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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:

Peer Review and the Future of Biomedical Research

Peer review of investigator-initiated grant proposals at the National Institutes of Health (NIH) has enormously advanced biomedical research and medical care during the last 50 years. Researchers have relied on the system to rank proposals based on investigator competence, novel prelim-

inary data, and logical argumentation, rather than perceived short-term utility, faddishness, risk aversion, and salesmanship. Today, however, the peer review process seems under siege: the work-load has ballooned, pay lines have shrunk, study section members have become frustrated and participation by the most experienced scientists has declined. Moreover, an increasing fraction of successful proposals address topics specified by administrators and legislators, while novel programs designed by innovative researchers, the origin of most historic scientific advances, fail more and more frequently. Worst of all, far too few beginning scientists are now launching their careers in the tried and true manner: with an initial R01 grant.

These changes are described by NIH Director Elias Zerhouni as "a perfect storm" and a special NIH advisory panel is working to address the problems of peer review. As part of this process, a GSA committee chaired by Board member Tim Schedl, solicited information from members about their study section service and recent review experience. A summary of their findings and recommendations appears on page 7. The entire report will be sent to the NIH panel members. Other peer review initiatives are also being discussed at NIH according to Dr. Alan M. Krensky, named Deputy Director of the Office of Portfolio Analysis and Strategic Initiatives (OPASI, the new NIH office charged by Congress with examining NIH's research portfolio) on July 8th.

The current study of difficulties with peer review suggests the possibility of improving the system. First, however, the unsatisfactory state of peer review must be distinguished from the short-term crisis in funding levels. The problems of peer review developed slowly over a period of years. The current funding crisis happened suddenly, when, after many decades of uninterrupted real growth, the NIH budget was cut by Congress in constant dollars for two consecutive years, 2006 and 2007. Some may argue that the biomedical research enterprise must now end its long era of expansion and radically readjust to a completely steady-state vision of scientific research. I think not.

Continued on page 8

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Dear Abbot:

A lthough my genetics students have a good textbook and a brilliant teacher, some of them seem to have difficulty understanding and remembering topics that we go over in class. Do you have any suggestions for how I might help my students become more engaged and remember more of what they learn?

- Concerned Professor



I, too, had difficulty getting people to pay attention! It was a rather long time before anybody retained what I had to say. Fortunately, there are now many good ideas and resources to help you increase student engagement, particularly in large classes. A simple way to begin is by typing "biology education" and "active learning" into Google, and investigating some of the many links that appear. Another is to communicate with colleagues teaching similar courses; faculty across the country are inventing many creative approaches to help students understand genetic concepts.

One recent example of active learning is the use of performance art to teach chromosome biology to advanced genetics students at the University of California, Davis. This is a large-enrollment course (~140 students) offered once per year, and taken primarily by genetics majors in their third year. In 2006, students were offered the opportunity to produce and perform (for a few extra credit points), an "interpretive dance" performance art project that would illustrate the bridge-breakage-fusion cycle. Nine videos were produced by 84 of the 146 enrolled students (58%). Submissions included sound tracks (some with original songs), drama, dance, and animations. The formation of groups was facilitated by an electronic discussion board on the course web page.

In addition to the formal course evaluation, 77% of the students who participated in the project filled out an informal survey on the activity. Students were enthusiastic about their participation. "Hands down the academic highlight of my year!"; "I met a lot of new people because of rehearsals. I'll never forget the pathway of anaphase breakage/fusion"; "I think it was a good way to help students gain knowledge of the subject matter in depth while in a stimulating manner"; "It was fun and I met a lot of new people"; and "It made me understand the process a lot more. I wish I had done it before Midterm II." Less positive comments focused on the time spent on the project and lack of expertise in using media technology.

For the 2007 course offering, students were given more latitude in their chosen topic and approach, which could use "performance art" to illustrate any aspect of chromosome dynamics. Group size was limited to 10 students. Two of the best videos submitted in 2006 were shown to the 2007 class as examples. In 2007, 95 of 137 students (69%) participated and produced 14 videos. Topics included reciprocal translocation, meiotic chromosome segregation, homologous recombination, non-homologous end joining, tumor progression, t-loop formation, plasmid shuffle, gene silencing and spreading of heterochromatin. Again, a majority of student comments were positive, although a few expressed concern about the use of class time to watch videos. Future modifications to this approach will include providing students with better resources to help them in video production and increasing student-faculty interaction by requiring submission of a draft video for comments prior to final production.

Interactive learning experiences can be an effective tool for helping students learn genetics, even in high enrollment courses. Those who participated were enthusiastic about their experience and reported that they had a more solid understanding of the genetic process they performed than if they had not participated. In the end, it is the process rather than the product that is critical; students internalize the genetic concepts as they design and participate in the creative activity. Another benefit is that the instructor gets to know students as individuals, and can interact with them in a less formal setting than the classroom. Finally, it is a fun way to see students express their creativity and enjoy learning genetics.

The Abbot

Sean Burgess, Section of Molecular and Cellular Biology University of California, Davis

New Design and Menus for GSA Website

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Genetics Sectors of America

The GSA website has a new look. It's at the same url: http://www.genetics-gsa.org,

but the design and menus are brand new. We think the clean looking design makes access to the information members' desire quickly available.

The cover of the most recent copy of *GENETICS* is in the upper left-side of the homepage. Click the cover and you're at the Journal website. Brief abstracts of upcoming papers in *GENETICS* scroll by at the top of the website homepage. The model organism databases and meeting information are still available both on the homepage and under the menu items, "Meetings/Model Organisms". Model organism databases can also be found under the menu item, "Education". If you're looking for a colleague, the first item on the menu bar, "Directory & Membership" leads right to the GSA Membership Directory search page.

Information posted on the new GSA homepage will be shorter and easier to read. More information on each item is a click away.

GSA staff members redesigned the website in collaboration with the GSA Board of Directors and the Board of Senior Editors. Please send us a message to let us know what you think of the new site: society@genetics-gsa.org.

GSA Awards Nomination Site Open

Help us recognize your colleagues who have had a major impact on genetics! From now until November 1st, nominations for the 2008 GSA Awards can be made online at http://www.geneticsgsa.org/pages/awards/gsaaward_nomination.shtml.

