Genetics Society of America

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# From the President's desk:

It was wonderful news to hear that GSA member, Andy Fire, together with Craig Mello won this year's Nobel Prize in Physiology or Medicine for their work on RNAi in *C. elegans*. Not only does it bring great pleasure to see the deserving achievements of our colleagues recognized with this highest honor, but in addition, their work stands as yet another testimony to the important fundamental discoveries, often unanticipated, that emerge when creative, dedicated, and skillful investigators have the opportunity to explore and to pursue their curiosity. The list of all Nobel recipients in Medicine contains numerous such examples – many for discoveries related to genetics.

It is thus all the more disheartening to read reports, such as those of Mandel and Vesell (*Science* 313:1387, 2006), documenting the precipitous erosion of NIH support for funding of investigator-initiated (R01) projects over the past several years, even as the NIH budget has doubled. To quote Mandel and Vesell, "Although the total number of applications has increased annually since FY 2002, not only success rates, but also total number of grants awarded and total dollars committed persistently decreased." For example, Mandel and Vesell report that in 1999, there were 8957 submissions of new, unamended, grant applications, of which 1761 were funded at a total of $456 million. In 2005, only 970 awards were made out of 10,605 applications at a total of $351 million. The trend is similar for competing renewals. Although the reasons for this decline are many and complex, current NIH policies that have diverted increasingly larger proportions of NIH funds away from R01's toward large-scale projects including Center grants, initiatives in nanotechnology, proteomics, and other earmarked projects, of which the Roadmap is part, have certainly contributed to the problem (see Weinberg, *Cell* 126:9, 2006). There is little objective evidence to indicate that this kind of centrally planned, top-down direction is an effective mechanism for scientific discovery or progress. In contrast, investigator-initiated small research projects have been the engine that has driven scientific discovery in this country for the past half century. It has made us world leaders in science, generated key breakthroughs in biomedicine (such as Fire's and Mello's) and spurred economic opportunity and growth. This paradigm has been thoroughly tested over time and has proved its merit.

The present funding situation, with paylines near or below the 10th percentile, has taken the peer-review system beyond its effective limits. This system was never designed to make such fine distinctions among many meritorious applications and it simply is not capable of doing so. Of

*Continued on page 4*

*Published three times a year and distributed by The Genetics Society of America*

"The Abbot" has taken a well-deserved break from his column for this issue. He will return in the May 2007 issue.

# A Tribute to Gregor Mendel

*by Sehoya Cotner, University of Minnesota, Minneapolis*

On a recent Sunday afternoon at Chicago's Field Museum, a handful of patrons found a quiet place (away from the lines to see King Tut's gold) in which to reflect on something revolutionary: the story of Gregor Mendel, the "father of genetics." It was the second week of the new exhibit, "Gregor Mendel: Planting the Seeds of Genetics," and the clamor over Mendel couldn't out-compete that for the giant *T. rex* dinosaur, Sue, in the museum lobby. Yet, students of heredity and fans of the history of science were nicely rewarded by this exhibit.

The exhibit, housed in a medium-sized room at the Field Museum, consists of a sampling of paintings, photographs and scientific equipment from Mendel's day, and provides some opportunities for hands-on application of Mendel's principles. Through original notebooks and photographs visitors learn a bit about his life beyond the garden pea experiment, from his childhood as the only son of a peasant farmer, to adulthood as a scientist who painstakingly developed the foundational theories of heredity. Little is known of young Johann's formative years beyond his birth in 1822 in Northern Moravia, and his early distinction as a musician and scholar. At age twelve, he left home to begin his religious training, and took the name Gregor when he became a monk. An especially memorable anecdote involves Mendel, the teacher, throwing dried peas at sleeping students! (Unless you're ready to confront a lawsuit, this is not a teaching technique recommended today.) Mendel's microscope – the same one he used for all of that painstaking single-grain pollination – is on display, along with an apparatus for comparing magnifying abilities from different eras. For those who grow weary of garden peas, there is an unexpected surprise in the form of "Art Inspired by Genetics," including a memorable photo series of frog development in a glass flask.

Details on the intellectual environment during the 19th century are especially rich. The exhibit describes pre-Mendelian thoughts on heredity, including the work of Aristotle and Hippocrates, as well as the practice of selective breeding prior to any articulation of the principles of inheritance. In the present day, we use the term "monastic" to describe a life of austerity and seclusion, yet this description is unequal to Mendel's experience as a friar at the Abbey of St. Thomas in Brno, Moravia, (now the Czech Republic). Abbey friars formed a vibrant community of scholars, with access to contemporary books on a range of subjects.

*Continued on page 3*

## Gregor Mendel: Planting the Seeds of Genetics

### TOUR SCHEDULE

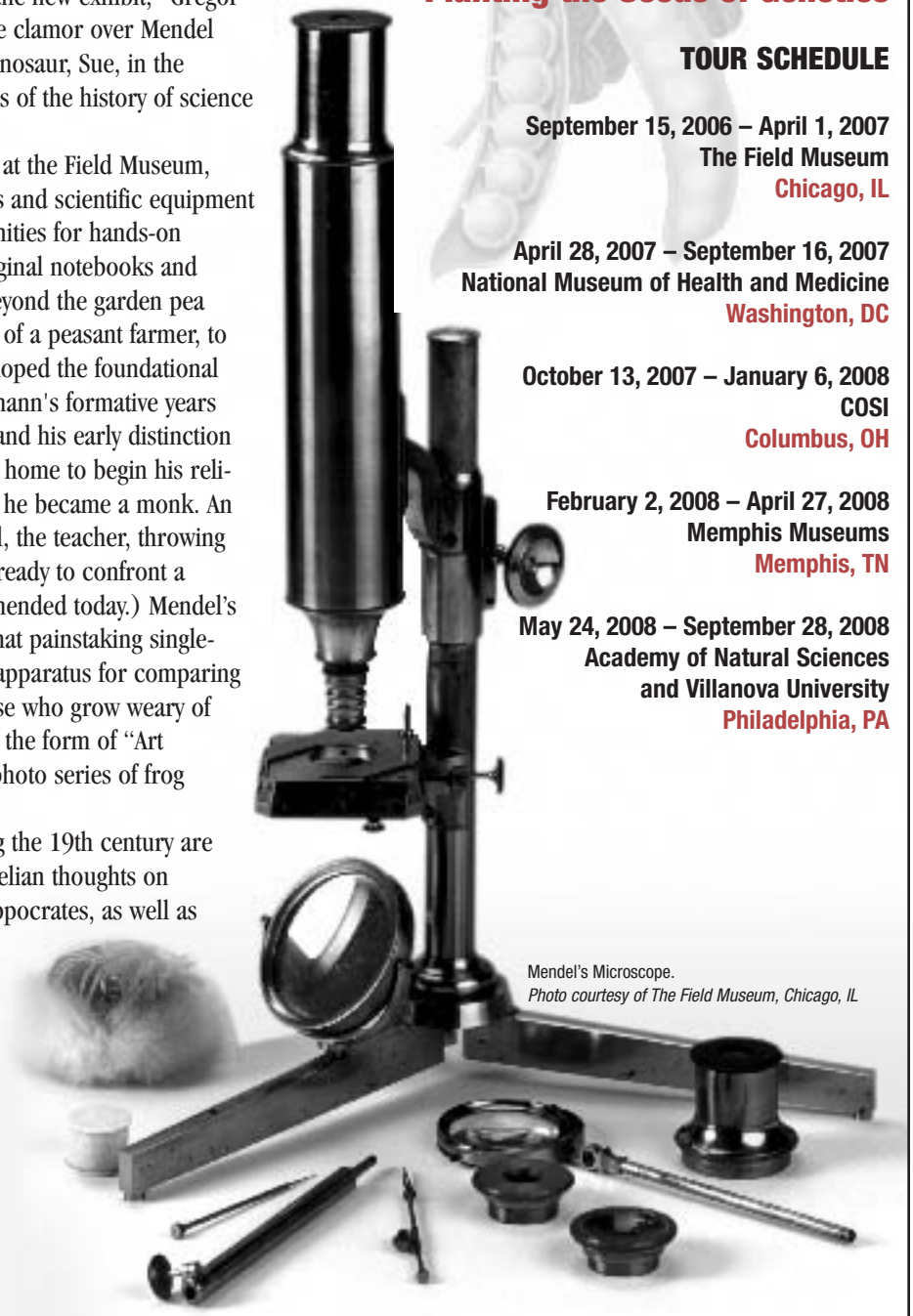
**September 15, 2006 – April 1, 2007**
**The Field Museum**
**Chicago, IL**

