Meeting Minutes of the 2011 Fly Board Meeting

The 2011 National Drosophila Board Meeting took place Wednesday, March 30 in the Pacific Ballroom, Salon 1 at the Town and Country Hotel in San Diego, CA from 3:00-6:00.

Attendees: Michelle Arbeitman, Eric Baehrecke, Dan Barbash, Hugo Bellen, Celeste Berg, Nancy Bonini, Gio Bosco, Michael Boutros, Kevin Cook, Steve Crews, Janice Fischer, Liz Gavis, Bill Gelbart, Pam Geyer, Leslie Griffiths, Karen Hales, Thom Kaufman, Krystyna Keleman, Jim Thompson, Allan Spradling, Teri Markow, Kathy Mathews, Helen McNeill, Stephanie Mohr, Denise Montell, Mike O'Connor, Terri Orr-Weaver, Leo Pallanck, Liz Perkins, Helena Richardson, Juan Riesgo-Escovar, Hanele Ruohola-Baker, Helen Salz, Jeff Sekelsky, Carl Thummel, Henry Sun

AGENDA

1. Introduction & Approval of 2010 Minutes	3:00-3:05	Report
2. Report from 2011 Fly Meeting Organizers	3:05-3:20	Page 8
3. Introduction of 2012 Fly Meeting Organizers	3:20-3:22	-
4. Report of the GSA Meeting Coordinator (Suzy Brown)	3:22-3:30	Page 30
5. Treasurer's Report (Pam Geyer)	3:30-3:40	Page 32
6. Drosophila Board Election Report (Carl Thummel)	3:40-3:50	Page 36
7. Image Award	3:50-3:50	Page 39
8. Sandler Lectureship Committee (Denise on behalf of Claude)	3:50-3:55	Page 39
9. Undergraduate Education Initiatives (Karen Hales)	3:55-4:00	Page 40
10. 1st Asia-Pacific Drosophila Research Conference (Henry Sun)	4:00-4:05	-
11. Discussion of national funding situation, NCRR, TRI, stock center funding (all)	4:05-4:30	-
Break	**4:30-4:50**	
COMMUNITY RESOURCES AND PROJECTS	**4:50-6:00**	
12. Upcoming White Paper (Denise Montell)		
12. Bloomington Stock Center (Kathy Matthews and Kevin Cook)		42
13. Possible Indian Stock Center Update		42
14. Berkeley Drosophila Genome Project (Sue Celniker)		43
15. ModENCODE and ModENCODE II (Sue Celniker)		45
16. Genome Disruption Project (Hugo Bellen)		47
17. Harvard Drosophila RNAi Screening Center and Transgenic RNAi Project (Stephanie Mohr)		50
18. Vienna Transgenic RNAi Project (Krystyna Keleman)		54
19. DIS (Jim Thompson)		54
20. DGRC		-
21. Species Stock Center		55
22. Flybase (Bill Gelbart) Drosophila		59
ADJOURN	6:00	

3:00pm Call to order.
Began Fly meeting organizer report – paused for introductions.

Fly meeting organizer report: Gio Bosco, Leslie Griffiths, Dan Barbash
Registration numbers slightly down (9%) from last year, but on par with previous three years. Things worked smoothly overall, the geographical separation of organizers wasn't a problem.

Next years organizers are Steve Crews, Celeste Berg, Kevin White, Erika Matunis.

Issue came up as to whether the session topics are too broad, for example "cell biology" - makes it difficult for people to choose a session when submitting abstracts for talks.

It was pointed out that there are secondary terms that can be chosen if people aren't sure which session is best and others agreed that being able to select two sessions gives sufficient coverage – also, the use of the secondary topics helps the organizers to spread talks and even out the number of talks considered for each session.

There was a discussion about the balance between ensuring that the same speakers/labs aren't chosen for talks year to year with ensuring high quality talks. The organizers didn't think that it was particularly important to make sure that the same lab didn't talk two years in a row, as long as it isn't the same talk, but they did try hard not to have more than one talk per lab per year.

Suzy Brown's report:
1) budget in pretty good shape, trying to break even and we will likely do so
2) meeting venues are booked through 2016, and the meeting will likely be held at this venue again in 2017 given that the rates are good and the staff are easy to work with – no complications with the current meeting.

Treasurer's report: Pam Geyer
The GSA requires that we have $150K to guarantee a meeting
Right now we have a total fund of $261K – we are making money
Registration for the fly meeting has been pretty constant

Should we spend down some of the accumulated funds?
Suzy reminded us that the Chicago meeting will be more expensive and typically loses money. Ideas for other ways to use money included travel awards, additional/better coffee breaks. Suzy explained that we did indeed add some things back that had been cut at previous meetings, like coffee breaks and that we are easing back into providing some niceties - this year we are subsidizing $1 of the drinks for the welcome reception.

This year we are also providing low cost undergraduate fees.

After continued discussion, there was consensus that a good way to spend money would be to institute travel awards. This raised the question of who would chose the recipients and

it was discussed whether the DeLill Nasser award committee could oversee selecting the fly meeting-specific travel awards. The DeLill awards are meeting-independent, however, so the committee would have to use different selection criteria. Support developed around the idea of a competitive award that would defer part (~$500) but not all of the costs to attend the meeting. This would have the benefit of giving winners something to put on their CV and might attract people to the meeting who would otherwise not go.

Denise proposed a new committee and Pam suggested that that committee could be made up of the regional reps – would be a good way for them to participate more actively. Everyone agreed with this idea.

Karen requested that there be some money set aside for undergraduate travel awards.

It was decided that Pam and Suzy will figure out how much money can be put toward travel awards and that the regional reps will form the selection committee.

Election report: Carl Thummel

The committee was maintained at 5 people this year, with Debbie Andrew and Susan Parkhurst joining Carl, Jay Hirsh, and Barry Ganetzky.

Voting is still extremely low – only 13% of those contacted actually voted.
Probably the community does not see what the board does and so is not motivated to vote. That is why we started Fly News, the quarterly Drosophila email newsletter that describes the board's activities and is mailed to the Flybase email address book.

There was a discussion about how regional reps could interact better with their constituency – so they would be more visible, play more of a role. Ideas included using blogs, providing email lists to reps for their specific regions, sending out a regional newsletter. It was decided to leave this up to the regional reps.

Bill suggested that regional reps could post their own newsletters on FlyBase so that everyone could see them and Thom urged people in general to send things they want posted to FlyBase – they're happy to post material, but they can only do it if they have the material.

Image award: Denise in lieu of David Bilder

Getting lots of submissions, working fine.

Sandler lecture: Denise in lieu of Claude Desplan

Claude was disappointed in the number of nominations received this year – the quality of the nominees was very high, but there were only 5 of them.