The Thomas Hunt Morgan Medal is for lifetime contributions to the field. The Genetics Society of America Medal is for outstanding contributions in the last 15 years. The George W. Beadle Award is for outstanding contributions to the community of genetics researchers. The GSA Excellence in Education Award, first presented last year, recognizes individuals or groups that have had significant, sustained impact on genetics education at any level, from K-12 through graduate school and beyond. New for 2008, the Novitski Prize honors long-time GSA member and Drosophila geneticist, Edward Novitski, and recognizes scientific achievement that stands out from the body of innovative work, that is deeply impressive to creative masters in the field, and that solves a difficult problem that may have evaded the genetics scientific community.

For more information about these awards and the nomination process, visit the GSA website, http://www.genetics-gsa.org/pages/awards.shtml.

In Memoriam

We are saddened by the passing of our colleague, Bob Metzenberg. One of the guiding lights of fungal genetics, Bob was a friend and colleague of many of us. His recent essay about the joy of doing research during his "retirement" (Research in Your **Retirement House**)

appeared in the January 2007 newsletter. A complete obituary will appear in an upcoming issue of GENETICS.







2nd Genetic Analysis: Model Organisms to Human Biology Meeting

The GSA invites you to join your colleagues at the 2nd Genetic Analysis: Model Organisms to Human Biology Meeting, a meeting that takes the lead in promoting communication and exchange of ideas among investigators using model organisms to inform human biology. The development and application of state-of-the-art methods of molecular genetic analysis to such problems will be emphasized. The meeting will be held January 5-8, 2008 at the Town and Country Resort & Convention Center in San Diego, California.

• Three poster sessions for contributed abstracts * Some abstracts selected for oral presentation

Response to the 2006 meeting was enthusiastic!

"Reassembly of geneticists working on different organisms has been fantastic."

"This is one of the most exciting meetings I have ever attended! Thank you."

"I think you may have to

opened my eyes to the diversity of model organism biology... I look forward to future ones!"

"This was an amazing,

invigorating meeting that

limit attendance when word gets out on this meeting."

The 2008 meeting promises to be even better!

DEADLINES

Abstract Submission: Wednesday, November 14, 2007 Advance Meeting Registration and Housing Reservation: Monday, December 3, 2007 Attendance is limited, so register early.

For more meeting information and to register online, visit the meeting website at www.gsa-modelorganisms.org/



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Andy Fire. Stanford University School of Medicine



GENETIC

Model

ANALYSIS:

Organisms

to Human

Biology

Richard Axel. HHMI. Columbia University College of Physicians and Surgeons



Francis Collins. National Human Genome Research Institute, NIH



From the August Issue of GENETICS

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

These are articles from the current issue of GENETICS that you shouldn't miss. The full text is at www.genetics.org/current.shtml.

Using reporter gene assays to identify cis regulatory differences between humans and chimpanzees

Authors: Adrien Chabot, Ralla A. Shrit, Ran Blekhman and Yoav Gilad

Humans are 95–99% similar to other apes at the nucleotide level, yet show pronounced phenotypic differences. To reconcile these two observations, King and Wilson proposed that modifications in gene regulation may be responsible for many of the observed phenotypic differences between humans and their close evolutionary relatives. This article describes use of reporter gene assays to identify differences in *cis* regulatory elements between human and chimpanzee for 10 genes that are differentially expressed between the species. For three of these genes, changes in *cis* regulatory elements altered the gene expression differences. Moreover, using site-directed mutagenesis, the authors identified three nucleotides that account for a regulatory difference between the species.

A genetic mosaic analysis with a repressible cell marker screen to identify genes involved in tracheal cell migration during Drosophila air sac morphogenesis

Authors: Hélène Chanut-Delalande, Alain C. Jung, Li Lin, Magdalena M. Baer, Andreas Bilstein, Clemens Cabernard, Maria Leptin and Markus Affolter

and

A clonal genetic screen for mutants causing defects in larval tracheal morphogenesis in Drosophila

Authors: Magdalena M. Baer, Andreas Bilstein and Maria Leptin

How does a developing organism direct cellular traffic during embryogenesis? These articles describe hunts for mutants that disrupt genes involved in fibroblast growth factor-dependent tracheal cell migration during embryogenesis in *Drosophila melanogaster*. The authors find a range of defects in terminal cells, including failure of lumen formation and reduced or extensive tracheal branching. Other mutations affect cell growth, cell shape, and cell migration.

Prediction of multilocus identity-by-descent

Authors: William G. Hill and Jules Hernández-Sánchez

The probability of identity-by-descent (IBD) is a fundamental quantity that has many applications in analysis of genotypes. Current theory for predicting its magnitude for multiple loci is either approximate or unwieldy. This article develops a fast and accurate chain-rule method for predicting IBD at large numbers of loci. The results can be used in quantitative trait loci mapping by predicting IBD of individuals at the locus from neighboring marker genotypes.

The Bro1-domain protein, EGO-2, promotes Notch signaling in Caenorhabditis elegans

Authors: Ying Liu and Eleanor M. Maine

A puzzling aspect of Notch signaling is the observation that endocytosis in the signaling cell promotes transduction of the signal in the receiving cell. The authors show that EGO-2, which contains a Bro1 domain characteristic of certain endosomal proteins, promotes Notch signaling in *Caenorhabditis elegans*. EGO-2 activity in the soma is critical for Notch signaling in the germline, consistent with a role for it in production of ligand by the signaling cell. The authors propose that EGO-2 functions in endosome-localized processes in the signaling cells that promote Notch signaling.

Genetic screens for Caenorhabditis elegans mutants defective in left/right asymmetric neuronal fate specification

Authors: Sumeet Sarin, M. Maggie O'Meara, Eileen B. Flowers, Celia Antonio, Richard J. Poole, Dominic Didiano, Robert J. Johnston, Jr., Sarah Chang, Surinder Narula and Oliver Hobert

This article describes comprehensive genetic screens that identify a large number of genes involved in an interesting cell-fate decision in the nematode *Caenorhabditis elegans*.

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GSA Position Statement on Alignment and Function of NIH Study Sections and IRGs

In response to the NIH Center for Scientific Review (CSR) request for input on the alignment and function of its Integrated Review Groups (IRGs) and component study sections (see: http://cms.csr.nih.gov/AboutCSR/OpenHouses.htm), the GSA surveyed its member PIs.

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Of the 193 members who responded to the survey, most (74%) have served on NIH study sections. The web-based survey obtained information in three areas: 1) From the perspective of the PI: Is genetics-based research appropriately evaluated within the current study section alignment? 2) From the perspective of past/present ad hocs or study section members: How can the review process be improved? 3) What are emerging areas of research that study sections will need to serve?