**April 28, 2007 – September 16, 2007**
**National Museum of Health and Medicine**
**Washington, DC**

**October 13, 2007 – January 6, 2008**
**COSI**
**Columbus, OH**

**February 2, 2008 – April 27, 2008**
**Memphis Museums**
**Memphis, TN**

**May 24, 2008 – September 28, 2008**
**Academy of Natural Sciences and Villanova University**
**Philadelphia, PA**



Mendel's Microscope.
*Photo courtesy of The Field Museum, Chicago, IL*

# Board Members for 2007 Elected

Congratulations to Trudi M. Schüpbach, Princeton University, NJ, who was elected as GSA Vice President for 2007. She will become GSA president in 2008, succeeding Allan C. Spradling, Carnegie Institution of Washington, Baltimore, MD, after his term in 2007.

Also elected as a Board officer was James E. Haber, Brandeis University, Waltham, MA, succeeding Anita K. Hopper, Ohio State University, Columbus, who completed her tenure as secretary on the Board. New directors elected to the Board this year are: Victor R. Ambros, Dartmouth Medical School, Hanover, NH; Nancy M. Bonini, University of Pennsylvania, Philadelphia; and Tim Schedl, Washington University of St. Louis, MO. These Board members replace Thomas W. Cline, University of California, Berkeley; Terry R. Magnuson, University of North Carolina, Chapel Hill; and John Harvey Postlethwait, University of Oregon, Eugene, all whose terms have ended.

The GSA congratulates and welcomes all the new Board members. In addition, the GSA wishes to thank the nearly 1,000 members who voted in this election; the outgoing Board members for their past years of service; and the Nominating Committee, chaired by Susan Lindquist, Whitehead Institute, Cambridge, MA; and with members William Dove, University of Wisconsin, Madison; David Begun, University of California, Davis; and Anita Hopper, *ex officio*, for the slate of officers they developed.

## New Board Members for 2007

Allan C. Spradling
President 2007

Trudi M. Schüpbach
Vice-President 2007

James E. Haber
Secretary

Victor R. Ambros
Director

Nancy M. Bonini
Director

Tim Schedl
Director

# A Tribute to Gregor Mendel

*Continued from page 2*

The Abbey's library is depicted in a wall-sized photomural in the exhibit, from which one can appreciate the likely sources of Mendel's ideas on the use of mathematics to understand biological phenomena.

It is unlikely this exhibit will have the extended appeal of those of King Tut and *T. rex*, nor will geneticists find the scientific explanations very illuminating. The interactive elements are best suited to advanced middle and high school students, and possibly beginning college students. But the collection has an appeal to patrons wanting to feel a greater connection to the friar who has become a legend. It's difficult not to be moved by the story of Gregor Mendel, who rose far above his birthright as a farmer's son, to become a highly educated, literate man of science. And how evocative to have his groundbreaking work ignored for decades past his death! Perhaps there is some justice in this sort of homage more than a century after his original work.

*"Gregor Mendel: Planting the Seeds of Genetics" is on display at The Field Museum of Chicago through April 1, 2007. For more information on the exhibit at the Field Museum, visit http://www.fieldmuseum.org.*

The Abbey Library. *Photo courtesy of The Field Museum, Chicago, IL*

# Preparations Underway for DNA Day 2007

*by Kenna Shaw, ASHG/GSA Education Director*

April 25, 2007 will mark the fifth annual celebration of National DNA Day. Each year GSA collaborates with the American Society of Human Genetics (ASHG) and the National Human Genome Research Institute (NHGRI) to coordinate genetics speakers in K-12 classrooms across the country. Geneticists, who are members of the ASHG/GSA Mentor Network, are contacted in early spring and paired with a teacher in their community who requests a geneticist to speak in the classroom. ASHG and NHGRI have developed resources to assist speakers in designing their presentations to fit the specific grade level and state standards they might need to address. Please help excite future generations of scientists about our field by becoming a part of the ASHG/GSA Mentor Network. Add your name to our growing list of potential speakers by visiting www.GenEdNet.org and following the links to "Mentor Network" and "Outreach to Teach," or contact the ASHG/GSA Education Director Kenna Shaw at kshaw@ashg.org.

Another way for geneticists to participate in DNA Day is to serve as judges for the DNA Day Essay Contest. This contest, now in its second year, is open to students in grades 7-12. All submissions and scoring are completed online, making judging very easy. The deadline for receipt of essays is March 16, 2007; help with judging will be needed in the few weeks after that. The two questions for this year's contest are:

1) If you could be a human genetics researcher, what would you study and why?

2) In what ways will knowledge of genetics and genomics make changes to health and health care in the U.S possible?

If you are interested in being a judge, please send a message to kshaw@ashg.org for more information.

Becoming a mentor or an essay contest judge are great ways to become involved in GSA and your community! We are looking forward to DNA Day and hope you will join our efforts to promote the exciting advances in genetics.