Some people felt that advisors view the bar as so high that their students won't get the award anyway. It was recommended that the conference organizer who introduces the Sandler award encourage students in the audience to encourage their advisors to nominate them.

It was suggested that it would help to extend the eligibility period to 18 months from graduation – this would likely increase the number of nominees. After a brief discussion an 18 month eligibility period was agreed on.

Undergrad institutions: Karen Hales
Karen has now served her first year as the PUI rep and it has been a successful year.

There are numerous undergrads events being held at the meeting for the first time this year. including a mixer on first night , undergraduate plenary session on Friday afternoon, also an event (a mixer) for the PUI faculty

On Thursday morning the Undergraduate Experience program will allow students and faculty from local schools to attending the fly meeting for part of the day

Karen pointed out that Beth Ruedi and Suzy Brown from GSA were very helpful in planning these events.

Two goals have not yet been met, however - travel funding for undergraduates and the institution of a pedagogy workshop at the meeting.

Henry Sun: Asia/Pacific

The Asia/Pacific conference has over 300 registrants with good coverage from many countries.
The meeting received support from Japan and Taiwan for student and postdoc travel funds – they gave 72 awards (100% of applicants for the awards were funded).

Discussion of the national funding situation:

An extended discussion was held concerning the national funding situation for Drosophila research and what the Drosophila community can and should do to ensure/enhance funding. Three challenges were recognized: advocating for the NIH budget at the national level by getting Drosophila researchers on the FASEB board; and educating other scientists and administrators within the NIH about the importance of this model organism; educating the general public about the contributions Drosophila research can and does make towards improving human health.

As a community, we should engage the public and advocate for Drosophila research as much as possible. We do not always do everything we can. For example, last year at fly meeting science writers affiliated with the GSA contacted speakers to meet with them, but only three of the speakers agreed to meet with the writers.

The next time a FASEB opening comes up we should suggest names of Drosophila people who would be willing to serve.

The idea was put forward that the community should develop a website to illustrate how Drosophila research can lead to medical advances. FlyBase is also developing tools for non-experts.

Two concrete suggestions emerged from this discussion. One is that the Drosophila board could use some of the community's accumulated funds to support a part time science writer to develop a website for educating the general public and drawing the attention of science writers for major newspapers to Drosophila research. Secondly there could be a new board member position for coordinating outreach and education who would then report to the board.

White Paper:

This year the White Paper will be updated to reflect new and emerging priorities for the Drosophila community, such as stock centers and clone banks, meeting the goals of having loss of function tools for every gene in the genome, etc. The suggestion was made that a third topic be added to the next White Paper – understanding the contribution of individual variation to disease, an important topic in human genetics community. Foundational work is going on in Drosophila. We should leverage genome-wide association studies, common alleles, and identifying disease alleles. Copy number polymorphisms are highly correlated with human disease, flies have a lot to offer for such population studies.

Bill Gelbart indicated that he would take responsibility for this section of the White Paper – will form a group with Trudy McKay, Langely etc. to write this part

Eric mentioned that production of antibodies has been part of the White Paper but never actually gets done – and proposed including synthetic technology being used at U of Toronto (Lipshitz lab).

Hugo reminded the Board that projects involving community resource development need lots of support – many letters required to get a resource project funded but agreed that it still needs to be in the White Paper

Discussed the idea that gene expression analysis could be separated from functional analysis and then antibodies could be put into expression analysis – can't interpret functional analysis without expression analysis

Updates from community resource projects

Bloomington stock center: Kathy Mathews – nothing to add over the report which is appended to the minutes.

Denise mentioned that the Indian stock center is still planning to move forward, nothing new to report.

BDGP/modENCODE: Sue Celniker

Summary is in the report appended to the minutes projects are well funded for next couple of years, they will
will have over 10,000 tagged expression ready clones that can be moved around

Sue raised the issue of the next phase, modENCODE2 – justified by the need for studying transcription factors, switching to tagged proteins, chromatin analysis to be done at developmental stages and tissues, goal of obtaining cellular resolution of transcriptional information – many areas to pursue

Bill suggested that we need to come back to this topic during the discussion of the White Paper and pointed out the need for the fly community at large to give their input. The key question is whether modENCODE2 should be a continuation of what was done before but at deeper levels or whether it should go in new directions

Gene disruption project: Hugo Bellen

Summarized report provided in the agenda,
800 Mi{Mic} lines have deposited at Bloomington, Mi{Mic} database can be accessed on Hugo's website and at Bloomington
They have obtained support for another 4 years

X chromosome duplications (transgenics and Kevin's duplications) are progression, there is a
poster available as PDF from FlyBase

DRSC: Stephanie Mohr

They are sending out more and more lines as people are setting up to do screens at their own institutions.

Stephanie also mentioned that there are many people who work in other organisms, like mouse, who are now coming to the center to do RNAi screens.

Harvard TriP: Liz Perkins

Liz is collecting letters of support for making TriP lines. She expressed concerns about funding. The Vallium 22 grant received a fundable score but was not funded because it went to NICHD whose budget is low. The resubmission will have to be delayed a cycle because it is reviewed at the same study section as the main TriP grant, which is going in for renewal.

VDRC:
Krystyna Kelemen described the VDRC collection

Species stock center: Teri Markow

Teri noted that they are getting a lot of requests for different strains of a particular species – people doing studies of polymorphisms, also many people seem to be interested in DNA rather than in live flies.

The stock center renewal was cut by half of what was requested and the grant period was cut to 4 years instead of 5 years. She also mentioned that the NSF wants to do a workshop to show them how to use a proper business model.

There was a brief discussion about how the NSF wants to stop supporting these sorts of projects.

Bill mentioned that he would be happy to post stories on FlyBase about why these different fly species are interesting if Teri can provide them.

The next discussion centered on a letter to Denise from Susan Gerbi, who has applied for funding for a Sciara genome sequencing project. Adam Felsenfeld at the NIH gave her feedback that the grant was hurt by the fact that Sciara was not mentioned in the White Paper.

Sciara is a valuable species to the fly community – stocks have been around for years, it is an important and interesting part of the phylogenetic tree, the term epigenetics originated from work in Sciara. The suggestion was made to make it an honorary Drosophila species.

On the other hand it was noted that there is already an arthropod wide genomics initiative that is doing this sort of work and perhaps we should not spread ourselves thinner by adding additional species that are not actually Drosophila. The suggestion was made to point Susan toward the arthropod wide genomics initiative.

The White Paper is not meant to advocate for specific projects, rather it is there to highlight important priorities for the whole community. Nevertheless, the funding agencies want to

see support for specific projects articulated– this make for a difficult situation because anything we leave out of the white paper will be perceived as lacking support. For each request, we need to think about what the value is to the whole community not just the person asking for support. The more funding that goes to other species, the less there is for Drosophila in the present funding climate. In the end, a motion was put forth to write a letter of support sequencing additional arthropod species including Sciara, however that motion failed to pass.