PI perspective on the review process:

There is uniform agreement that peer review is the only way to ensure that research of the highest quality and significance is funded. The formation of the GVE (Genetic Variation and Evolution) and GCAT (Genomics, Computational Biology and Technology) study sections were viewed as important additions. Two major recommendations emerged from the survey:

1 With the organization of study sections around biological questions, genetics-based research proposals are distributed to a number of IRGs. There is a strong consensus that more geneticists are needed on these study sections. Genetic analysis relies on *in vivo* organism-based deductive research that is exploratory in nature and that can be either hypothesis driven or hypothesis generating. These approaches are often very different from those utilized by the biochemists, molecular biologists, cell biologists and physiologists that populate many study sections.

The GSA can provide CSR with a web-based key word searchable database containing CVs of qualified geneticists who are willing to serve on study sections.

2] There is a strong consensus that study sections need more mid-career and senior level reviewers with previous review experience, who have a broader perspective and are less distracted by details.

Study section ad hoc and members' perspective on the review process

Reviewers uniformly feel that study sections appropriately judge advancement of the field, rather than disease relevance. The online system where scores and critiques are posted prior to the meeting is viewed very favorably, but the following recommendations emerged from the survey:

1] To increase the pool of mid-career/senior reviewers: a) reward regular study section members with immunity from administrative time/budget cuts to their own NIH grants; b) allow members to attend two of the three meetings per year; c) have a large reserve of experienced ad hoc reviewers who would attend once per year; d) give more than two weeks grace for grant submission for study section members; e) reduce the workload by shortening the proposal length to 15 or 20 pages without assigning more grants to reviewers.

2] The SRA and Chair should be proactive in establishing the review culture to ensure: a) the discussion focuses on the big picture: the potential for advancing the field and the significance of the research; b) that reviewers are not parochial; c) that a small number of individuals do not dominate the meeting; and d) that reviewers spread their scores. After receiving the proposal packet, first-time reviewers should receive formal training from the SRA and Chair on the process and expectations. These points are in the CSR Guidelines but often there is a lack of follow through.

3] There is a strong consensus against internet-based review, or asynchronous electronic discussion, for IRG study sections. Face-to-face discussions were viewed as essential for evaluating merit, obtaining input from nonreviewers on the significance of the work and calibrating the group of proposals.

Challenges for CSR in the next 10 years

CSR asked, what will be the most important questions and/or enabling technologies within your discipline in the next 10 years? In the past 50 years the most revolutionary discoveries (e.g. epigenetic silencing mechanisms, oncogenes) and technologies (e.g. microarrays, RNAi knockdown) in this country come from unanticipated results of investigator-initiated (R01) research that was at best only indirectly targeted to these findings. Rather than attempt to guess at an unknown future, CSR should empanel study sections that are open to new ideas and approaches and do not require that the answer is almost at hand.



Research in the next 10 years will become increasingly multidisciplinary, both from individual PIs and from collaborative projects. For example, genomics, bioinformatics and modeling are generating large amounts of data and predictions, the *in vivo* relevance of which must be validated through genetic analysis. Conversely, genetic analysis of complex traits and environmental interactions, particularly in humans, generates candidate genes that must be validated through forward/reverse genetic analysis along with other approaches. Therefore, there will be an increasing need for geneticist reviewers on review panels to evaluate this multidisciplinary research.

Much of our understanding of human biology and disease has come from studies of model organisms. Research with model organisms also drives technology development (e.g. RNAi, embryonic stem cells) and advances treatment and prevention of disease by laying the foundation for our understanding of its biology, genetics and biochemistry. Reviewers with relevant model organism expertise remain essential for the evaluation of research that will advance our understanding of human biology and disease.

– Reported by a Committee of GSA Board Members Stan Fields, Trudy Mackay, Terry Magnuson, Tim Schedl, Chair

From the President's desk:

Continued from page 1

Leadership in scientific research and entrepreneurship is widely recognized as a major engine of the United States economy. Many nations try to emulate the U.S. system of higher education and its research infrastructure, despite the acknowledged cost, the multi-decade minimum time scale, and the real possibility of failure. Nations recognize that a thriving U.S.-style research system is an extremely valuable asset. In an increasingly interdependent, competitive world, U.S. research can continue to grow, and continue to serve as an engine of innovation that more than repays its costs. Research and entrepreneurship are complex processes, and increasing world economic prosperity does not guarantee the development of equivalent enterprises. The peculiar U.S. genius for research and innovation has the potential to become even more economically important in the future than it is today.

The size of the biomedical research enterprise will ultimately be determined by the public and their representatives. But the NIH committee should reform peer review on the assumption that there is still room to grow. We can't afford to accept a new dumbed-down version of peer review; we need to make it better. Science truly is an "endless frontier"; today we know very little compared to what we could learn tomorrow about our genomes and how they animate multi-cellular creatures such as ourselves. Gaining this knowledge requires a peer review system that empowers scientists to pursue their own best ideas beginning at an early stage of their careers. This has always been the secret of America's research success. The system must reward truly innovative accomplishment, rather than grantsmanship, citation counting and journal shopping. Yes, the demands on PIs will be greater than in the past due to the increasingly interdisciplinary nature of biological research and the rapidly expanding knowledge base. However, there are plenty of talented young scientists ready, willing and able to thrive in such an environment, if given the opportunity.

An interesting new tool for encouraging these young scientists might involve OPASI. Currently, each study section works in isolation, judging grants relative to its own experience, without reference to NIH as a whole. This can skew the NIH research portfolio. For example, as Dr. Krensky pointed out recently at a FASEB Workshop, NIH currently funds more than 400 grants on VEGF that were reviewed in a wide range of study sections. Would the research portfolio actually be better off with 200 grants on VEGF and 200 on new topics not currently being studied adequately? The inability of study sections to take into account how a proposal fits in with related grants and proposals remains a significant weakness of the existing peer review system. Currently, Institute Councils try to consider such factors, but they lack the time, expertise and deliberative process of a study section. An improved peer review process would enable study sections to get away from details and to access the information necessary to consider strategic factors as well as scientific merit in evaluating proposals. Only expert peer reviewers will be able to accurately estimate the marginal value of a proposal within the NIH universe. A top-down portfolio system will give NIH 200 grants that contain the word "VEGF," but peer reviewers could give it the 200 best grants.

