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From the President's desk:

(Please note: By the time you read this I will be the Past President. Look for current President Terry Orr-Weaver's column in the next newsletter)

I am pleased to announce that the GSA is organizing a new conference entitled **"Genetic analysis: From model organisms to human biology"** to be held in **San Diego, January 5-8, 2006**. The GSA Board of Directors and I believe this is an important event for the Society and its members.

Our rationale for this meeting is twofold. First, the time is right for a meeting that highlights and emphasizes the value of model organisms in understanding biology. Research on a select few organisms that serve as models for all creatures, including humans, has provided much of what we know about fundamental life processes. The genome sequencing projects reemphasized the fact that all organisms are built from the same genes, and underscored the value of model organisms for understanding gene function.

Second, with impending budget cuts and uncertain support for basic research, it is more important than ever to keep model organism genetics at the front of the research agenda. A meeting that puts on display the research advances being made with model organisms can help do that. It is logical that the GSA, with its large constitutency of model organism geneticists, should lead this endeavor.

Our inspiration for this meeting comes from two very successful meetings on "Yeast and human disease" held in 1996 and 1999 that were co-organized by Phil Hieter (of the GSA) and David Valle (of The American Society of Human Genetics). Those meetings were held not long after the sequence of the yeast genome was determined, and people came away from them excited and energized by the awesome power of yeast genetics to inform human biology. With the genome sequences of the other major model organisms in hand, now is a great time to hold a meeting similar to these, but expanded to include the other models for human biology.

The meeting sessions will be designed to highlight both human and model organism genetics in a complementary way. Speakers for the following sessions are now being lined up:
1) Cancer and cell cycle; 2) Complex traits; 3) Epigenetics; 4) Stem cells; 5) Cell biology of diseases; 6) Comparative genomics; 7) Innovative Technologies.

We would welcome your ideas and suggestions for this meeting. Please send them to society@genetics-gsa.org.

This will be the first regular meeting of the GSA in more than a decade. We hope it will establish a strong foundation for future regular (annual or biennial) GSA meetings. We intend to keep the cost

Continued on page 3

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GSA Profile

Timing and Mentors Shape Career Path of Amy Pasquinelli, First Rosalind Franklin Young Investigator Awardee

(Based on a conversation with Judith Benkendorf, MS, CGC)

One morning this past spring, University of California –San Diego, Assistant Professor of Molecular Biology Amy Pasquinelli's cell phone rang at an unusual time. She reflexively answered it — in spite of not recognizing the number on the caller ID—and learned that she was selected as the first recipient of the prestigious Rosalind Franklin Young Investigator Award.

The Rosalind Franklin Young Investigator Award, given by the Peter Gruber Foundation, and administered and selected by the Genetics Society of America and the American Society of Human Genetics, is a $75,000 prize for a young woman geneticist who is in her first three years of an independent faculty position in any realm of genetics. The award honors the groundbreaking contributions of Rosalind Franklin and is designed to inspire and support new generations of women geneticists. Pasquinelli was selected from among 130 applicants worldwide and was presented with her award at the Annual Meeting of the American Society of Human Genetics, in Toronto, Canada, on October 27, 2004.

Pasquinelli's career path started in a small town in northwestern Pennsylvania. She "had never heard of anyone getting a PhD in science. I thought that being a biology major meant [having] a career in medicine." Pasquinelli, however, credits her parents, her schoolteacher mother and her factory worker father as supportive of the path she chose to take. "There are no scientists in my family, but my parents always stressed the importance of education."

As an undergraduate at Bucknell University, Pasquinelli had a summer job in a lab and something clicked. With encouragement from her undergraduate advisor, Mitch Chernin, Pasquinelli pursued graduate studies at the University of Wisconsin-Madison. When she started looking for a research home, she "was repeatedly struck by the contagious enthusiasm of the professors. I landed in Jim Dalberg's lab where I worked with graduate students and other investigators, studying how RNAs are exported from the nucleus." This was Pasquinelli's first foray into the RNA field and she is grateful to Dalberg for his mentoring and Elsebet Lund, a senior scientist in the lab, for hands-on training.