2. REPORT OF 2011 MEETING ORGANIZERS (Giovanni Bosco, Daniel Barbash, Leslie Griffith)

The formation of this year's organizing committee started in spring of 2009, when Gio Bosco contacted Dan Barbash and Leslie Griffith to explore the possibility of the three of us organizing the 2011 meeting in San Diego. We got input from the organizers of the 2010 meeting and began to get on track with the invaluable help of Suzy Brown soon after that. Organization went smoothly, with most things done by email (couple of conference calls). Most items were decided by consensus with particular tasks delegated to individuals for completion. The geographic distance between the three organizers did not negatively impact the meeting organization efforts.

Program Book & Registration:
Only the schedule and lists of talks and posters are in the Program Book. All abstracts are available online and a meeting Wi-Fi will be set up for on-site access to abstracts.

Pre-registration for the meeting is strong but lower than last year. 1,414 people had registered for the meeting as of March 2, 2011, down 9% from 2010, but comparable to previous years. For comparison, pre-registration numbers for several recent years are as follows: 1,516 (2010), 1,383 (2009), 1,343 (2008), 1,345 (2007), 1,241 (2006), 1,451 (2005), and 1,470 (2004). Interestingly, the number of abstracts submitted is higher than any other year (see below)

The meeting organizers, plenary speakers, and panelists for the historical lecture were given a free conference registration. (However, a few decided to pay registration fees in order to support the conference and the GSA.) This policy is a continuation of what was offered the year before. Everyone had to cover their own room fees and travel costs. The Larry Sandler Award Winner receives complementary airfare, registration, hotel accommodations and GSA membership. The organizers did receive a handful of requests for registration/travel "grants" none of which were granted, keeping with past practices.

Invited Speakers:
During May 2010, the organizing committee compiled a list of possible Plenary Speakers. Our criteria were (as usual) representation of the breadth of research done with Drosophila, equal gender representation, and a mix of up-and-coming junior and well-known senior investigators. We eliminated people who had given plenary talks recently (see below) and then decided based on email/phone conversations on a final list at the end of May. We invited Dr. Francis Collins, director of the NIH, but he was unavailable. We decided that it was overdue to have a plenary speaker from Russia, and were happy that Igor Zhimulev was able to accept. We decided to continue the (sort-of) recent tradition of having one speaker working on non-Drosophila insects, and invited Anna Dornhaus who works on ant social behavior, as this topic would complement the other plenary presentations.

2011 Plenary Speakers:
Linda Partridge, Paul Garrity, Brian Lazzaro, Larry Goldstein, Patricia Wittkopp, Igor Zhimulev, Kami Ahmad, Therese Markow, Vivian Budnik, Eric Lai, Anna Dornhaus, Eric Weischaus. We sent email invitations to the speakers by the end of May and heard back from everyone pretty quickly. It took several tries to obtain abstracts from some of the plenary speakers, so clarity on this requirement in the invitation is probably a good idea.

Historical Panel:
The Organizing Committee agreed that the panel discussion format for the Historical Lecture from the last few year seemed to work, so we decided to highlight behavioral studies in Drosophila. We recruited Michael Rosbash, one of the leaders in the field of circadian biology, to help select the speakers and be the moderator of the event. Michael was in charge of communicating with the speakers and arranging the order of their short (~12 minutes each) presentations. The speakers include Michael himself, Scott Waddell (a leader in the field of olfactory memory), Ulrike Heberlein (pioneer in development of fly models for drug and alcohol abuse) and Stephen Goodwin (expert in sex determination and its behavioral consequences).

Abstracts and Platform Sessions:
Feedback we received from the previous year (2010) meeting organizers informed us that poster judging was one task session chairs spent too much of their conference time and was difficult to complete in timely manner. We decided to have co-chairs for all sessions, which we felt would be particularly helpful for handling the poster judging. For most sessions, we invited a single person and asked them to nominate a co-chair. We ended up accepting all the co-chair suggestions because we felt it was important that the co-chairs know each other and be able to work together effectively. Each pair of co-chairs worked out their own system of abstract reviews and have been informed that they can share poster judging responsibilities as they see fit—as long as it gets done on time.

The number of abstracts submitted per topic area varied widely. The largest number was for Cell Biology and Signal Transduction (115), but this was due to a mistake of not having a separate choice of Cell Biology and Cytoskeleton during abstract submission. We therefore assigned about half of the abstracts to Cell Biology and Cytoskeleton based on the keywords of abstracts submitted under Cell Biology and Signal Transduction.

With the schedule available, 4 topic areas could be chosen for double sessions. Drosophila Models of Human Diseases, Evolution and Quantitative Genetics, and Gametogenesis and Organogenesis had the largest number of abstracts submitted and were chosen. For the fourth, we chose Regulation of Gene Expression, because it had a very large number of abstracts listing it as the secondary topic. This gave us flexibility to move abstracts from many areas to this session.

Cell Cycle and Checkpoints and Cell Death had small numbers and were merged into one session. RNA Biology, and Immunity and Pathogenesis also had a small number of abstracts. We therefore asked the session chairs to choose additional abstracts from among those that listed these areas as secondary topics.

A sample letter giving instructions to session chairs about choosing abstracts is attached. Chairs with double sessions were instructed to indicate ~20 candidate abstracts for talks.

Notes: We didn't realize at that time that some sessions have 7 rather than 8 slots; we don't think that this mistake had much impact.

We asked the chairs to check last year's program in order to not have the same people/labs speaking 2 years in a row. We're not sure if anyone did this, and we found it difficult ourselves to try to enforce this. We also found it challenging to follow who the PI was for any given abstract. This was an important fact to know since we made every effort possible to distribute presentation slots to as many different PIs/labs as possible. We noted junior/assistant professor PIs and/or their students wishing to present, and tried our best to have a fair representation of talks from junior PI labs. The session co-chairs were instructed to keep this in mind when selecting abstracts, and they were also asked to select only a few PI presenters—favoring students and post-docs whenever possible. A suggestion for future conferences is that a searchable database of session chairs, session speakers and the lab PIs be set up. This may be as easy as excel files with lists of names that could be handed down by organizers. Currently, a list of session chairs and speakers (such as the one shown below) are found in reports and can be used by meeting organizers. The general issue of striving to balance fairness with featuring the highest quality science is a challenge that the Board may wish to discuss further.

Final abstract assignments:
One or two session chairs asked for our advice on assigning talks, for example one session had many PIs selected which seemed to go against the tradition of the conference. We worked with them to choose instead 1-2 junior people. We made a few other adjustments, and also picked highly rated abstracts from various topic areas to fill the second half session of Regulation of Gene Expression. In general, things went smoothly in part due to the advice from last year's organizers about being very clear on first author as speaker and selection of only those who checked the box for talks.