# From the President's desk:

*Continued from page 1*

additional concern to many members of our community, the composition and character of the newly re-constituted study sections have produced an orientation that is not favorably disposed toward research on simple model organisms such as yeast, worms, and flies. This situation is especially difficult to understand in light of the many fundamental contributions studies on these organisms have made, not only to basic science, but also to understanding human biology and disease. Elimination of the Genetics Study Section, whatever its original rationale, has proven to be an ill-considered decision that has been harmful to many investigators in our field. The overall climate is having a devastating and demoralizing impact on new as well as established investigators. Many top graduate students and post-doctoral trainees are beginning to re-evaluate their career plans and decisions because of what they see happening to their mentors and because they perceive dim prospects for future support of basic research. Unless these disturbing trends are reversed soon, it can only be to the detriment of scientific progress in this country and to the health and welfare of its citizens.

On behalf of its members, the GSA leadership has expressed these concerns in response to a request from NIH for input concerning new Roadmap initiatives. We strongly urge that new Roadmap funding be maximally directed for R01 support, particularly for basic research on model organisms and we emphatically call upon the leaders of NIH to recognize, value, defend, and support a vigorous program of basic research and discovery through investigator-initiated projects. This paradigm, which has served the United States so well for so long needs to be sustained and nourished. The GSA welcomes the opportunity to work together with the NIH leadership to achieve our common goals.

Sincerely,

Barry Ganetzky
Past President (2006)

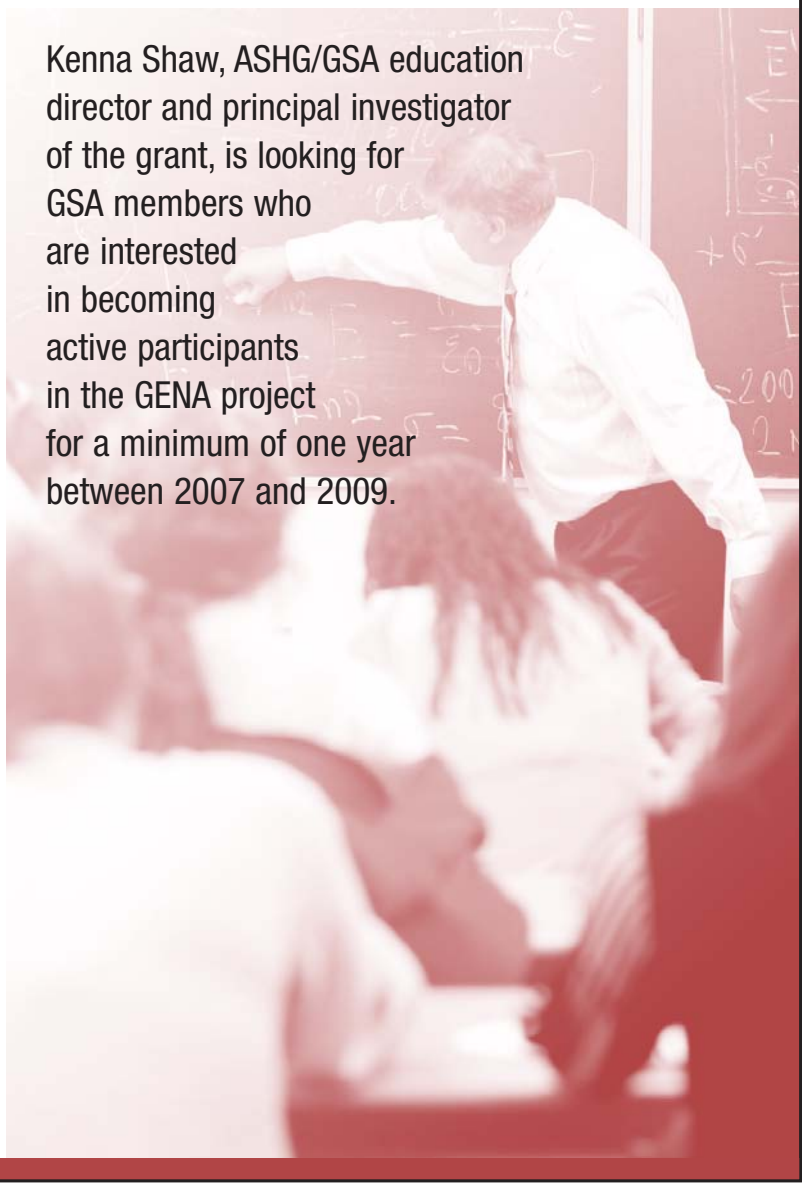
# GENA Receives NSF Funding

*by Kenna Shaw, ASHG/GSA Education Director*

The GSA is proud to announce that in partnership with three other professional scientific societies, it has received a $1.1 million grant from the National Science Foundation (NSF) for the Geneticist-Educator Network of Alliances (GENA) project. The grant provides three years of funding for a project designed to develop a model for establishing long-term collaborations between high school science teachers and genetic scientists and an infrastructure to support meaningful scholarship by scientists in the high school classroom.

The GENA project grew out of NSF's concern that institutions of higher learning may not pay enough attention to the scholarship of teaching and learning among scientists, particularly when these activities take bench scientists away from their laboratories and into K-12 classrooms. Consequently, the objectives of this project include exploring ways in which a secondary science education outreach effort, monitored by professional scientific societies, can positively enhance career development of junior (pre-tenure) and as well as senior genetics faculty. In addition, by pairing geneticists with high school teachers within their local community, each team of a geneticist and teacher will design teaching materials in genetics education for secondary students that are in line with their state education standards and that address common misconceptions about genetics.