Sincerely,

Allan Spradling GSA President society@genetics-gsa.org or GSA2008@ciwemb.edu

GSA Voting Open until Midnight September 28th

There's still time to vote for the GSA vice-president and directors for 2008. Please cast your ballot for the individuals you want to join the GSA leadership team by midnight, Friday, September 28th.

An e-mail with the ballot and candidate bios was sent to all members in July and a reminder in August. A final e-mail reminder will be sent shortly to those who have not already voted. Paper ballots were mailed to all GSA members who do not use e-mail. If you do not use e-mail and did not receive a paper ballot, please contact the GSA administrative offices at (301) 634-7300.

We thank for their service Past President Barry S. Ganetzky and Directors Susan K. Dutcher, Stanley Fields, and Geraldine Seydoux, whose terms on the Board end this year. Continuing on the Board in 2008 will be President Trudi M. Schüpbach, Past President Allan C. Spradling, Treasurer Trudy F. Mackay, Secretary James E. Haber, Elizabeth W. Jones, Editor-in-Chief, *GENETICS*, and Directors Victor R. Ambros, Kathryn M. Barton, Nancy M. Bonini, Tim Schedl, Michael P. Snyder, and Mariana F. Wolfner.

Listed on the next few pages are the candidates for officer and directors. Please vote for one candidate for vice-president and for a total of three candidates as directors (one in each section).

Candidates for Vice-President: (vote for one)

Philip Hieter, Ph.D.

Director and Professor, Michael Smith Laboratories; Professor, Department of Medical Genetics, University of British Columbia.

Advanced Degree(s): Ph.D. in Biochemistry, Johns Hopkins University (1981).

Career Summary: Assistant Professor, Associate Professor, and Professor (1985-1997), Molecular Biology and Genetics, Johns Hopkins University School of Medicine; Professor (1997 –), Medical Genetics, University of British Columbia; Associate Director (1997-2001), Senior Scientist (1997 –), Centre for Molecular Medicine & Therapeutics; Director and Professor (2001 –), Michael Smith Laboratories, University of British Columbia.

Honors and Awards: International Research Scholar, Howard Hughes Medical Institute (2006); Fellow, Royal Society of Canada (2005); Fellow, American Association for the Advancement of Science (2005); Senior Scientist Award, Medical Research Council (2000); Fellow, American Academy of Microbiology (1998); Faculty Research Award, American Cancer Society (1991); Pew Scholar in the Biomedical Sciences (1986-1990); Council of Graduate Schools/University Microfilms International Dissertation Prize (1981).

Professional Service Activities: Board of Scientific Counselors for the National Human Genome Research Institute, NIH (2001-2006, Chair, 2004-2006); Advisory Board, Saccharomyces Genome Database (1994 –); Chair, Eukaryotic Division, American Society for Microbiology (1996); Advisory Board, NRC/NIH Resource Center for Comprehensive Biology (1997 –); Institute Advisory Board, Institute of Genetics, Canadian Institutes for Health Research (2001-2005); Chair, Planning and Priorities Committee, Integrating the Physical and Applied Sciences into Health Research, CIHR (2003 –); Genome Research Review Council, NIH (1997-2001); Board of Directors, Genetics Society of America (1994-1997); *Editorial Boards: Chromosoma* (1990 –), *Human Molecular Genetics* (1992-1997), and *Genome Research* (1995-2001).

Major Research Interests: Molecular genetics, chromosome transmission, centromere function, mitosis, cell division cycle, mechanisms of aneuploidy, genome analysis, model organism research and human biology.

Fred Winston, Ph.D.

Professor of Genetics, Department of Genetics, Harvard Medical School.

Advanced degree(s): B.A., University of Chicago (1974); Ph.D., Massachusetts Institute of Technology (1980).

Career Summary: *Postdoctoral Training:* Postdoctoral Fellow, Department of Biochemistry, Cornell University (1980-1982); Postdoctoral Fellow, Department of Biology, Massachusetts Institute of Technology (1982-1983). *Employment:* Assistant Professor (1983-1988), Associate Professor (1988-1992), Professor (1993 –), Department of Genetics, Harvard Medical School.





Honors and Awards: Fellow of the Helen Hay Whitney Foundation (1980-1983); Recipient, National Science Foundation Presidential Young Investigator Award (1985-1990); Keynote Speaker, Northeast Regional Yeast Meeting, Montreal, Canada (1997); Fellow, American Academy of Microbiology (1998 –); Award for Teaching, Biological and Biomedical Sciences Graduate Program, Harvard Medical School (2000, 2004, 2006); AAAS Fellow (2003); NIH MERIT Award (2004).

Professional Service Activities: Co-director, Genetics Training Grant, Harvard Medical School (1984-2003); Scientific Advisory Committee on Personnel for Research (1987-1991), Scientific Advisory Committee on Virology and Molecular Genetics (1992-1996) American Cancer Society; Instructor, Yeast Genetics Course, Cold Spring Harbor Laboratory (1987-1990); Visiting Professor, Department of Microbiology, University of Sao Paolo (1989); Member (1989-1993), Co-chair (1994-1996) Yeast Genetics and Molecular Biology Program Committee, Co-organizer, FASEB Conference on Chromatin and Transcription (1997); Chair, Genetics Society of America Nominating Committee (1997); Ad hoc member, NIH Molecular Cytology Study Section (1997); Ad hoc member, NIH Microbial Physiology and Genetics Study Section (1998); Treasurer, Genetics Society of America (1999-2001); Member, NIH Cell Development and Function 2 Study Section (1999-2002); Member, Scientific Review Board, The Medical Foundation (2001–); Committee on Election to Fellowship of the American Academy of Microbiology (2007-2012). *Editorial Boards: Molecular and Cellular Biology* (1986–), *Genetics* (1992–).

Major Research Interests: Gene expression and chromatin structure in yeast.

Candidates for Directors: (vote for one in each section)

Sally A. Camper, Ph.D.

James V. Neel Professor and Chair, Department of Human Genetics, University of Michigan.

Advanced Degree(s): Ph.D. Biochemistry, Michigan State University (1983).

Career Summary: *Postdoctoral training*: Case Western Reserve University (1983-1984); Fox Chase Cancer Center (1984-1986); Princeton University (1986-1988). *Faculty appointments:* Assistant Professor (1988-1993), Associate Professor (1993-2000), Professor (2000 –), Chair (2004 –) Department of Human Genetics, University of Michigan.