Main Topic	Total # of Abstracts	# Requesting Platform	# Requesting Poster	Secondary Topic Total # Abstracts	# Requesting Platform	# Requesting Poster
Cell Biology and Signal Transduction	**115**	**62**	**53**	**129**	**69**	**60**
Cell Cycle and Checkpoints	**19**	**8**	**11**	**24**	**13**	**11**
Cell Death	**28**	**19**	**9**	**17**	**10**	**7**
Cell division and growth control	**53**	**33**	**20**	**59**	**28**	**31**
Chromatin and epigenetics	**64**	**28**	**36**	**36**	**16**	**20**
Drosophila models of human diseases	**82**	**35**	**47**	**77**	**33**	**44**
Evolution and quantitative genetics	**93**	**46**	**47**	**45**	**24**	**21**
Gametogenesis and organogenesis	**83**	**41**	**42**	**71**	**31**	**40**
Immunity and pathogenesis	**39**	**18**	**21**	**16**	**11**	**5**
Neural physiology and behavior	**58**	**32**	**26**	**44**	**17**	**27**
Neurogenetics and neural development	**49**	**27**	**22**	**72**	**37**	**35**
Pattern formation	**39**	**19**	**20**	**81**	**45**	**36**

Physiology and aging	**42**	**23**	**19**	**50**	**29**	**21**
Regulation of gene expression	**62**	**30**	**32**	**147**	**65**	**82**
RNA biology	**35**	**15**	**20**	**15**	**10**	**5**
Stem cells	**38**	**23**	**15**	**23**	**18**	**5**
Techniques and functional genomics	**55**	**25**	**30**	**48**	**28**	**20**

Sample instruction letter for choosing abstracts

Dear Bill and Liz,

Thank you for agreeing to chair a session on RNA biology at the 2011 Drosophila Conference. Please read this carefully, and reply (using the attached spreadsheet) by Dec. 2, 2010. We the organizers will do the final sorting and session assignments to make sure that there is a good distribution of quality talks and that particular labs are not overrepresented.

Your job is to go through the abstracts and pick the best of the abstracts for your platform session. Please pick from the abstracts that have requested a platform presentation (marked with asterisks in the website).

Your session has a small number of abstracts based on primary session choice. Therefore we are asking you to please select from those that indicated RNA biology as either primary or secondary choice.

Abstracts sorted by primary session choice are available for review at: http://www.drosophila-conf.org/cgi-bin/dros11-cgi/rpt/pcmain.pl?st=1.

Abstracts sorted by secondary session choice are available at: http://www.drosophila-conf.org/cgi-bin/dros11-cgi/rpt/pcmain.pl?st=2.

Please note that you have options for viewing all abstracts for your session on the website, or only those requesting platforms.

SPECIFIC INSTRUCTIONS

1) First, quickly review ALL abstracts (poster and platform) in your session to ensure they have some scientific merit. It is a rare event to reject an abstract, but we don't want to include anything inappropriate or embarrassing to the GSA/Drosophila community.

2) Your session will have 8 platform talks. Please recommend to us approximately 10-12 for talks by marking on the attached spreadsheet (yellow column). You do not need to rank these choices individually, but please group them into 2 or 3 levels of priority. For example: 1 = excellent, definite platform. 2 = very good, platform if available.

3) For the abstracts you've selected only, if it seems more or equally appropriate for a different session, please indicate that in the pink column.

4) For the abstracts you've selected only, please indicate the lab group/PI that the abstract is coming from (green column). This will help us distribute talks over the meeting as a whole.

5) Please check last years program to ensure that a similar talk was not given by the same person/lab. http://www.drosophila-conf.org/cgi-bin/dros10-cgi/drosSOE.pl

OTHER CONSIDERATIONS:

1) High quality is the most important criterion, but please strive for fairness. If 2 groups have similar abstracts, either both should be selected for posters or both for platforms.

2) Please ensure that your choices reflect the diversity of research in your field, and include a range of speakers from both junior and senior research groups.

3) If you find you do not have enough high-quality abstracts to make a strong session, please inform the organizers. We can probably move some good abstracts into your session from other groups.

The above plan will allow us flexibility to move some talks to different sessions if needed, and to ensure that no lab is over-represented for platform talks.

THANKS!!!

Leslie, Dan and Gio

Abstract Submission:
Abstracts were solicited in 18 topic areas with associated keywords (see table above). We received 974 abstracts by the early deadline (10 withdrawn), and 102 late abstracts for a total of 1066 abstracts. Totals in recent years were: 1046 in 2010, 1020 in 2009; 993 in 2008, 897 in 2007, 910 in 2006, 1043 in 2005, 982 in 2004, 1016 in 2003, 1003 in 2002 and 966 in 2001. There were 484 requests for platform presentations for 156 available slots, allowing accommodation of (on average) 32% of the requests, close to that of recent years. In one case where an abstract did not report any conclusions or observations (seemed be a place holder) the PI was contacted directly and allowed to revise the abstract (which took two tries). There were no abstracts rejected.

Workshops:

The workshop proposals were all strong, and with the exception of two that had significant overlap, were distributed in topic. The two groups that overlapped were asked (and agreed) to combine forces and form a single workshop (Cell competition and tissue growth regulation); all the other applications were accepted. The scheduling was done so as to have 4 concurrent workshops in each slot with the exception of modENCODE, which was felt to be a sufficiently big draw that it was scheduled with no competition. Ecdysone retained its traditional early singleton slot on Wednesday.

Workshop organizers were strongly encouraged to adopt presentation formats that were different from session presentations, e.g. something other that a 15 minute talk with 5 minutes of questions. This suggestion was made based on feedback from past workshop attendees that felt that most workshops were just extensions of platform session presentations. Despite

repeated suggestions that more discussion group formats be adopted, only a few (ModEncode and Chromosome Pairing) workshop organizers have responded favorably to this suggestion.

As recommended by last year's organizers, to prevent people from speaking at more than one event (and potentially giving essentially the same presentation), we provided a list of the platform speakers to the Workshop chairs when they were notified that their Workshop proposal has been accepted. There was at least one case where a workshop presenter had to withdraw because he had been selected for a session oral presentation.