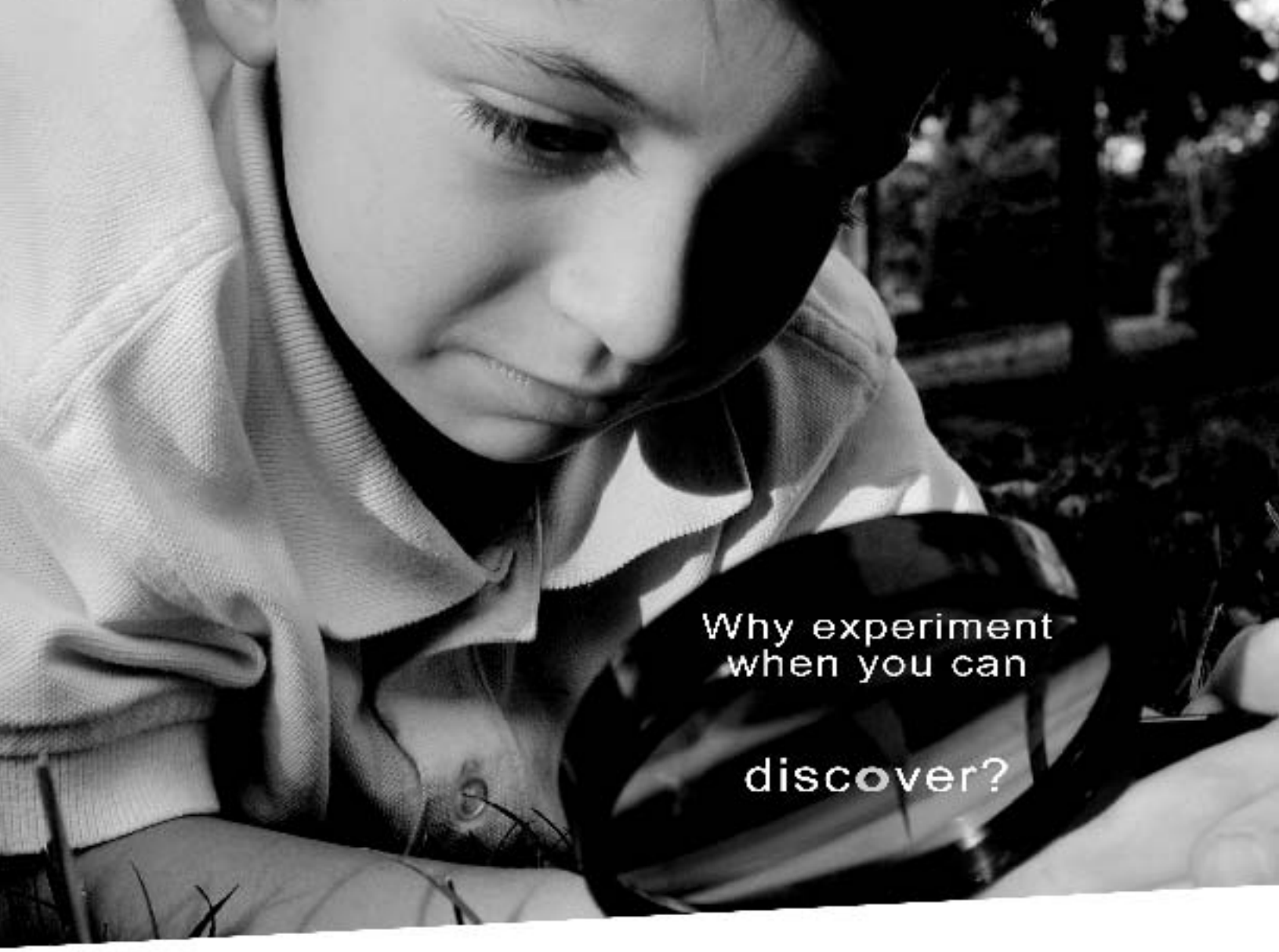
Kenna Shaw, ASHG/GSA education director and principal investigator of the grant, is looking for GSA members who are interested in becoming active participants in the GENA project for a minimum of one year between 2007 and 2009. During this period, 92 geneticist-educator alliances will be developed (184 participants). To gauge the impact this program has on the institutional policies at schools of higher education, participating geneticists must be a faculty member in a science department at a tenure-granting institution.




Participants in GENA, both scientists and teachers, will attend a two and one-half day training workshop, which will provide them with tools to instruct, facilitate and measure the effect of their participation in a secondary school science classroom. In subsequent years, these teams will serve as training leaders within their school districts so that the innovative teaching programs they develop can be easily used by other geneticists, resulting in the maximum effectiveness of their interaction with high school students.

In addition to developing genetic education lesson plans, the teams, along with the GENA project professional staff, will make presentations at national meetings of their partner societies and co-author articles for publication in journals to communicate their experiences to other scientists. Resources and ideas developed by these teaching teams will also be disseminated through the project's website.

If you are interested in applying to participate in the GENA project or in learning about what involvement will entail, please contact Kenna Shaw at kshaw@ashg.org in the ASHG/GSA Education Office.

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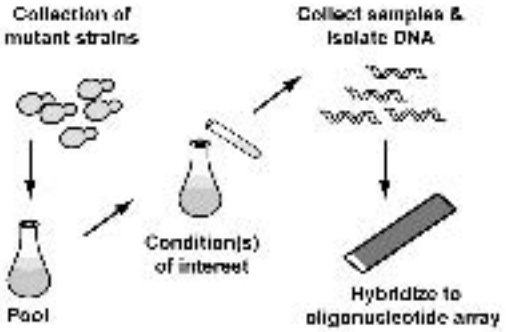
[1]Tong et al (2001) *Science* **294**, 2364–2368
[2]Pan et al (2004) *Molecular Cell* **16**, 487–496

Whole-Genome Parallel Analysis

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**Bob Metzenberg**, the 2005 winner of the GSA's Thomas Hunt Morgan Award for lifetime contributions to genetics, had a long and very productive career studying nutrient acquisition and utilization in Neurospora (see *GENETICS*, Vol. 169, 503-505 2005 for a brief summary). Several years ago he retired from his academic position, but not from his research. Here he describes what many of us might look forward to.

# Research in Your Retirement House

*by Robert L. Metzenberg, Department of Biology, California State University-Northbridge*

Retirement can be one of the most productive and satisfying times of your scientific career. All you need is a spare, dedicated room, an understanding and patient companion, neighbors who don't suspect you of brewing up anthrax bacilli, and a small amount of money. I have benefited greatly from a small NSF Grant, but the setup cost for a workspace at home was necessarily borne out of pocket. It compared favorably with that of a weekend for two with golf at a comfortable to pricey resort. The largest continuing cost that must be borne personally, even if you have a grant, is electricity used by the freezer(s). (The latter are best kept in the garage where they do not become heat-sources fighting the indoor air conditioning.) Disposable supplies are comparable in cost to an occasional evening out at a restaurant and a movie. You do need to maintain a nominal institutional connection of some sort, purely to give you access to library, electronic resources, and purchasing of chemicals.

Do not be shy about doing a bit of dumpster-diving at an institution near you. A great deal of shopworn but serviceable equipment ends up at the curb when a professor retires or changes institutions, simply because storing the equipment in expensive space is even less economical than discarding it. A friend at the institution can alert you when this is about to happen. Younger people will see you as a harmless eccentric, but their consciences will be eased by knowing that some use is being made of the equipment. In other words, you are doing them a favor.

While the five-second commute and the possibilities of either a 10-minute or 10-hour workday are welcome, the biggest change is to one's way of thought. During our employed lifetimes, we must meet payroll, get grants for fundable research and renew them, and point student and postdoctoral personnel toward sure-fire projects that will produce publishable results. Until these constraints are suddenly removed, it is difficult to realize how severely they limit our ability to follow up high-risk, high-payoff ideas.