She was looking to expand her horizons for her post-doc. "I had little experience in either genetics or developmental biology but I could see that genetics was a powerful tool and I was attracted to the *C. elegans* system; of course, the worm genome had just been sequenced at that time." An interview with Gary Ruvkun at Harvard Medical School was key. "His lab, together with Victor Ambros, had described some strange small RNA in worms that regulated development. I thought this might be a good way to bring together my RNA expertise with learning about genetics and development. By the end of the interview Ruvkun invited me to join a post-doc and graduate student in his lab who had embarked on studying a gene that regulated development, which they postulated to be a small RNA. I joined their lab in early 1999 and was totally hooked on the project."

Pasquinelli and her colleagues demonstrated that the small RNA encoded by *let-* is present in most animals, including humans. Following this discovery, several other groups identified multitudes of tiny RNA genes, now generally called miRNA. This explosion of interest in tiny RNAs that control the expression of protein-coding genes was anointed as the 2002 Breakthrough of the Year by *Science*.

Pasquinelli's transition from post-doc to faculty member was "pretty drastic." When she first walked into her new lab, "there was no lab equipment and there were no people. Luckily, this only lasted a short time. I now have a new, young lab up and running. We are continuing to learn more about how microRNAs are made and how they function, primarily using *C. elegans*."

Pasquinelli names many women scientist role models, including Elsebet Lund who taught her bench skills, Judith Kimble, with whom she interacted during graduate school, Barbara Meyer, a current collaborator, and her colleagues Cori Bargmann, Brenda Bass, and Cynthia Kenyon, all top researchers in her field.

The lessons Pasquinelli has learned are paying off. "I already have three graduate students, who came to me totally excited about *C. elegans*, microRNAs, and RNAi. One of my favorite moments came when I was in my office and overheard two of my students discussing microRNAs and other things I had talked to them about. I suddenly knew that my lab would be fun and exciting."

Continued on page 3

New GSA Officers


Barry Ganetzky


Geraldine Seydoux


Susan Dutcher


Stan Fields

Congratulations to Barry Ganetzky (University of Wisconsin, Madison) the new GSA Vice President. Barry has been a GSA stalwart, having previously served on the Board of Directors as treasurer. We are pleased he has agreed to play a leadership role in the GSA for the next three years. We also welcome newly-elected Board members Stan Fields (University of Washington, Seattle), Geraldine Seydoux (Johns Hopkins University, Baltimore), and Susan Dutcher (Washington University, St. Louis). We thank all who used GSA's first online ballot for voting.

Our thanks also to outgoing Board members Gerry Smith (Fred Hutchinson Cancer Research Center, Seattle), Andy Clark (Cornell University, Ithaca), Ken Kemphues (Cornell University, Ithaca) and to retiring Past President Cynthia Kenyon (UCSF) for their past three years of service to the GSA.

From the President's desk:

Continued from page 1

low so that as many people as possible can attend. We especially want to see a large contingent of students and postdocs attend the meeting.

It is an exciting time to be a geneticist. The rich information resource of the genome sequences along with the fantastic technical abilities we have acquired provide exciting new opportunities that promise deep insight into biology. If we are to fully realize this potential, investigators working with different organisms, including humans, must communicate with each other and exchange ideas. We all attend meetings, but increasingly those meetings are focused sharply on specialized areas of study. Yeast geneticists go to yeast meetings, fly geneticists go to fly meetings, and similarly for geneticists working with other organisms. But rarely do folks working on two different model organisms get together to discuss what they have in common (and we have a lot in common!). And almost never do model organism geneticists get together with human geneticists. GSA is taking a leadership role in promoting these kinds of interactions because our future depends on it.