Honors and Awards: Basil O'Connor Award; NARSAD Young Investigator Award; University of Michigan Career Development Award, Faculty Recognition Award, Distinguished Faculty Achievement Award; Boezi Memorial Alumnus Award in Biochemistry; NIH Merit Award; Roy O. Greep Research Award from the Endocrine Society.

Professional Service Activities: *Meeting and Course Organization:* 9th International Mammalian Genome Society Meeting; Mouse Initiatives Meetings, Jackson Laboratory, Bar Harbor, ME; Frontiers in Reproduction course, Woods Hole, MA; Endocrine Society, Annual Meeting Steering Committee. *International Mammalian Genome Society:* Co-chair of mouse Chr 11 committee; Nominating and Election Committee; Secretariat. *Advisory boards:* Jackson Laboratory, Mouse Genome Database, Induced Mutant Resources. *NIH Review activities:* Mammalian Genetics Study Section. *University of Michigan:* Director of the University of Michigan Transgenic Animal Model Core Facility. *Editorial Boards: Mammalian Genome, Current Biology, Genomics, Molecular Endocrinology, Mechanisms of Development.*

Major Research Interests: Mouse models of human genetic disease, homeobox gene transcription factor and cell-cell signaling regulation of pituitary gland development, genetic and hormonal contributions to deafness and hearing impairment.

John C. Schimenti, Ph.D.

Professor of Genetics, Dept. of Biomedical Sciences, Cornell College of Veterinary Medicine; Adjunct Professor, Dept. of Molecular Biology & Genetics, Cornell University.

Advanced Degree(s): Ph.D. in Developmental Biology, University of Cincinnati Children's Hospital (1985).

Career Summary: Postdoctoral fellow, Princeton (1985-1987); Assistant Professor, Department of Genetics, Case Western Reserve University School of Medicine (1987-1992); Associate Staff Scientist, Staff Scientist and Senior Staff Scientist, The Jackson Laboratory (1992-2004); Professor, Cornell (2004 –); Director, Cornell Center for Vertebrate Genomics (2004 –).







Professional Service Activities: Eukaryotic Genetics review panel, NSF (1993-1998); NIH priority settings committees for mammalian and non-mammalian Genomic resources (1998, 1999); Mammalian Genetics study section, NIH (1999-2003); Secretariat, International Mammalian Genome Society (2001- 2004); Advisory Board, Academia Sinica mouse mutagenesis program (2002- 2004); Organizing committee, International Congress of Genetics (2003, 2007); GSA nominating committee (2003); ad hoc reviewer for mouse (KOMP) and zebrafish genomics grants (2006).

Major Research Interests: Meiosis; spermatogenesis; recombination; mouse genetics; functional genomics; cancer; maintenance of genome stability.

Michael Lichten, Ph.D.

Senior Investigator, Laboratory of Biochemistry and Molecular Biology, Center for Cancer Research, National Cancer Institute, National Institutes of Health.

Advanced Degree(s): Ph.D. in Biology, Massachussetts Institute of Technology (1982).

Career Summary: Postdoctoral research associate (1982-1987), Department of Biology and Rosenstiel Center, Brandeis University; Senior Staff Fellow, Research Microbiologist and Senior Investigator, Laboratory of Biochemistry and Molecular Biology, Center for Cancer Research, National Cancer Institute (1987 –).

Honors and Awards: Damon Runyon-Walter Winchell postdoctoral research fellow; Leukemia Society of America special fellowship; Fellow, American Association for the Advancement of Science.

Professional Service Activities: Scientific Advisory Board, Mycology Department, American Type Culture Collection (1989-2004); Organizing Committee, Yeast Genetics and Molecular Biology Meeting (1996-2000); Vice-chair (1998) and Chair (2000), Gordon Research Conference on Meiosis; NSF grant review panels (Microbial Genetics, 2000; Eucaryotic Genetics, 2002-2004); NIH study sections (Genetics, 1996; Nuclear Dynamics and Trafficking, 2005-2006; Molecular Genetics C, 2007); Associate Editor, *Genetics* (1998-2006); *Editorial Boards: PLoS Biology* (2003 –), *PLoS Genetics* (2006 –), *PLoSOne* (2006 –)

Major Research Interests: Genome, chromosome and chromosome structure, function and evolution; DNA damage repair and response; homologous recombination; regulation of cell cycle progression in mitosis and meiosis. Primary organism of study: *Saccharomyces cerevisiae*.

Susan T. Lovett, Ph. D.

Professor, Department of Biology and Rosenstiel Basic Medical Sciences Research Institute, Brandeis University.

Advanced Degree: Ph. D. in Molecular Biology, University of California, Berkeley, 1983.

Career Summary: Postdoctoral Fellow, Lawrence Berkeley Laboratory (with R. Mortimer, 1983-1986); Postdoctoral Fellow, Dana Farber Cancer Institute (with R. Kolodner, 1986-1989); Assistant Professor (1989-1995), Associate Professor (1995-2003), Professor (2003 –), Brandeis University.

Honors and Awards: Fellow, American Academy of Microbiology (2006); Davis Fellow for Experiential Teaching (2005-2006); American Cancer Society Fellowship (1986-1989); Cornell National Scholar (1973-1977).

Professional Service Activities: Associate Editor, *Genetics* (2003-2007); Instructor, Cold Spring Harbor Advanced Bacterial Genetics Course (2006 –); Section Editor, American Society for Microbiology "EcoSal" Web Publication: "DNA synthesis and processing" (2006 –); Chair, Advisory Committee, *E. coli* Genetic Stock Center (2001 –); Contributor, Faculty of 1000, Microbial Growth and Development (2005 –); NSF Review Panel Prokaryotic Genetics (2007); NIH Special Emphasis Review Panel (2006); NCI Review Panel (2005), NIH Microbial Physiology II Study Section (1998-2003); NIH Ad Hoc Reviewer (1991, 1993, 1995); DOE Review Panel (1993); Organizer and Co-organizer, FASEB Conference on Genetic Recombination and Genomic Rearrangements (2001, 2003).

Major Research Interests: Mechanisms of recombination; genomic rearrangements; replication fork repair; mismatch repair; mutation hotspots; DNA exonucleases; bacterial cell cycle control.





David J. Begun, Ph.D.

Professor, Department of Evolution and Ecology, University of California at Davis.

Advanced Degree(s): Ph.D., Cornell University (Section of Genetics and Development), 1994.

Career Summary: Assistant Professor, University of Texas (1996-2000); Assistant Professor (2000-2002), Associate Professor (2002-2005), Professor, University of California at Davis (2005 –).

