason to believe [the 27 institutes] will produce the efficiencies that can be achieved by a logically unified structure."

Genetics Society of America

9650 Rockville Pike · Bethesda, MD 20814-3998

Public Policy Update

by Matt Zonarich, Joint Steering Committee for Public Policy

Proposed NIH & NSF Funding Disappointing

President Bush's $2.57 trillion FY 2006 budget includes a 2.1% increase ($840.3 billion) for discretionary programs; however, it is dedicated to homeland security and defense programs. All other discretionary funding will be cut 0.6%, which the President considers necessary to meet his target of halving the federal deficit within four years. Republican leadership strongly supports the President's extremely tight budget.

This tight budget has ramifications for both the National Institutes of Health (NIH) and the National Science Foundation (NSF). The Department of Health and Human Services is slated to receive a 0.5% cut in funding compared to FY 2005, although the President has proposed NIH funding to be increased by 0.7% or $196 million. Despite this increase, this is the third year in a row that the proposed NIH budget does not keep pace with the 3.5% biomedical inflation rate. The proposed budget will fund only 38,746 research project grants, 402 fewer than this year. Non-competing grants will be reduced by 658 to 27,092, down from 27,750 in 2005. It is anticipated that the NIH grant application success rate will drop to 21% in FY 2006.

Although the Senate has shown its support for the NIH by approving an amendment to the FY 2006 Budget Resolution to increase the NIH appropriation by $1.5 billion over FY 2005, the amendment does not guarantee an increase in NIH funding.

For the NSF, the President has proposed a budget of $5.61 billion reflecting a 2.4% increase ($132.2 million). A substantial portion of the proposed increase would be transferred to the Coast Guard for operating icebreaker ships that assist NSF-funded polar research. This proposed increase follows a 2005 cut of $105 million and still results in an NSF budget total that is less than the 2004 level. It is anticipated that the NSF will fund 10,010 grants in FY 2006 about 100 fewer projects than this year.

Continued on page 11