I hope you will plan to join me and our GSA colleagues at this new meeting, "Genetic analysis: From model organisms to human biology." Please save the dates January 5-8, 2006 to join us in San Diego, CA, and to help us open a new chapter of the GSA.

Mark Johnston

GSA Profile

Continued from page 2

Amy Pasquinelli

Along with a contagious enthusiasm for her research, Pasquinelli is grateful for award opportunities. "Awards and fellowships from private groups have helped much of my career. My post-doctoral fellowship was from the Helen Hay Whitney Foundation." The Rosalind Franklin Young Investigator Award "is a huge benefit to our lab at a time when we are still thinking about every penny we're spending. It will allow us to look at some state of the art equipment and techniques that we might otherwise have delayed or been unable to try."

The Franklin award will also bring into reach the goals Pasquinelli has set for herself for the next five years. "Hopefully we will continue to be an active lab, doing solid science and making important contributions to the microRNA field, to *C. elegans* genetics, and to RNAi. Five years from now, I'll be graduating my first students, which is another amazing thing to think about: To help produce young scientists, influence their career paths, and help them decide where they will go next." Pasquinelli teaches molecular biology to undergraduate students which she finds is "more a learning than a teaching experience for me."

When she isn't seeking thrills from her research, Pasquinelli enjoys the thrill of international travel. She's been to the jungles of Ecuador, the crowded cities of India, and she celebrated the millennium among the pyramids of Egypt. Pasquinelli hopes to continue her global explorations in between her exploration of microRNAs in her lab.

New Web Site Design Unveiled

The GSA Web site (http://www.genetics-gsa.org) has been redesigned! On the left margin are eight buttons (the "Ascus of Knowledge") linking the user to the most frequently used features, including our journal, *GENETICS*, our membership directory, information on upcoming meetings, positions available, and more. The right panel of the Web site includes buttons that link to model organism databases and meetings sponsored by the GSA. A new feature that we think visitors to the Web page will appreciate is a constantly updating news-feed that links to information of interest to geneticists.

The Web site will continue to highlight prominently important activities of the society, such as the Conversations in Genetics project, and news regarding our members. An area for population and statistical genetics is under construction. Also, we are creating a link to useful resources for teaching and instruction in collaboration with the GSA Education Committee.

Web editor R. Scott Hawley, GSA Executive Director Elaine Strass and Web consultant Donald Price are to be commended for their efforts to improve this useful resource. They will continue to strive to increase the Web site's utility, and are interested in hearing your reaction to the new site (especially the news-feed feature) and your suggestions. Comments should be sent to Scott at rsh@stowers-institute.org. Visit our new Web site soon (and often).

Education Committee Establishing Its Role

by Tim Stearns

The mission of the GSA Education Committee is to foster and support efforts of Society members in education. Each of the committee members, Tim Stearns, Stanford University, chair; Ken Burtis, University of California, Davis; Malcolm Campbell, Davidson College; Mike Cherry, Stanford University; Graham Hatfull, University of Pittsburgh; Dan Klionsky, University of Michigan; Phil Meneely, Haverford College; Pat Pukkila, University of North Carolina; and Wendy Raymond, Williams College, is devoted to science education, and future columns will highlight some of their innovative efforts. The committee is in the process of establishing roles for the GSA in supporting education efforts, three of which are described here.

An important role of scientific societies is to recognize exceptional achievements of our members who are leading by example and setting the high standards in our field. The GSA currently gives three awards for outstanding contributions to the field of genetics: the Thomas Hunt Morgan Medal, the Genetics Society of America Medal, and the George W. Beadle Award. These awards are for excellence in research (see announcement of the 2005 winners in this issue). Beginning in 2006 the GSA will also give an award for contributions to genetics education.