Honors and Awards: University of California at Davis Chancellor's Fellow (2005); Dobzhansky Prize (1995), Society for the Study of Evolution; American Society of Naturalists Young Investigator Prize (1995); Larry Sandler Memorial Lecture (1995), Annual Drosophila Research Conference.

Professional Service Activities: Associate Editor, Genetics (2003 –).

Major Research Interests: Evolutionary genetics.

Charles H. Langley, Ph.D.

Professor, Section of Evolution and Ecology and the Center for Population Biology, University of California–Davis. Advanced Degree(s): Ph.D. in Zoology, University of Texas–Austin (with K. Kojima, 1971).

Career Summary: Postdoctoral researcher, Genetics Department, University of Wisconsin–Madison (with J.F. Crow, 1971-1973); Staff Fellow, NIEHS/NIH (1973-1977); Research Geneticist, NIEHS (1977-1989); Professor of Genetics, UC-Davis (1990 –).

Honors and Awards: Genetics Society of America Medal (1999); Fellow of the American Academy of Arts and Sciences (2007).

Professional Service Activities: Drosophila Board of America (1994 –); Chair, International Program Committee, the 2003 International Congress of Genetics; Member, NIH Genetic Variation and Evolution Study Section (2006 –); Co-chair, Program Committee, 2008 International Congress of Genetics.

Major Research Interests: After decades as a theory-rich and data-poor discipline, advancing genomic technology is turning the intellectual dynamic in population genetics on end. Rapidly mounting data revealing the patterns of genomic variation among individuals and closely related taxa are challenging available analytic methods and demanding richer models of the underlying mechanisms. The research in my lab focuses on this revolutionary increase in the scope of population genetic data. In particular I pursue (1) theoretical modeling of genetic and ecological mechanisms that shape the patterns of genomic polymorphism and divergence, (2) large-scale population genomic resequencing, (3) empirical evolutionary population genomics in Drosophila, conifers and Arabidopsis and (4) rigorous computational approaches to population genomic analysis.







Rising Above the Impact Factor

by Tracey DePellegrin Connelly, Managing Editor, GENETICS

[This is part one of a two-part series discussing the use of metrics to evaluate scientific journals. Part two will be published in the January 2008 issue of GENEtics. For the complete article with tables, see www.genetics-gsa.org/pages/newsletter.htm]

Today's high volume of scientific literature has made evaluating journal impact, quality and usage increasingly complex. Authors deciding where to submit manuscripts, committees conducting professional evaluations, and librarians and advertisers allocating resources often use the "Impact Factor" to take the measure of a journal (and each paper therein). How is the impact factor calculated? And how can impact be measured accurately?

When people refer to the impact factor, they usually mean (whether or not they realize it) the Thomson Institute for Scientific Information (ISI) Impact Factor (IF). But there are at least two other ways to measure impact and value: the Eigenfactor, and the Bergstrom-McAfee Index. Precisely what are these metrics, and how do they reflect on our journal, *GENETICS*?

ISI Impact Factor

In scholarly publishing any ranking can be controversial, giving rise to debates on what journals, article types, metrics and categories are included, manipulated, and interpreted. But whether it's a number feared, revered, inflated, or touted, the ISI Impact Factor (listed to three decimal places), isn't going away. The IF is the oldest of the metrics, arising from an idea first proposed in a groundbreaking paper on citation indexing in a 1955 issue of *Science*.

Put simply, the Impact Factor is the average number of times a journal's papers are cited for two years after publication. It is the number of citations to journal papers published in the preceding two year period divided by the total number of source items – research papers, notes, reviews and proceedings only – published in the journal during that time.

The IF provides a convenient, seemingly objective measure of quality and impact for overburdened promotions committees. For many scientists it has become the single most important metric for evaluating journals: Of over 2600 authors recently surveyed, 96% said the IF is "important" or "very important" when deciding where to submit an article. Journals reinforce this behavior by advertising high Impact Factors as symbols of success and importance.

But the Impact Factor of a journal depends upon the citation rates of its individual articles – not vice versa. And as most know, review articles boost a journal's IF because they tend to attract citations. it's not surprising, then, that half of the 50 journals with the highest Impact Factor (≥ 14.780) are review journals. While editors may not be trying to manipulate the impact factor, publishing review articles certainly doesn't hurt. It is important, then, to consider the number of review articles (in proportion to research articles) when comparing Impact Factors.

Journals that publish large amounts of "front matter" – news, commentaries, editorials – at the expense of research articles also move up in the standings. Any citation to these "other items" counts in the IF numerator, but does not appear as a "penalty" in the denominator. Many high-IF, high-profile journals have a substantial amount of front matter. For example, one top-ten journal in 2006, published a 1:1 ratio of articles to "other items" (plus a 5:1 ratio of research articles to reviews). Citations to the latter, which count in the plus but not the minus column of the IF, are worth their weight in science reporters. The IF-advantage over journals like *GENETICS*, which publish little or no front matter, is substantial.

Evolution of the Impact Factor

The IF arose from Eugene Garfield's groundbreaking paper on citation indexing in the July 15, 1955 issue of *Science*. Garfield's 1961 meeting with the NIH Genetics Study Section resulted in the NIH-funded *Genetics Citation Index*, a pilot to test the utility of a citation metric. That led to the *Science Citation Index* covering 562 journals and 2 million citations, which became the Journal Citation Reports that ISI publishes annually.

Garfield still works at the ISI, the Philadelphia-based company he founded in 1960. Approachable and energetic at 82, he recently spoke with *GENETICS* about the Impact Factor. Initially intended simply as a way to compare journals whose absolute publication and citation counts varied greatly, Garfield acknowledges that the IF has taken on a life of its own as an indicator of journal—even author—prestige. "I don't know if you can say that high-impact articles are high-quality," says Garfield. "A lot of quality is in the eyes of the beholder."

"Your journal is respectable," says Garfield of *GENETICS*' IF of 4.232, quickly adding that any IF by itself says little. He is a proponent of relatedness analysis – looking at the big picture of which journals cite one another. Garfield notes that "*GENETICS*' is clearly cited by



high-impact journals." *GENETICS* articles are cited most by papers in *Molecular Ecology, Theoretical and Applied Genetics, PNAS, Molecular Biology & Evolution, PLOS Genetics, JBC, Heredity, Molecular and Cellular Biology, Journal of Evolutionary Biology, Current Biology, and Development.* Conversely, *GENETICS*' articles most often cite work published in *PNAS, Nature, Science, Cell, MCB, JBC, Genes & Development, MBE, Development, EMBO Journal, Evolution, Nucleic Acids Research, and Nature Genetics.*

How does *GENETICS* stack up in the 2006 ISI Journal Citation Reports?