Employees also eat up time. Keeping an industrious technician busy and happy takes more time and energy than is commonly realized. As I look back over my notebooks, I am struck by how much of my time was spent designing, recording, and interpreting experiments that kept my technician from getting depressed, but yielded little in terms of real information. A retiree, though, has no need for busy-work since there is always more than enough to do around the house. The result, I am finding, is that experiments done in retirement often have a higher density of useful information than those done during one's years of employment.

Finally, there is the matter of defending a turf. Every department seems to house at least one "colleague" who is aggressively trying to build an empire. If you are temporarily over-endowed with space, it can be difficult to prevent encroachments and, more important, even more difficult to reclaim this space when you really do need it again. Hence you must spend time and effort to make all your space look occupied and busy. Thinking back to those times, I can't help noticing how much of my own activity resembled that of a wolf or a hippo marking territory against incursions by conspecific animals. Presumably in one's own house, this is completely unnecessary.

Consequently, the plusses of doing research at home are far greater than any minuses and the results are conclusive: retirement is highly recommended!

*This is the first of what we hope will be a periodic column on career trajectories and opportunities. We invite your contributions. Please send them to pedelman@genetics-gsa.org.*

# A Conversation with John Carlson

GSA member John R. Carlson is the Eugene Higgins Professor of Molecular, Cellular and Developmental Biology in the MCDB Department at Yale University in New Haven, CT. Carlson, whose lab is supported by the NIH and a five-year Grand Challenge in Global Health Initiative grant funded by the Bill and Melinda Gates Foundation, recently spoke to *GENEtics* about his work, his ties to GSA and advice he would give to students.

*GENEtics*:

*Was there any particular person or event that got you interested in genetics and in particular, olfaction in flies?*

**John R. Carlson:** My first exposure to genetics was in the summer research program at the Jackson Lab in Bar Harbor, ME. Then as an undergrad at Harvard I did bacterial genetic research with Wally Gilbert.

I was a grad student with Dave Hogness at Stanford. I learned a great deal from Dave, had a wonderful time, and developed a deep appreciation for flies. I also became intrigued by the elegant behavioral genetics done by Seymour Benzer and read all his articles.

I started thinking about olfaction while a grad student in Hogness' lab. Hundreds of researchers were working on the fly's visual system, but the only lab I could find that was working on its olfactory system was Obaid Siddiqi's lab in India. I spent a couple of weeks visiting him in India, and he was very generous and encouraging.

*GENEtics*:

*I read in an article about you and your work and it said you worked on flies as a grad student and then switched to yeast and then when you came to Yale you switched back to* Drosophila*. Why did you do this?*

**John R. Carlson:** I was planning on working on *Drosophila* as a postdoctoral fellow, but my last year of grad school I had an idea that I was very excited about and that could best be explored in yeast, so I stayed at Stanford in Irv Weissman's lab and worked on yeast. Through great luck, Lee Hartwell was on sabbatical in the lab and I learned an enormous amount from him. Yale knew when they hired me that I would start work on a new system in which I had no experience whatsoever – fly olfaction. In retrospect, switching to a new system as a beginning assistant professor was risky, and I was lucky that things worked out as well as they did. Risk-taking is even more difficult today, but on the other hand, I think it's important to work on something you're excited about.

*GENEtics*:

*Can you explain briefly the research that's going on in your lab now?*

**John R. Carlson:** Our lab studies both olfaction and taste in *Drosophila*. We identified two families of 60 genes each, the *Or* genes and the *Gr* genes, which encode odor and gustatory receptors. We've analyzed these genes to understand how the fly encodes chemosensory information. We developed an *in vivo* functional expression system to identify the ligand specificities of individual odor receptors. A mutation that deletes two adjacent *Or* genes is used to eliminate the response of a particular neuron to all tested odors. This "empty" neuron is used as a "decoder": we introduce into it another receptor gene and determine the odor specificity conferred by the transgenic receptor. This allows systematic investigation of the odor receptor repertoire. Some receptors respond strongly to many of the tested odors, and others respond strongly to only one or none. Likewise, some odors strongly activate many receptors, and some odors activate only one. This work has allowed us to gain some understanding of how the fly encodes odors. It also allowed us to deduce which receptors are expressed in which types of neuron in the antenna and thus to establish a receptor-to-neuron map of the olfactory system.

We've extended this approach to express odor receptors from the malaria vector mosquito *Anopheles gambiae* in *Drosophila*. We found that the female-specific receptor AgOr1 responds to 4-methylphenol, a component

of human sweat. We're now identifying ligands for other mosquito receptors using the empty neuron system. Some odors that potently activate or block mosquito receptors could be useful as attractants in mosquito traps or as repellents. So we hope that basic research in *Drosophila* will lead to new means of controlling malaria, of which there are 500 million clinical cases a year.

*GENEtics*:

*When you started working on insect olfaction were you aware of all the practical/clinical applications of your research?*

**John R. Carlson:** Yes, I realized that insects transmit diseases to hundreds of millions of people each year and that they cause enormous agricultural damage. Since these insects find their human and plant hosts largely through chemosensory cues, it seemed that basic research in *Drosophila* olfaction might eventually be applicable to the real world.

*GENEtics*:

*Were there any "Aha!" moments during your research?*

**John R. Carlson:** It was very exciting when we realized that we'd identified what were surely insect odor receptor genes. We and many others had been searching for them for many years, in many insects, using many strategies, so to all of a sudden see them looking up at us was quite exhilarating.

And it was a thrill to discover the taste receptor genes, which were found by Peter Clyne, a superb student. Peter found them just days before he was scheduled to finish and leave on a trek in the Himalayas. The allure of these genes proved more seductive than the lofty peaks of Nepal, so he cancelled the trip and explored taste reception instead.

*GENEtics*:

*How important is teaching/mentoring to you?*

**John R. Carlson:** I teach an intro course, "Principles of Molecular, Cellular and Developmental Biology" to about 200 freshmen and sophomores. I enjoy explaining things that I find elegant or intriguing and it's very rewarding when students get excited about them too. I think it's terribly important to keep genetics thriving as a field and to get both undergraduate and graduate students interested in it. I've had terrific graduate students at Yale and feel very lucky to be here.

*GENEtics*:

*If you could offer one bit of advice to these students and to up and coming scientists, what would it be?*

**John R. Carlson:** I think it's important to learn several different approaches to solving biological problems. The goal is not just to gain different technical skills, but to gain intellectual skills – to learn different ways of thinking about biological problems. A student's education should be interdisciplinary – in addition to genetics it should also include some other fields such as molecular biology, computational biology, physiology, or behavior. Mastering several different approaches also gives students the courage and confidence to adopt new approaches when they need them later in their careers.