Day/Date	Time	Proposed Workshop Title
Wednesday, March 30	12:00 PM	Ecdysone Workshop
Friday, April 1	1:45 PM	Cell Competition
Friday, April 1	1:45 PM	Apoptosis, Autophagy and other cell death mechanisms
Friday, April 1	1:45 PM	Chemical Genetics and Drug Screening
Friday, April 1	1:45 PM	Mechanisms and functions of chromosome pairing
Saturday, April 2	9:30 PM	modENCODE workshop
Saturday, April 2	6:45 PM	Confocal Imaging
Saturday, April 2	6:45 PM	Drosophila Research and Pedagogy at Primarily Undergraduate Institutions (PUI)
Saturday, April 2	6:45 PM	Quantitative biology of cell signaling and pattern formation
Saturday, April 2	6:45 PM	Emerging Model Arthropods
Saturday, April 2	6:45 PM	Everything You Ever Wanted to Know About Sex

In addition to these workshops, the following events will take place at this years' meeting in order to augment GSA's efforts to advance education and career development:
*Undergraduate Plenary Workshop (Friday afternoon)
*Undergraduate Mixer (Thursday night)
*Undergraduate Experience (They will attend a portion of the 1st Plenary Session then get together to discuss the session as a group - led by Beth Ruedi)
*GSA Career Luncheon (this isn't new, it has just been renamed)
*PUI Workshop (listed above as a workshop-- not new this year but another educational initiative)
*There will also be a Special Interest Group Mixer on Thursday night for those PIs interested in getting more involved in undergrad education at GSA.

Poster awards:
The award committee consists of all the platform session chairs for the initial judging, and the meeting organizing committee for the final selections. The session chairs are responsible for examining all the posters in their sessions and nominating three per session (one postdoc/PI, one graduate student and one undergraduate poster, if possible) via e-mail to Gio Bosco by 5 p.m. Friday April 9. The initial nominations will be forwarded to the other organizing committee members, and all organizing committee members will view the nominated posters and vote on the winners by Saturday morning. Ribbons (1^{st}, 2^{nd}, 3^{rd} place, Honorable Mention) will be pinned on the posters at that time, so that conference attendees will have sufficient time to examine the winning posters. Winners will be recognized during the final plenary session, and

the winning posters will also be displayed in front of the plenary session room. The GSA provides cash prizes and copies of Conversations in Genetics videos to give to the award recipients. Only 1st, 2nd and 3rd place winners get the prizes. Honorable mention does not get a cash prize. This year a category has been added so that undergrads can also win (first, second or third). Undergraduate posters should be easily identified. Gio Bosco will be responsible for reminding session chairs of this duty and for distributing the prizes.

Interaction with the GSA office:
Suzy Brown again did a fantastic job helping the organizing committee with all aspects of meeting organization. She has a detailed timetable that is very helpful, and readily (and speedily) answers every question. This meeting would not have been possible without her.

INFORMATION USEFUL FOR PLANNING FUTURE MEETINGS:

PLENARY SPEAKERS, FROM 1995 THROUGH 2011:

Susan Abmayr	1995
Kami Ahmad	2011
Ravi Allada	2007
David Anderson	2008
Kathryn Anderson	1999
Deborah Andrew	1997
Doris Bachtrog	2005
Bruce Baker	1996, 2002
Utpal Banerjee	1997, 2005
Daniel Barbash	2009
Konrad Basler	2003
Amy Bejsovec	2000
Phil Beachy	1998
Eric Baehrecke	2010
Hugo Bellen	1997
Marianne Bienz	1996
Ethan Bier	2002
Mark Biggin	2008
David Bilder	2008
Seth Blair	1997
Grace Boekhoff-Falk	2003
Nancy Bonini	2000
Juan Botas	1999
Andrea Brand	2001
Sarah Bray	2005
Nick Brown	2009
Vivian Budnik	2000, 2011
Ross Cagan	1998
John Carlson	1999, 2002
Sean Carroll	1995, 2006
Richard Carthew	2005
Elizabeth Chen	2010
Sara Cherry	2008
Bill Chia	2006
Chiara Cirelli	2010
Andrew G. Clark	2002
Tom Cline	2000
Steve Cohen	2008
Francis Collins	2004
Lynn Cooley	2010
Claire Cronmiller	1995
Ilan Davis	2001
Rob Denell	1999
Wu-Min Deng	2009
Claude Desplan	2007
Michael Dickinson	1995, 2009
Barry Dickson	2006

Daniella Drummond-Barbosa	2009
Chris Doe	1996
Anna Dornhaus	2011
Ian Duncan	2001
Bruce Edgar	1997
Mike Eisen	2007
Sarah Elgin	2005
Sharyn Endow	2010
Anne Ephrussi	2001
Mel B. Feany	2002
Martin Feder	1998
Janice Fischer	1998
Nicole Francis	2008 (accepted but withdrew March 7th)
Matthew Freeman	2004
Minx Fuller	2003
Barry Ganetzky	2009
Paul Garrity	2011
Ulrike Gaul	2007
Elizabeth R. Gavis	2002
Pam Geyer	1996
Richard Gibbs	2003
David Glover	2000
Larry Goldstein	2011
Kent Golic	2001
Ralph Greenspan	2005
Leslie Griffith	2006
Ernst Hafen	2005
Iswar Hariharan	2003
Dan Hartl	2001
Scott Hawley	2001
Tom Hayes	1995
Ulrike Heberlein	1996, 1998
Martin Heisenberg	1998
Steve Henikoff	2009
David Hogness	1999
Joan Hooper	1995
Ken Irvine	2010
Yuh Nung Jan	2005
Wayne Johnson	2000
Laura Johnston	2005
Gary Karpen	2006
Timothy Karr	2003
Thom Kaufman	2001
Manolis Kellis	2008
Rebecca Kellum	1999
Christian Klambt	1998
Elisabeth Knust	2010
Artyom Kopp	2008
Thomas B. Kornberg	2002
Mark Krasnow	2004
Henry Krause	2004

Ed Kravitz	2004
Mitzi Kuroda	2003
Eric Lai	2011
Chuck Langley	2006
Paul Lasko	1999
Cathy Laurie	1997
Brian Lazzaro	2011
Thoma Lecuit	2007
Ruth Lehmann	2002
Mike Levine	2003
Bob Levis	1997
Haifan Lin	1995
Susan Lindquist	2000
John Lis	2001
Troy Littleton	2006
Liqun Luo	2003
Trudy Mackay	2000
Richard Mann	2006
Therese Markow	2011
J. Lawrence Marsh	2004
Erika Matunis	2004
Dennis McKearin	1996
Mike McKeown	1996
Gero Miesenbock	2006
Jon Minden	1999
Marek Mlodzik	2006
Antonia Monteiro	2010
Craig Montell	2010
Denise Montell	2002
Mohamed Noor	2007
Roel Nusse	1997
David O'Brochta	1997
Michael O'Connor	2005
Terry L. Orr-Weaver	2002
Linda Partridge	2004
Mark Peifer	1997
Trudy MacKay	2000
DJ Pan	2010
Linda Partridge	2011
Nipam Patel	2000
Norbert Perrimon	1999
M. Ramaswami	2001
Robert Rawson	2003
John Reinitz	2009
Don Rio	2007
Pernille Rorth	1995, 2007
Gerry Rubin	1998, 2001
Eric Rulifson	2007
Hannele Ruohola-Baker	1999
Babis Savakis	1995
Paul Schedl	1998