- At 4.232, *GENETICS*' Impact Factor ranks it 32nd among 131 journals in the Genetics and Heredity category. (For determining Genetics' IF, see www.genetics-gsa.org/pages/newsletter.shtml)
- *GENETICS* is #4 in total cites only *Nature Genetics, Oncogene*, and *Genes and Development* had more total citations in Genetics and Heredity journals.
- *GENETICS*' Cited Half Life of 8.6 the median age of articles cited in the current year—indicates that *GENETICS*' articles have long-lasting impact.

Eigenfactor

A recent and promising adjunct to the Impact Factor is the Eigenfactor, devised by Carl Bergstrom, an evolutionary biologist at the University of Washington, with a long-running interest in the economics of scientific publishing.

Bergstrom's approach is similar to that used by Google to rank popularity of web pages. "ISI provides a big table of how often each of its indexed journals has cited one another. Influential journals are highly cited by other influential journals...we recursively calculate the overall influence of each journal from our data."

The Eigenfactor accounts for five years' worth of citations, rather than the two years covered by the IF. The Eigenfactor also adjusts for differences in citation patterns across disciplines. Eigenfactor rankings account for variations in prestige among citing journals; citations from top-tier journals are valued more highly than those from journals with narrower readership.

"I'd hate to see hiring, tenure, or funding decisions made based on Eigenfactor or any other simple statistic," Bergstrom says, careful to point out the obvious: no metric is a substitute for actually reading the papers.

"But some large-scale questions (i.e. How influential is *Science* relative to *Nature*? How has the prestige of *Cell* changed over the past 30 years?) can only be answered with bibliometric statistics."

"Our data suggest that *GENETICS* is somewhat undervalued by the Impact Factor," Bergstrom says. With an EF of .16, *GENETICS* ranks 6/298 among Genetics and Heredity journals categorized by Eigenfactor. "According to Impact Factor, *GENETICS* is in the top 6% of all scientific literature; our measures rank *GENETICS* in the top 4%. Given the high quality of other top-ranked journals, this difference is substantial." (See www.genetics-gsa.org/pages/newsletter.shtml for how the Eigenfactor was determined.)

Bergstrom-McAfee Index

The Bergstrom-McAfee index was created by economics professors Ted Bergstrom [father of Carl, (UC-Santa Barbara)] and Preston McAfee (Cal Tech) to evaluate the relative cost of journals. It is especially useful to acquisitions librarians deciding what journals to buy. This index reveals that Genetics is an economic bargain; its relative cost index of .22 puts Genetics in the highest category of cost-effectiveness – the top 5% of all 1192 biology journals in the index.

Faculty of 1000 Biology

A traditional way of evaluating articles seems to be gathering support: actually reading them. That's how more than 2000 leading international researchers that form the Faculty of 1000 (which includes many *GENETICS*' Associate Editors and GSA Board members) evaluate papers. The focus is on the article's perceived scientific merit. "It was clear that the community felt something was needed to 'level the playing field' in terms of putting the emphasis back on scientific merit.... rather than on which journal a paper was published in," explains Steven Lokwan, Director of F1000 Biology. "One of the main aims of Faculty of 1000 Biology was to tackle existing journal hegemony."

The articles' evaluators reveal themselves because "Few scientists we talked with valued the opinion of anonymous evaluators or those perceived as being too junior," Lokwan explained. "They really wanted an authoritative resource." Papers are labeled 'recommended', 'exceptional', or 'must-read'" on the F1000 website. The "hidden jewels" list is designed to promote the visibility of papers from less widely-read journals.

The process by which journal and article impact and quality are measured continues to (and well should) evolve. More about this will be in Part II.

Next issue: Distinctions between impact, journal quality, prestige, seminal work, and other factors that don't lend themselves to measurement; common misperceptions about journal metrics. See www.genetics-gsa.org/pages/newsletter.shtml for Part I in more detail.

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?



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.

Science and Art Mix at the C. elegans Meeting

Victor Ambrose, Dartmouth Medical School

The 16th biennial International *C. elegans* meeting on the UCLA campus, June 27 - July 1, attracted researchers from more than 30 countries. There were five plenary sessions and 17 concurrent symposia. Throughout the meeting more than 1000 posters were on display on the gym floor of Pauley Pavilion, which became a lively meeting place each evening.

The meeting was kicked off Wednesday night with Gary Ruvkun (Massachusetts General Hospital and Harvard Medical School) as keynote speaker presenting an amusing and stimulating discussion of the state of *C. elegans* research and prospects for the future. He reviewed the history of his work on microRNA mechanisms and developmental timing, and followed with more recent findings from his laboratory's genome-wide RNAi screens for worm genes involved in RNAi and microRNA mechanisms. Ruvkun also presented the status of his work on insulin signaling, fat metabolism and longevity in *C. elegans*. Departing from the topic of the lowly worm, he closed with the question of life in the solar system more generally, outlining his NASA-funded project to test for universally conserved ribosomal RNA genetic material in Martian soil.

Other highlights of the meeting included the 5th Annual Worm Art Show, organized by Ahna Skop (University of Wisconsin, Madison), featuring a lengthy and rather

astonishing claymation video (by the Roy lab at McGill) that showed the adventures of worms with bizarre RNAi phenotypes, and offered a salute to the 2006 Nobel **Prize for Craig** Mello and Andy Fire. Morris Maduro (UC-Riverside) and **Curtis Loer** (University of San Diego) presented a hilarious new Worm Comedy Show that included numerous quips, songs, skits, and even a short film featuring "Morat" interviewing people in the Sternberg lab about their work. A DVD of the Worm Comedy Show

Stri International C. elegans Art Show,



can be obtained by visiting http://www.faculty.ucr.edu/~mmaduro/wormshow07/ws07.htm .

Three students, David Harris (MIT), Christopher Schoff (University of Washington) and Maria Catarina Silva (Northwestern University and Universidade de Lisboa, Portugal), were awarded first-place prizes by GSA for their outstanding posters. An additional 42 students received second place or honorable mention awards for their posters.