*GENEtics*:

*Why did you join GSA and why do you continue to be a member?*

**John R. Carlson:** I joined GSA shortly after becoming a faculty member at Yale, around 1986. I thought then and still do that it's an excellent organization. One reason I've renewed my membership year after year is that the fly meetings are terrific. A second reason is that I like to settle down on the couch once a month and leaf through a hard copy of *GENETICS*. I always learn something interesting from the research articles, and I often enjoy the historical commentaries such as the ones by James Crow. A third reason is that I like to support an organization that accurately represents my views on issues such as government funding for research, the teaching of evolution, and stem cell policy. Our elected officials need to hear from scientists and not just from corporate and religious interests. Finally, I want to support genetics as an intellectual discipline. I want my students to know not only the molecular definition of a null allele, but also the genetic definition developed by fly geneticists. There is a long and venerable intellectual tradition of genetic research, and I feel that the GSA helps preserve it.

*GENEtics*:

*Where does your research go from here?*

**John R. Carlson:** I've been working on fly olfaction for 20 years and have always felt that intriguing questions are just coming into view. We still know very little about how the responses of neurons in the antennae translate into behavior. And it would be wonderful if work in the fly could lead to a new way of helping people in Africa avoid malaria.

*GENEtics*:

*Did you ever imagine as a child that you would be working with flies?*

**John R. Carlson:** When I was very young I wanted to be a zookeeper. Now, many years later I find myself in charge of a different kind of zoo – a zoo of odd *Drosophila* stocks.

# FlyBase: New and Improved!

*by Thom Kaufman, Indiana University, Bloomington, and Bill Gelbart, Harvard University, Cambridge, MA on behalf of FlyBase*

The FlyBase Consortium is pleased to announce a completely new web interface and integrated database for exploring the genes and genomes of *Drosophila*. The first official version of the New! FlyBase (FB2006_01) is accessible through http://flybase.org/.

The website contains a completely new design intended to simplify navigation with "Matryoshka" nested subreports (named for the Russian nested dolls) that can be toggled open or shut, and a simpler menu of options for querying the data.

Simple QuickSearch and Google entry forms provide direct query access to the major FlyBase datasets. Other major entry points to the sequenced *Drosophila* genomes (BLAST and GBrowse) and genes (TermLink, QueryBuilder and ImageBrowse) are represented with icons on the home page. The BLAST facility allows similarity searches for all sequenced insect genomes. For the 12 fully sequenced *Drosophila* species, BLAST results are directly connected to the convenient GBrowse genome browser, where one can view all sequence-level data that are aligned to a particular segment of each genome. These data in turn are linked to various sections of FlyBase, that report on genes, alleles, transgene insertions, transcripts, proteins, and many other features of the genome.

Alternative and generally more powerful entries into FlyBase datasets are provided by QueryBuilder, TermLink and ImageBrowser. TermLink permits the user to access datasets by migrating through hierarchically organized FlyBase controlled vocabularies such as the Gene Ontology lists, and anatomy, development and phenotypic classifications. ImageBrowser provides graphical access to *Drosophila* anatomy and developmental stages, and then to TermLink. QueryBuilder is a powerful interface for carrying out complex queries of the many FlyBase datasets and can be used to answer more involved questions. For those who wish to carry out their own data analysis, the entire database underlying the website and various precomputed files are available for downloading.

In coming months, FlyBase will be refining the website according to feedback from the community. Moreover, additional datasets for the new species' sequenced genomes, for transcriptional arrays, cell-based RNAi phenotypes and macromolecular interactions will be integrated into FlyBase.

We encourage all interested geneticists to explore FlyBase and provide feedback on problems or suggestions to improve it. Please use the data entry web form at http://flybase.org:7055/cgi-bin/mailto-fbhelp.html or e-mail flybase-help@morgan.harvard.edu.

# A Dozen Fly Genomes: an Update

*by Bill Gelbart, Harvard University, Cambridge, MA and Thom Kaufman, Indiana University, Bloomington, on behalf of the 12 Fly Genomes Coordinating Committee*

The initial community analysis of 12 sequenced *Drosophila* species' genomes is coming to closure. All assemblies are now in GenBank, with reference alignments and annotation. Other canonical datasets for the initial analysis are also available. We urge members of the community to share the use of these canonical datasets so that the results of independent analyses can be readily integrated and compared.

Two papers summarizing the major results of the initial analysis are currently being prepared: one focuses on the use of comparative analysis to annotate the *Drosophila melanogaster* genome; the other on understanding gene and genome evolution through comparative analysis. It is anticipated that the community will submit companion papers to various journals, including *GENETICS*, concurrently with the submission of the two main papers.

We are grateful to Michael Eisen, Univ. of California, Berkeley, and his colleagues for setting up the AAA website (Assembly/Alignment/Annotation: <http://rana.lbl.gov/drosophila/>) that serves as a clearinghouse for accessing the canonical datasets. See the News section of FlyBase for updates to plans for publication and for contact information, the most recent is entitled "Community Genome Papers": http://flybase.org:7055/static_pages/news/articles/2006_11/genomes_papers.html.

# Upcoming GSA Meetings

**Mark your Calendars**


## Mark your calendar now for several GSA meetings coming up in 2007 and 2008.

**48th Annual Drosophila Research Conference** will be held **March 7-11, 2007** at the Philadelphia Marriott Hotel in Pennsylvania. There's still time to send in late abstracts, register for the conference and reserve hotel space. Note the deadlines below:

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|---|---|
| January 22, 2007 | Deadline for late abstract submission. (Note: Late abstracts will only be assigned poster presentations and given space in the back of the poster area, not in the requested area of interest. Late abstracts will not be available in the Abstract book or through the searchable online database.) |
| February 2, 2007 | Deadline for Early Conference Registration. (Registration fees increase after this date.) |
| February 7, 2007 | Deadline for Hotel Reservations |

Spyros Artavanis-Tsakonas, Ph.D., Harvard Medical School, Massachusetts General Hospital Cancer Center, will be presenting the historical address. Other highlights include The Larry Sandler Memorial Lecture, a dozen plenary talks, and awards to students and postdocs for the best poster presentations.

Program Chairs are Steve DiNardo, University of Pennsylvania, Philadelphia; Liz Gavis, Princeton University, NJ; Tom Jongens, University of Pennsylvania; and Jessica Treisman, New York University, NY.

For information about the meeting, visit the GSA website at http://www.drosophila-conf.org/genetics/gsa/dros/dros2007/.

**24th Fungal Genetics Conference** will be held from **March 20-25, 2007** at the Asilomar Conference Center, Pacific Grove, CA. All deadlines – abstract submission, meeting and housing registration – for the conference have passed. Four sets of concurrent sessions, for a total of 25 sessions are planned. June Kwon-Chung, National Institutes of Health, NIAID, will be presenting the Invited Lecture on Saturday evening.