Dietmar Schmucker	2008
David Schneider	2009
Gerold Schübiger	1996
Trudi Schüpbach	2004
Thomas Schwarz	2007
Kristin Scott	2007
Matthew P. Scott	2002
John Sedat	2000
Amita Sehgal	2003
Pat Simpson	2008
Marla Sokolowski	1998
Allan Spradling	2008
Ruth Steward	1996
Daniel St. Johnston	2005
Tin Tin Su	2002
Bill Sullivan	1996
John Sved	1997
John Tamkun	2000
Barbara Taylor	1996
William Theurkauf	2002
Jessica Treisman	2005
Tim Tully	1995
Tadashi Uemura	2009
Talila Volk	2004
Leslie Vosshall	2006
Barbara Wakimoto	2001
Lori Wallrath	2007
Steve Wasserman	1996
Kevin P. White	2004
Kristin White	2004
Eric Wieschaus	1996, 2011
Rachel Wilson	2008
Patricia Wittkopp	2011
Mariana Wolfner	2009
Ting Wu	1997
Ting Xie	2010
Tian Xu	1997
Jennifer Zallen	2009
Philip Zamore	2003
Igor Zhimulev	2011
Larry Zipursky	2010
Susan Zusman	1998

SESSION TOPICS AND KEYWORDS 2011

Note that these were used for abstract submission, but final sessions were adjusted to fit demand

01 Cell biology & signal transduction

cytoskeleton
cell polarity

intracellular transport
secretion
endocytosis
migration
hedgehog
wingless
dpp
Notch
receptor tyrosine kinase/phosphatase
JAK/STAT
Rho GTPases
live imaging
other

02 Cell cycle and checkpoints
checkpoint
kinase/phosphatase/cyclin
developmental modulation
DNA repair
DNA replication
APC
other

03 Cell death
caspases
death mutants/genes
inhibitors of apoptosis (iaps)
transcriptional regulation
autophagy
physiological apoptosis
other

04 Cell division and growth control
mitosis
meiosis
centrosome
kinetochores and cohesion
spindles and motors
cytokinesis
cell growth
tissue growth
tumor suppressors and oncogenes
cell competition
insulin
other

05 Chromatin and epigenetics
chromatin structure
chromatin assembly
heterochromatin
remodeling complexes

histone variants and modifications
insulators/boundary elements
polycomb/trithorax complexes
other

06 Drosophila models of human diseases
neural degeneration
cancer
cardiovascular
diabetes and obesity
addiction
developmental disorders
drug discovery
small RNAs
other

07 Evolution and quantitative genetics
genome evolution
population variation
evolution and development
quantitative traits
speciation
phylogenetics
other

08 Gametogenesis and Organogenesis
spermatogenesis
oogenesis
pre-gametogenic germ cell development
sex determination
sex-specific traits and molecules
dosage compensation
endodermal derivatives
mesodermal derivatives
ectodermal derivatives
extracellular matrix/cell adhesion
imaginal disc morphogenesis
other

09 Immunity and pathogenesis
cellular immunity
humoral immunity
transcriptional regulation
stem cells
host/pathogen interaction
Wolbachia
other

10 Neural physiology and behavior
sensory
synapse

neurotransmitters
neuropeptides
ion channels
homeostasis
learning/memory
courtship and mating
circadian rhythms
eating
aggression
hormones
other

11 Neurogenetics and neural development
axon guidance
dendrites
synaptogenesis
neuronal specification
neuronal morphogenesis
programmed cell death
glia
hormonal control
CNS
sensory
postembryonic
stem cells
other

12 Pattern formation
segmentation
homeotics
axis specification
compartments and boundaries
cell migration and motility
commitment
eye disc
wing disc
leg disc
non-Drosophila patterning
other

13 Physiology and aging
stress response
metabolism
nutrition
nutrient sensing
endocrine function
dietary restriction
oxidative damage
physiology of adult organs
other

14 Regulation of gene expression
core promoters and general transcription factors
enhancers
activators/coactivators
repressors/corepressors
position effect variegation
other

15 RNA Biology
miRNA
small RNAs
non-coding transcripts
RNA binding proteins
RNA localization
RNAi (RNA interference)
RNA elongation and stability
splicing and its regulation
UTRs
other

16 Stem cells
somatic stem cell
germline stem cell
niche
maintenance
signaling
other

17 Techniques and functional genomics
microarrays
RNAi
microscopy
gene disruption and targeting
gene and transcript mapping
computational analyses
mutational screens
molecular interactions
small compounds
ChIPchip
ChIPseq
recombination systems
other

18 Educational initiatives

SESSION CHAIRS, THROUGH 2011 SAN DIEGO, CA

Cell Biology & Cytoskeleton
2009 Elizabeth Chen

2010 Rick Fehon
2011 Tom Hayes & Anna Marie Sokac

Cell Biology & Signal Transduction
2009 Henry Chang
2010 Andreas Jenny
2011 Michael Welte & Yashi Ahmed

Cell Cycle, Checkpoints & Cell Death
2009 Mary Lilly & Jamie Rusconi
2010 Tian Xu

Cell Cycle & Cell Death
2011 Helana Richardson & Tin Tin Su

Cell Division & Growth Control
2006 Thomas Neufeld
2007 Moberg
2008 John Kiger
2009 Iswar Hariharan
2011 Iswar Hariharan & Nick Baker

Cell Division & Growth Control, Cell Death
2010 Laura Johnston

Chromatin & Gene Expression
2008 Elissa Lei

Chromatin & Epigenetics
2009 Ting Wu
2010 Francois Karch
2011 Lori Wallrath & Keith Maggert

Cytoskeleton & Cell Biology
2003 Sisson / Miller
2004 Schoeck
2005 Helmut Kramer
2006 David Bilder (1/2 session…)
2007 Zallen
2008 McCartney (two sessions)
2009 changed to Cell Biol & Cytoskeleton

Drosophila Models of Human Disease:
2005 Ming Guo
2006 Mark Fortini
2007 Mark Fortini
2008 Ethan Bier (two sessions)
2009 Mel Feany
2010 Karen Ocorr (replaced Rolf Bodmer, late)
2011 Hannele Ruhola-Baker & Ethan Bier

Evolution & Quantitative Genetics
2003 McAllister & Gleason
2004 Andolfatto
2005 Long
2006 Greg Gibson
2007 Stern
2008 Wittkopp (two sessions)
2009 Sergey Nuzhdin
2010 Lisa Nagy
2011 Yun Tao & Todd Schlenke

G**ametogenesis & Sex Determination**
2003 Matunis / Godt
2004 Brill
2005 Arbeitman
2006 Rick Kelley
2007 Mark Van Doren
2008 Xie Chen

Gametogenesis & Organogenesis
2009 Celeste Berg
2010 Mark Van Doren
2011 Sharon Bickel & Mary Lilly