The organizers, Victor Ambrose (Dartmouth Medical School) and Anne Hart (Massachusetts General Hospital and Harvard Medical School) are grateful for the sponsorship of Carl Zeiss, Divergence, Inc., Integrated DNA Technologies, Leica Microsystems, Photonic Instruments, Union Biometrica and Constant Systems, Inc. The full meeting program and abstracts can be accessed at http://genetics.faseb.org/genetics/Celegans/2007meeting/.

(*Page 16*) 1] Morris Maduro, left, and Curtis Loer performing during their Worm Comedy Show. 2] Caroline Goethe, left with students at the Student-Mentor Luncheon. 3] Tim Schedl, left, GSA Board member with Anne Hart, Meeting Co-chair. 4] Ann Rougvie, right, with a student at the Student-Mentor Luncheon. 5] Victor Ambrose, left, Meeting Co-chair, with Local Organizer, Alex van der Bliek (UCLA). 6] Ahna Skop, Worm Art Show organizer with some of the submitted works. 7] Gary Ruvkun, center, Keynote Speaker, talking informally with meeting participants. (*Right*) 8] David Harris, one of the three First Place GSA Poster Award winners with his new iPod. 9] Second Place GSA Poster Award winners.



Fly Researchers to San Diego in April

The A9th Annual Drosophila Research Conference sponsored by the GSA is scheduled April 2-6, 2008 at the Town & Country Resort and Convention Center in San Diego.

Important dates are:

Monday, September 24 Thursday, November 1 Monday, November 5 Thursday, February 21

Saturday, March 1

Abstract submission site opens. Deadline for Abstract Submissions Conference Registration Opens Deadline for Early Conference Registration Deadline for Hotel Reservations

For more information about the 49th Annual Drosophila Research Conference, visit the GSA website at http://www.drosophila-conf.org/genetics/gsa/dros/dros2008/.

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Public Policy Update

Continued from page 20

The uncertain fate of most of the spending bills means Congress will face an end of year showdown with the Bush administration. Members of Congress are already preparing for the following scenarios: an omnibus bill so big the President could not sustain a veto, a government shutdown, or another long-term continuing resolution like the one Democrats passed this year.

★ F* ★ ★

* This analysis is one of a series of AAAS R&D Funding Updates on FY 2008 congressional appropriations. The complete series of AAAS Updates, is available at http://www.aaas.org/spp/rd in the "FY 2008 R&D" or the "What's New" sections.

August Issue of GENETICS

Continued from page 6

SYP-3 restricts synaptonemal complex assembly to bridge paired chromosome axes during meiosis in *Caenorhabditis elegans*

Authors: Sarit Smolikov, Andreas Eizinger, Kristina Schild-Prufert, Allison Hurlburt, Kent McDonald, JoAnne Engebrecht, Anne M. Villeneuve and Mónica P. Colaiácovo

and

Synapsis-defective mutants reveal a correlation between chromosome conformation and the mode of double-strand break repair during *Caenorhabditis elegans* meiosis

Authors: Sarit Smolikov, Andreas Eizinger, Allison Hurlburt, Eric Rogers, Anne M. Villeneuve and Mónica P. Colaiácovo

How do cells ensure that only aligned pairs of homologous chromosomes form synaptonemal complexes (SCs)? This article describes SYP-3, a coiled-coil protein that helps ensure that assembly of the SC occurs only in the appropriate context. Analysis of *syp-3* mutants provides insight into the relationship between chromosome conformation and the repair of meiotic double-strand breaks.

Electronic Forums Launched

A new program of electronic forums has been developed by the ASHG/GSA Education Office. Instead of signing-up for specific topic-based listserves, members can sign on to a current forum topic or post their own forum topic by logging on to www.ashg.org/forum/and entering the user name and password that was recently e-mailed to you.

The current forums are divided into three categories related to trainees, education and general information. Within those categories are more specific topics including professional development and mentoring for trainees; K-12, medical student and public education; and under general issues are topics such as women and minorities in science, and recent articles in *GENETICS* and *AJHG*. If



you have something to say about any of the topics listed just click on it and post your comment. You can read previous postings and comment on what others have written on the same topic. Or, you can start a new topic – from job searches to textbook reviews. Older topics will be archived so messages can be searched later. And if you want to gauge your colleagues' interest on a certain issue or topic you can post an (unscientific) opinion "poll".

The success of these electronic forums will be determined and measured by your use. The Education Office will provide guidance and information opportunities, but only you can provide the content and interaction needed for this new resource to have traction within the genetics community. We encourage you to use this resource.

To start interacting with your colleagues visit: www.ashg.org/forum/ and enter your user name and password.

If you have questions or if you are interested in moderating a specific topic and are willing to accept responsibility for generating and soliciting content for that topic, please contact Kenna Shaw in the Education Office, kshaw@ashg.org.



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Public Policy Update

by Lynn Marquis, Joint Steering Committee for Public Policy

NIH Budget: Future Uncertain

It was summer in Washington and Congress was in the heat of the appropriations process; the process that funds all the federal government agencies and the many programs under each agency's umbrella. President Bush issued a veto threat on 10 of the 12 annual appropriations bills, leaving the outcome for the National Institutes of Health (NIH) for Fiscal Year 2008 (FY08) far from certain.

Spending levels are the main reason for the veto threat. The President wants to freeze spending on all nondefense programs, but Democrats want to provide more funding for domestic, nondefense programs. Accordingly, the House and Senate have recommended funding the NIH at levels higher than the President's recommendation.

The JSC, with other leaders in the NIH advocacy community, worked with Congressional supporters seeking a 6.7% increase for the NIH's FY08 budget. The JSC will continue to advocate for the NIH to ensure its budget is increased by at least the rate of biomedical inflation.

In mid-July, the House of Representatives passed their version of the appropriations bill that funds the NIH. The House voted to give the NIH a total budget of \$29.9 billion for FY08, an increase of \$701 million or 2.4 percent over the current year, and \$1.0 billion more President Bush's request. The Senate committee proposed funding the NIH at \$30.1 billion, an increase of \$950 million or 3.3 percent over the current year and \$1.3 billion more than the President requested.

According to the American Association for the Advancement of Science (AAAS), the Senate plan would allow NIH funding to stay ahead of the general economic inflation, projected at 2.4 percent next year. But because of other NIH funding initiatives in the Office of the Director, most NIH institutes and centers (IC's) would see smaller increases -- between 2.3 and 2.5 percent in the Senate plan and between 1.5 and 1.7 percent in the House bill. The Senate would enable most IC's to just keep pace with inflation, while the House and the Administration's budget plans would mean another year of decline in real terms.*