Another way to recognize the education efforts of GSA members is to hold sessions on education at the GSA-sponsored meetings, which are attended by scientists at all levels, including many with a deep interest in education. At last summer's "Yeast Genetics and Molecular Biology" meeting in Seattle, an education workshop was successful in providing a forum for the discussion of classroom and laboratory methods, as well as strains, reagents, and other resources available for teaching. We will continue to include education sessions at these meetings. We welcome volunteers to help us organize one of these sessions.

Lastly, it is important to involve our most talented undergraduates in the GSA-sponsored meetings. These students, carrying out research in our labs, are our next generation of geneticists, yet many do not choose careers in research. Providing them with the experience and the excitement of attending a scientific meeting including the presentation of their work, may help attract these students as future colleagues. A group of Stanford undergraduates attended the summer Yeast Genetics meeting and won honorable mention in the GSA poster contest, a thrill rivaled only by their amusement at the dance moves of some of the more senior scientists at the social. With this kind of educational reinforcement we now have scientists for life! We will work with the meeting organizers to enable undergraduates to attend the GSA-sponsored meetings.

We will continue to feature education activities in this newsletter, and on the GSA web site. Stay tuned, and get involved! Please let us know your suggestions and ideas (society@genetics-gsa.org).

News from the Databases

by Paul Sternberg (with help from many wonderful curators)

The databases have become indispensable tools for our research. Here's some of what's new with them:

dictyBase (dictybase.org)

The genome sequence of *Dictyostelium discoideum* (all 34 Mb on its 6 chromosomes) has been completely determined! There are approximately 12,500 genes encoding proteins (of at least 80 amino acids).

dictyBase is your portal to curated literature, manually curated genes, automated and manually assigned Gene Ontology terms, results from two different microarray gene expression projects, alignments of over 155,000 ESTs to the genome and *in situ* hybridization patterns for nearly 200 genes.

WormBase (www.wormbase.org)

WormBase now includes the results of 38,531 RNAi experiments, 234 microarray experiments (with millions of individual measurements), 11,655 yeast two-hybrid experiments, and 3,583 anatomic expression patterns including over 800 new unpublished patterns from the British Columbia Genome Sciences Centre.

ZFIN (zfin.org)

ZFIN gives access to gene expression data from the Thisse lab, *in situ* hybridization experiments that utilize various cDNA libraries and I.M.A.G.E. clones. Gene Expression pattern images are annotated by developmental stage using terms from the zebrafish anatomical dictionary. These data will be released at the rate of roughly 500 expression patterns a month. The data can be easily searched according to anatomical feature or gene name.

SGD (www.yeastgenome.org)

The genome sequence of the reference yeast strain (S288C) has been updated. The sequence of 16 ORFs has been updated, three new ORFs have been added, and one ORF has been merged with a neighboring ORF.

SGD now uses a new underlying database architecture; while not obvious to users, it allows SGD to incorporate new types of data. During the transition, much of the data has been checked and updated.

FlyBase (www.flybase.org)

The genome sequence and annotation for *Drosophila melanogaster* (Release 4.0) continues to improve. A new version (Release 4.0, Nov. 2004) is now available in FlyBase. It includes over a megabase of new DNA sequence.

A first release of the *D. pseudoobscura* genome is also available at FlyBase. All the sequence and annotations can be easily downloaded.

Mouse Genome Informatics (MGI; www.informatics.jax.org/)

MGI now hosts the International Mouse Strain Resource (IMSR) database, a catalog of mouse strains available at facilities around the world. The IMSR already contains strain data from four major sources. Users can search for available strains by strain designation, strain status (e.g., live mice, cryopreserved embryos, sperm, etc.), mutations they carry, and chromosome.

Rat Genome Database (rgd.mcw.edu/)

RGD has 24 new tracks on its genome browser, including SNPs, and ontology tracks showing annotations from Gene Ontology, Mammalian Phenotype Ontology, Disease Ontology and RGD's Pathway Ontology.