Genome & Chromosome Structure
2003 Dernburg / Gallant
2004 Brock
2005 Biessmann
2006 Geyer
2007 Ahmad
2008 Hoskins
2009 became Chromatin & Epigenetics

Immune System & Cell Death
2003 McCall & Bergmann
2004 Manoukian 2005
Brachman 2006 Bergmann
2007 David Schneider
2008 White (Kristin)

Immunity & Pathogenesis
2009 Louisa Wu & Kurt McKean
2010 Ylva Engstrom
2011 David Schneider & Ionnis Eleftherianos

Mitosis, Meiosis & Cell Division
2003 Su / Johnston
2004 Campbell
2005 Scholey
2006 became Cell Division & Growth Control

Neurogenetics & Neural Development
2003 Tanya Wolff / Mark Seeger
2004 Yong Rao
2005 Kai Zinn
2006 Kwang-Wook Choi
2007 Grueber
2008 Matthew Freeman
2009 Dietmar Schmucker
2010 Wei Xie and Yi Rao
2011 Daniela Zarnescu & Tom Jongens

Neurophysiology & Behavior
2003 Smith / Taylor
2004 Gabrielle Boulianne
2005 Krantz
2006 Troy Littleton
2007 Blau
2008 Clandinin
2009 Ravi Allada
2010 Jay Hirsh
2011 Subhatrata Sanyal & Carsten Duch

Organogenesis
2003 Abmayer / Cripps
2004 Godt
2005 Manfred Frasch
2006 Debbie Andrew
2007 Mary Baylies
2008 Justin Kumar
2009 merged with Gametogenesis

Pattern Formation I
2003 Horabin & Rogers
2004 Laura Nilson
2005 Raftery
2006 Justin Kumar
2007 Stathopoulos
2008 Richard Mann
2009 Chip Ferguson
2010 Paul Adler
2011 Angela Stathopoulos & David Umulis

Pattern Formation II
2003 Pollack & Jones
2004 Tepass
2005 Stuart Newfeld
2006 Rushlow
2007 Ken Irvine
2008 (only one session of eight)

Physiology & Ageing

2006 Pletcher
2007 Tatar
2008 Drummond-Barbosa
2009 Rolf Bodmer & Eric Rulifson
2010 Eric Rulifson
2011 John Tower & LeAnne Jones

Regulation of Gene Expression
2003 Arnosti / Orenic
2004 Vett Lloyd
2005 Coury
2006 Scott Barolo
2007 Small
2008 Arnosti (two sessions)
2009 Steve Crews
2010 Ilaria Rebay
2011 Judy Kasis & Pam Geyer

RNA Biology
2008 Lopez
2009 Andrew Simmonds
2010 Richard Carthew
2011 Bill Theurkauf & Liz Gavis

Signal Transduction I
2003 Jiang / Robinow
2004 Marc Therrien
2005 Erica bach
2006 Xinhua Lin
2007 Ilaria Rebay
2008 Barolo
2009 merged with Cell Biology

Signal Transduction II
2003 Halder / McNeill
2004 Bruce Reed
2005 Marques 2006
2007 Wharton
2008 (only one session of eight talks)

Stem Cells
2009 Haifan Lin
2010 Haifin Lin
2011 Yukiko Yamashita & Craig Micchelli

Techniques & Genomics
2003 Christenson & Dearolf
2004 Westwood
2005 Amy Kiger
2006 Chen
2007 Dasgupta

Techniques and Functional Genomics
2008 Bernard Mathey-Prevot
2009 Mike Eisen
2010 Yikang Rong
2011 Hugo Bellen & Julie Simpson

HISTORICAL SPEAKERS, THROUGH 2011

1999: Dan Lindsley (introduction) and Iris Sandler (Keynote) followed by Gerry Rubin (introduction) and David Hogness (Keynote)
2000: Seymour Benzer
2001: Gerry Rubin
2002: Ed Lewis
2003: Michael Ashburner
2004: Peter Lawrence
2005: Chrstiane Nusslein-Volhard
2006: Thom Kaufman
2007: Spyro Artavanis-Tsakonas
2008: Antonio Garcia-Bellido
2009: Scott Hawley (moderator), Mel Greene, Thom Kaufman, Ruth Lehmann, Dan Lindsley, Tony Mahowald, Eric Wieschaus
2010: Hugo Bellen (moderator), Thom Kaufman, Gerry Rubin, Bill Gelbart, Norbert Perrimon and Susan Celniker
2011: Michael Rosbash (moderator), Scott Waddell, Ulrike Heberlein, Stephen Goodwin

ORGANIZING COMMITTEES

39th Annual Drosophila Research Conf - March 25-29, 1998 * Washington, DC
Program Chairs
Kristin White, Massachusetts General Hospital
Laurel A. Raftery, Massachusetts General Hospital
Terry L. Orr-Weaver, Whitehead Institute

40th Annual Drosophila Research Conf - March 24-28, 1999 * Bellevue, WA
Program Chairs
Barbara Wakimoto, University of Washington
Susan Parkhurst, Fred Hutchinson Cancer Research Center

41st Annual Drosophila Research Conf - March 22-26, 2000 * Pittsburgh, PA
Program Chairs
Pamela K. Geyer, University of Iowa
Lori L. Wallrath, University of Iowa

42nd Annual Drosophila Research Conf - March 21-25, 2001 * Washington, DC
Program Chairs
Mariana Wolfner, Cornell University
Michael Goldberg, Cornell University
Organizing Committee
Charles Aquadro, David Deitcher, John Ewer, Michael Goldberg, John Lis,
Ross MacIntyre, Mariana Wolfner, Cornell University

43rd Annual Drosophila Research Conf - April 10-14, 2002 * San Diego, CA
Program Chairs
Kenneth C. Burtis, University of California, Davis
R. Scott Hawley, Stowers Institute for Medical Research
Charles H. Langley, University of California, Davis
Organizing Committee
David J. Begun, Kenneth C. Burtis, Linda M. Hall, Scott Hawley, Deborah A. Kimbrell, John A. Kiger, Charles H. Langley, Jeanett E. Natzle, Sergey V.Nuzhdin

44th Annual Drosophila Research Conf - March 5-9, 2003 * Chicago, IL
Organizing Committee
Dennis McKearin, University of Texas Southwestern Medical Center
Helmut Krämer, University of Texas Southwestern Medical Center
John Abrams, University of Texas Southwestern Medical Center

45th Annual Drosophila Research Conf - March 24-28, 2004 * Washington, DC
Organizing Committee
Paul Lasko, McGill University, Montreal, Canada
Howard Lipshitz, Hospital for Sick Children, Toronto, Canada

46th Annual Drosophila Research Conf - March 30-April 3 2005 * San Diego, CA
Organizing Committee
Kavita Aurora, University of California, Irvine
Rahul Warrior, University of California, Irvine
Frank Laski, University of California, Los Angeles