Barbara Howlett, The University of Melbourne, Australia, and Joseph Heitman, Duke University Medical Center, Durham, NC are the scientific program co-chairs.

For information about the meeting, visit the GSA website at http://www.genetics-gsa.org/genetics/fungal-conf/.

**16th International *C. elegans* Meeting** will be held **June 27-July 1, 2007** at the University of California, Los Angeles campus. Abstract submission and meeting registration will open in February. See important dates below:

| | |
|---|---|
| February 16, 2007 | Abstract submission site opens |
| February 21, 2007 | Meeting registration opens; Housing registration opens |
| March 22, 2007 | Abstract submission closes |
| May 1, 2007 | Financial Aid Application deadline |
| May 25, 2007 | Meeting registration closes |
| May 26, 2007 | Housing reservation closes |

Gary Ruvkun, Massachusetts General Hospital and Harvard Medical School will provide the Keynote Address. Other features of the meeting include the Worm Art Show, organized by Ahna Skop, University of Wisconsin, Madison, a student mentoring luncheon and a faculty mentoring social organized by senior *C. elegans* faculty for current and new junior faculty members.

Meeting co-organizers are Victor Ambros, Dartmouth Medical School, Hanover, NH; Anne Hart, Massachusetts General Hospital and Harvard Medical School; and Alex van der Bliek is the local organizer at the University of California, Los Angeles.

For information about the meeting, visit the GSA website at http://genetics.faseb.org/genetics/Celegans/2007meeting/.

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# From the December Issue of *GENETICS*

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

Here are article highlights from the December 2006 issue of *GENETICS.* Read the full text at http://www.genetics.org/current.shtml.

### ***emb-4*** **is a conserved gene required for efficient germline-specific chromatin remodeling during** ***Caenorhabditis elegans*** **embryogenesis**

Authors: Paula M. Checchi and William G. Kelly and

### **EMB-4: A predicted ATPase that facilitates** ***lin-12*** **activity in** ***Caenorhabditis elegans***

Authors: Iskra Katic and Iva Greenwald

The establishment and maintenance of the embryonic germline is essential for fertility of the adult and hence maintenance of the species. Repressive mechanisms provide this maintenance in many organisms, including *Caenorhabditis elegans*. One mode of repression in *C. elegans* germ cells involves chromatin remodeling, and this requires the gene *emb-4,* which encodes a highly conserved protein with orthologs in fly, mouse, and human. The embryonic phenotype of *emb-4* mutants is consistent with a defect in the efficient and timely activation of developmental programs, including germline chromatin remodeling. The *emb-4* gene encodes a conserved nuclear-localized ATPase that functions cell autonomously to enhance LIN-12/Notch signaling.

### **Centromere-proximal crossovers are associated with precocious separation of sister chromatids during meiosis in** ***Saccharomyces cerevisiae***

Authors: Beth Rockmill, Karen Voelkel-Meiman and G. Shirleen Roeder

In virtually all eukaryotes, the frequency of recombination is reduced near the centromere, as might be expected if centromere-associated crossovers have deleterious effects on meiotic chromosome segregation. Indeed, studies in humans and *Drosophila* demonstrate that centromere-associated crossovers predispose chromosomes toward meiotic missegregation events that are the equivalent of meiosis II nondisjunction. In budding yeast, centromere-associated meiotic crossovers are also associated with meiotic chromosome missegregation, in this case with premature separation of sister chromatids (PSSC). The authors propose an elegant model in which crossovers disrupt structures that are essential for meiotic centromere function. This model can account for the differing meiotic defects caused by centromere-associated crossovers in different species.

### **Chemical inactivation of Cdc7 kinase in budding yeast results in a reversible arrest that allows efficient cell synchronization prior to meiotic recombination**

Authors: Lihong Wan, Chao Zhang, Kevan M. Shokat and Nancy M. Hollingsworth

A chemical genetic approach was used to create a novel conditional allele of the highly conserved protein kinase Cdc7 (*cdc7-as3*) that enables cells to be synchronized immediately prior to recombination. When Cdc7-as3 is inactivated by addition of inhibitor to sporulation medium, cells undergo a delayed premeiotic S phase, then arrest in prophase before double-strand break (DSB) formation. The arrest is easily reversed by removal of the inhibitor, after which cells rapidly and synchronously proceed through meiosis. Using the synchrony resulting from the *cdc7-as3* system, DSB-dependent phosphorylation of the meiosis-specific chromosomal core protein, Hop1, was shown to occur after DSBs. The *cdc7-as3* mutant provides a valuable tool both for understanding the role of Cdc7 in meiosis and for facilitating studies of recombination.

### ***roX*** **RNAs are required for increased expression of X-linked genes in** ***Drosophila melanogaster*** **males**

Authors: Xinxian Deng and Victoria H. Meller

The male-specific lethal (MSL) ribonucleoprotein complex is necessary for equalization of X:A expression levels in *Drosophila* males, which have a single X chromosome. The MSL complex binds selectively to the male X chromosome and directs acetylation of histone H4 at lysine 16. *roX1* and *roX2* noncoding RNAs are essential but redundant components of this complex. Simultaneous removal of both *roX* RNAs reduces X-localization of the MSL proteins and permits their ectopic binding to autosomal sites and the chromocenter. Microarray

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analysis revealed that the loss of the *roX1* and *roX2* RNAs resulted in a decrease in X chromosomal gene expression, but did not enhance gene expression at autosomal sites of MSL binding. These results indicate that it is the failure to compensate X-linked genes, rather than inappropriate upregulation of autosomal genes at ectopic sites of MSL binding, that is the primary cause of male lethality upon loss of *roX* RNAs.

### Enhancer–promoter communication at the *yellow* gene of *Drosophila melanogaster*: Diverse promoters participate in and regulate trans interactions

Authors: Anne M. Lee and C.-ting Wu

The *yellow* locus of Drosophila is useful for investigating the mechanisms of *trans* interactions due to its ability to support transvection and the relative ease with which it can be altered by targeted gene replacement. Through the analysis of *yellow* alleles whose promoters have been replaced with wild type or altered promoters from other genes, the authors show that mutation of single core promoter elements of two of the three heterologous promoters tested can influence whether *yellow* enhancers act in *cis* or in *trans*. This finding parallels studies of the *yellow* promoter, suggesting that the manner in which *trans* interactions are controlled by core promoter elements describes a general mechanism. The authors further demonstrate that heterologous promoters can themselves be activated in *trans* as well as participate in pairing-mediated insulator bypass. These results highlight the potential of diverse promoters to partake in many forms of *trans* interactions.