A new tool, GViewer, provides a genome-wide overview of the locations of genes and quantitative trait loci annotated with these various ontology terms. Mouse and select human quantitative trait loci are now available in RGD's VCMap tool for comparative mapping of complex traits among the three species.

Reactome (www.reactome.org)

The Reactome project is developing a resource of core pathways and reactions in human biology. The information in this database is authored by researchers with expertise in their field, maintained by the Reactome editorial staff, and cross-referenced with PubMed, Gene Ontology, and the sequence databases Ensembl and UniProt. The latest release includes modules on Apoptosis and Hemostasis.

Generic Model Organism Database (GMOD; www.gmod.org)

Model organism databases have been working together on software development to unify the access to data. SGD, dictyBase, RGD, FlyBase and WormBase are now using the same genome browser, **Gbrowse**.

FlyBase is leading the development of **chado**, a generic database system that is allowing them to fuse the information from FlyBase and the Berkeley Drosophila Genome Project. **Apollo** is a facile, interactive tool for annotating genome sequence using data from either local or remote **chado** databases.

Textpresso (www.textpresso.org), developed for *C. elegans* literature, now has a pilot Neurospora search engine with over 500 papers, and SGD and FlyBase are implementing systems. Textpresso splits full-text of papers into sentences and indexes them according to categories such as "gene," any word that means "interaction," and so forth.

From the January Issue of *GENETICS*

by R. Scott Hawley

These upcoming articles may be of special interest to our readers.

GENETICS/2004/033191

Characterization of the *grappa* gene, the *Drosophila* Histone H3 Lysine 79 methyltransferase

Authors: Gregory A Shanower, Martin Muller, Jason L Blanton, Viktor Honti, Henrik Gyurkovics, and Paul Schedl

The roles of chromatin modification in early *Drosophila* development are explored by the analysis of a novel gene called *grappa (gpp)*, which encodes a histone methyltransferase that modifies Histone H3. Mutants in this gene disrupt the gene silencing mechanisms that operate on the *Bithorax complex*, suggesting a role for this chromatin modification in early *Drosophila* development. *grappa* mutants display additional phenotypes that suggest a role for this protein at multiple sites in the genome.

GENETICS/2004/032300

Communication between parental and developing genomes during Tetrahymena nuclear differentiation is likely mediated by homologous RNAs

Authors: Douglas L. Chalker, Patrick Fuller, and Meng-Chao Yao

Following conjugation, the development of new somatic micronuclei in Tetrahymena involves the removal of some 6000 DNA elements totaling nearly 15 megabases. Regions to be eliminated are targeted by a process that involves comparison of the germline genome with that of the parental somatic genomes. Excision of a specific DNA segment from the developing somatic nucleus is inhibited if the homologous sequence is placed within a parental somatic nucleus. These authors demonstrate that the protection of such sequences in the maturing new somatic nucleus by the parental genome does not require direct genetic exchange, but rather appears to be mediated by small sRNAs.

GENETICS/2004/032870

Sperm competitive ability in *Drosophila melanogaster* associated with variation in male reproductive proteins

Authors: Anthony C. Fiumera, Bethany L. Dumont, and Andrew G. Clark

Previous experimental work links sperm competition in *D. melanogaster* to variation in genes that encode proteins in the seminal fluid. In this paper the authors assess the extent to which variation in sperm competition within natural populations of *Drosophila* can be ascribed to differences in such genes. Chromosome 2 substitution lines were scored for sperm competitive ability, genotyped for markers in 10 male reproductive genes and assayed for the level of transcription of each of those genes. A large number of significant associations between polymorphisms in the male reproductive genes and sperm competitive ability support the view that natural variation in sperm competition reflects divergence at such genes.

GSA Supports NIH Open Access Publishing Proposal

The NIH has proposed that researchers be required to submit their manuscripts accepted for publication to PubMed Central, which will make them freely available six months after publication (see: http://www.nih.gov/about/publicaccess/index.htm). The GSA Board of Directors expressed support of this proposal, but noted a few concerns. The complete text of GSA's response can be viewed at http://genetics.faseb.org/genetics/g-gsa/gsa-response-nih.shtml.

2005 GSA Awards

The three annual GSA awards and their recipients for 2005 are:

- **The George W. Beadle Award**, for outstanding contributions to the community of genetics researchers: **Thom Kaufman**, University of Indiana.
- **The Genetics Society of America Medal**, for outstanding contributions in the last 15 years: **Steve Elledge**, Harvard University.
- **The Thomas Hunt Morgan Medal**, for lifetime contributions to genetics: **Robert Metzenberg**, University of Wisconsin and UCLA.

Congratulations to our award recipients. Watch upcoming issues of *GENETICS* for descriptions of the awardees' contributions.

Public Policy Update *Continued from page 8*

the chopping block, grassroots efforts by scientists are going to be essential for protecting the research enterprise.

The GSA recognizes that publicly funded scientists have a responsibility to explain the value of their research to their elected officials, and encourages its members to join the Congressional Liaison Committee (CLC) of the Joint Steering Committee for Public Policy. The CLC is a direct link for bench scientists to public policy and legislative information affecting biomedical research funding and policy. The CLC provides scientists nationwide with the opportunity to help educate their member of Congress and advocate for many of the important issues facing the scientific community. To join the CLC, sign up at http://www.jscpp.org/clc.cfm.

United Nations Won't Seek Comprehensive Cloning Ban

After nearly two years of debate, the United Nations abandoned the pursuit of a global ban on reproductive and therapeutic cloning. While there is near unanimous support among the 191 member countries of the U.N. to ban reproductive cloning, they have wrestled over the right of countries to clone human embryos in pursuit of cures for life-threatening diseases.

The Sixth Legal Committee of the General Assembly had been considering rival resolutions: One offered by Costa Rica and heavily supported by the Bush administration, sought to ban all forms of cloning. The other, co-sponsored by pro-research nations such as Belgium, the United Kingdom, Japan and Singapore allowed cloning for research purposes. It was clear neither side had enough support for ratification and with the threat of procedural delays looming, both sides agreed to an 11th hour compromise proposed by Italy. Italy's proposed non-binding declaration contained language ambiguous enough to allow countries to establish cloning laws on an individual basis. The draft declaration will be the basis for discussions that will resume in February.

The Genetics Society of America

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Public Policy Update

by Matt Zonarich, Joint Steering Committee for Public Policy

A Decisive Victory for Stem Cell Research

On Election Day, California voters passed the California Stem Cell Research and Cures Initiative. Passage of this measure makes California poised to become a global leader in stem cell research and is a clear denunciation of President Bush's stem cell policy. The measure creates the California Institute for Regenerative Medicine, which in 2005 will start distributing $295 million per year for ten years, to support embryonic stem cell research. Modeled after the National Institutes of Health, funds will be dispersed on a competitive, peer-reviewed basis.

NIH/NSF Funding Update

After the November elections, Congress returned to a lame-duck session to complete the remaining FY 2005 appropriation bills. The White House, coming off significant political gains in the election, insisted on maintaining strict spending limits. In order to meet these limits, Congress cut nearly $8 billion from the remaining appropriation bills, approving before the Thanksgiving recess a $388 billion measure. This represents a total freeze in funding for domestic programs over last year. The bill provides the NIH with $28.6 billion, an increase of $800 million, or 2% over last year's figure. But with mandatory cuts the total NIH appropriation will be approximately $28.4 billion. The National Science Foundation was hit with substantial cuts, receiving $5.47 billion, 2% less than last year's budget.

Join the CLC

With the federal budget deficit expected to reach an all time high over the next few years, it is likely the Bush administration will recommend significant cuts in FY 2006 for many popular domestic programs, including the NIH and the NSF. With these programs on

Continued on page 7