### Structure–function analysis of Delta trafficking, receptor binding and signaling in *Drosophila*

Authors: Annette L. Parks, Jane R. Stout, Scott B. Shepard, Kristin M. Klueg, Ana A. Dos Santos, Todd R. Parody, Martina Vaskova and Marc A. T. Muskavitch

The transmembrane proteins Delta and Notch act as ligand and receptor in a conserved signaling pathway required for a variety of cell fate specification events in many organisms. The binding of Delta to Notch results in a proteolytic cascade that releases the Notch intracellular domain, allowing it to participate in transcriptional activation in the nucleus. While the Delta N-terminal domain is necessary and sufficient for binding to Notch, the integrity of epidermal growth factor-like repeat (ELR) 2 is also required for Notch binding. Screening of 117 *Delta* mutant lines for proteins that exhibit aberrant subcellular trafficking has led to the identification of 18 *Delta* alleles, most of which result from missense mutations in ELRs within the Delta extracellular domain that encode "trafficking-defective" Delta proteins. However, the authors also find that two $Dl^{rp}$ alleles contain lysine missense mutations within the Delta intracellular domain (DeltaICD) that may identify residues important for Delta endocytosis and signaling.

### The X chromosome in quantitative trait locus mapping

Authors: Karl W. Broman, Śaunak Sen, Sarah E. Owens, Ani Manichaikul, E. Michelle Southard-Smith and Gary A. Churchill

Most quantitative trait locus (QTL) mapping methods, including widely used computer packages, fail to account for the fact that the X chromosome requires special treatment in the mapping of QTL. In this article the authors develop a method for appropriate treatment of the X chromosome for QTL mapping in experimental crosses. They show that if the X chromosome is treated like an autosome, a sex difference in the phenotype can lead to spurious linkage on the X chromosome. Tests of significance need to be tailored to the X chromosome, and failure to do so can make the test too liberal. The methods are implemented in the R/qtl software package.

### Unexpected high polymorphism at FABP4 gene unveils a complex history for pig populations

Authors: Ana Ojeda, Julio Rozas, Josep M. Folch and Miguel Pérez-Enciso

Agriculturally important animals provide excellent models for genetic architecture of important traits. Fatty acid binding protein 4 (FABP4) plays a key role in fat regulation in mammals. Resequencing of FABP4 identified exceptional nucleotide diversity for a mammal (0.01) and a gene genealogy that did not show any geographical or breed clustering. Additional genotyping showed that distant breeds often share similar haplotypes and that some of the most inbred breeds had high levels of heterozygosity. The coalescence time for FABP4 is older than the estimated time of domestication of pig, suggesting an exceptional duration of maintenance of high variability in the face of inbreeding.

# Public Policy Update

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## The Doubling of the National Science Foundation (NSF) Budget

In 2002, in a low-key ceremony, President Bush signed into law a bill to double NSF's budget in five years, to $9.8 billion by 2007. As we enter the fiscal year 2007, the Congress, at the request of the President, increased the NSF budget 8% over 2006 to $6.0 billion. While this funding level is still a far cry from the goal of the doubling bill, the NSF funding will reach an all-time high in real dollar terms after years of flat funding. The congressional increases would go not only to NSF's investment in the physical sciences but across the entire NSF research portfolio.

The NSF is benefiting this year from President Bush's proposed "American Competitiveness Initiative" (ACI) announced in his 2006 State of the Union address. The ACI proposes to double funding for three key physical sciences agencies over the next decade, and the 2007 budget requests the first installment of this ambitious plan. NSF and the Commerce Department's National Institute of Standards and Technology (NIST) laboratories, and the Department of Energy's Office of Science will all benefit from the ACI.

# Upcoming GSA Meetings

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**Genetic Analysis: Model Organisms to Human Biology II** is planned for **January 5-9, 2008** in San Diego, CA.

All organisms, including humans, are built from the same basic set of genes, yet most of us can only follow work on just a few species. It is more important than ever for investigators working on different organisms, including humans, to communicate with each other and exchange ideas. The GSA is taking the lead in promoting this kind of interaction with the MOHB II meeting that will highlight research on diverse systems that inform human biology.

The first GSA model organism meeting in 2006 received an overwhelmingly positive rating from attendees.

Characteristics that contributed to its success were:

1) relatively small meeting size: 300-400;
2) all meals provided to facilitate interactions;
3) most participants (including speakers) present throughout the entire meeting; and
4) inclusion of multiple keynote speakers and special workshops on education and research funding.

Our goal is to provide a premier forum focused on the underlying unity of major biological mechanisms and on the genetic technology that is needed to understand them. Toward this end, there will be sessions on:

- Prokaryotes and pathogens
- chromosomes, chromatin
- RNA-mediated regulation
- new technology for metazoan analysis
- stem cells and cancer
- populations and evolution
- neurobiology and behavior
- aging, and engineering

Allan Spradling, 2007 GSA president, is the organizer of the 2008 MOHB. For more information on this meeting, check the GSA website, http://www.genetics-gsa.org/, in late spring 2007.

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# Public Policy Update

*by Lynn Marquis, Joint Steering Committee for Public Policy*

## Biomedical Research and the Democratic Congress

The 110th Congress has officially been sworn-in; Democrats have resumed full control of both the House of Representatives and the Senate, and now begins the daunting challenge of following through on the promises made on the campaign trail.

**What does this all mean for biomedical research?**

Democratic control may bring some changes in congressional policy on scientific research and training not seen in recent years. The new Democratic leadership gives reason for the scientific community to be optimistic. In speeches and in actions, it is clear they are aware of the impact recent budgets have had on the research community, including the decrease in the buying power since the end of the doubling of the National Institutes of Health (NIH) budget.

Rep. David R. Obey (D-WI), the chairman of the full House Committee on Appropriations has often criticized Republicans' failure to sufficiently fund biomedical research and the NIH. On the Senate side, Senator Tom Harkin (D-IA), the new chairman of the Senate Labor-Health and Human Services-Education Appropriations Committee has been a staunch supporter for biomedical research, working hand in hand with his Republican counterpart Sen. Arlen Specter (PA) to fund and support the NIH. Together, they have provided leadership and vision as they champion for biomedical research.

But members from both the House and Senate caution against heightened expectations. The country still has a large budget deficit and wars in Iraq and Afghanistan that need funding. A Democratic Congress and the Republican administration will have to work together to agree on funding for biomedical research and the myriad other programs that compete for tax dollars.

Still the change in leadership opens the door for the research community to be heard. Do not let this opportunity pass by. Your voice must be heard as your Member of Congress prioritizes limited federal dollars. Researchers can only be successful when the whole community is involved. **For more information on how to be involved, visit www.jscpp.org or contact Lynn Marquis at lmarquis@jscpp.org.**

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