47th Annual Drosophila Research Conf - March 29-April 25, 2006 * Houston, TX
Organizing Committee
Hugo J. Bellen, Baylor College of Medicine, Houston, Texas
Ron Davis, Baylor College of Medicine, Houston, Texas
Georg Halder, The University of Texas, M. D. Anderson Cancer Center, Houston, TX
Graeme Mardon, Baylor College of Medicine, Houston, Texas

48th Annual Drosophila Research Conf – March 7-11, 2007 * Philadelphia, PA
Organizing Committee
Liz Gavis, Princeton University
Steve DiNardo, U Penn School of Medicine
Tom Jongens, U Penn School of Medicine
Jessica Treisman, NYU Medical Center

49th Annual Drosophila Research Conf – April 2-April 6, 2008 * San Diego, CA
Organizing Committee
Susan Celniker, LBNL
Nancy Bonini, U Penn
Brian Oliver NDDK
John Tamkun UCSC

50th Annual Drosophila Research Conference – March 4-8, 2009 in Chicago, IL
Organizing Committee
John Carlson, Yale University
Lynn Cooley, Yale University
Rick Fehon, U Chicago

51st Annual Drosophila Research Conference – April 7-10, 2010 in Washington, DC
Organizing Committee
Steven Hou, National Cancer Institute
Leslie Pick, U Maryland
Debbie Andrew, Johns Hopkins University School of Medicine
Mark Fortini, Jefferson University

52nd Annual Drosophila Research Conference – March 30-April 3, 2011 in San Diego, CA
Giovanni Bosco, University of Arizona
Daniel Barbash, Cornell University
Leslie Griffith, Brandeis University

REPORT OF THE GSA MEETING COORDINATOR
(Suzy Brown, CMP)

52nd ANNUAL DROSOPHILA RESEARCH CONFERENCE

As you can see from the information in the treasurer's report, while I budgeted for a loss of approximately $30,000, it looks like we will be able to turn that loss into a modest gain thanks in part to lower anticipated payroll (some processes have been streamlined) and catering costs.

Registration:

The total registration number for 2011 as of March 2 is 1,441. This number is down 9% from last year at this time. The registration cut-off is March 22 so we may see a few more come in before we close out advanced registration.

Registration income at this point is about $18,000 below the total budgeted registration income of $391,740. The number of individuals registering as GSA members is up 2% over last year. Currently over 68% of the people attending the conference are GSA members.

Hotel Rates and Pick-up:

The sleeping room rate is $157-$178 (depending on location) which is up to 27% less than last year. The hotel cut-off is still a few days away and we still have rooms left. We should be able to meet our contractual commitments.

Exhibitors/Sponsorship/Advertising:

We sold twenty booths this year which is even with last year. We have seen a rise in our print and web advertising. Overall revenue for exhibits/ads/sponsorship is up 8% .

Other Items:

This year we do not have the option of onsite poster printing and pickup. We felt that there was not a good option in terms of service/price but that shouldn't be a problem in Chicago where it will be offered again.

Full abstract text will only be available on-line as in the past few years. Additionally, we will again offer the option, through a third part vendor, of printing the abstracts in book format for an additional cost.
As in past years the abstract search and program planner is available through the website to customize your schedule and full abstracts can be printed as a group or individually for no charge.

Last year we had great success using PSAV and their content management system for our plenary and platform speaker presentations. All speakers uploaded their presentations in advance with little if any difficulty and were shown how to use the equipment from the podium. All speakers are encouraged to check in at the speaker ready room and in only "glitches" happened where the speakers skipped this step. So, this will again be encouraged this year.

FUTURE CONFERENCES

As we look at promotional efforts for future conferences, we need to make sure that the experience is such that the positive word of mouth promotion continues. The organizers have once again done an outstanding job of putting together a scientific program that is second to none. I have complete faith that this will continue. We also need to look at things that have been cut from the program in the last couple of years that may seem insignificant in some cases (no sodas on breaks, limited

coffee, technology/A/V, Wifi, etc.) but impact the overall experience. The convention surveys that are done after the meeting will provide additional feedback to the Fly and GSA Boards for use when considering a registration price increase.

Dates and rates have been confirmed through 2016 and the Town & Country is holding space for us for 2017. Detailed below is the schedule for the next five years:

2011 – 52nd Annual Drosophila Conference: March 30-April 3, The Town and Country Resort Hotel, San Diego. $176/$186/$196.

2012 – 53rd Annual Drosophila Conference: March 7-11, Sheraton Chicago Hotel and Towers. $209/$229 – 10% drop

2013 – 54th Annual Drosophila Conference: April 3-7, Marriott Wardman Park Hotel. $235

2014 – 55th Annual Drosophila Conference: March 30-April 3, The Town and Country Resort Hotel, San Diego. $192/$202/$232.

2015 – 56th Annual Drosophila Conference: March 4-8, Sheraton Chicago Hotel and Towers. $219/$239.

2016 – 57th Annual Drosophila Conference: March 2-6, Philadelphia Marriott. $179

Registrations - 2011

	Number	Amount
Faculty/Lab Tech Members	421	$89,420
Faculty/Lab Tech NonMembers	128	$49,683
Postdoc Members	196	$36,655
Postdoc Nonmembers	112	$33,490
Grad Student Members	292	$27,000
Grad Student Nonmembers	191	$31,640
Undergrad Members	69	$2,525
Undergrad Nonmembers	17	$1,975
Complimentary	15	0
Early/Regular	**1,441**	**$272,388**

Registrants by country

United States	1090
Canada	51
United Kingdom	37
France	31
Germany	31
China	22
Japan	23
Spain	17
Switzerland	16
Korea	15
Taiwan	14
Mexico	10
Sweden	11
Portugal	9
Israel	8
Italy	7
Australia	6
Russian Federation	6
Hungary	6
Brazil	5
Austria	4
India	4
Finland	3
Czech Republic	3
Turkey	2
Argentina	2
Netherlands	2
Chile	2
Singapore	1
Belgium	1
Norway	1
Slovakia	1
Malta	1
New Zealand	1

Total Number of Registrants: 1441
Total Number of Countries: 28

TREASURER'S REPORT (Pam Geyer)

Drosophila Main Fund: After the 2010 meeting, the main fund is **$261, 359**, which is substantially over the required minimum that GSA requires of **$150,000**. This year we are projected to lose a little (~$3,600). Over the last ten years, we have increased our reserves **$218,889**, and have only lost money three of these years [2003, Chicago $22,993; 2008 San Diego, $5,410; and 2009, Chicago $47,935; Total $**76,338**]. In 2008-2009, the losses included providing box lunches for a networking luncheon for all participants. In the last four years, sponsorship appears to be growing (~40% to current $40,500). Overall, registration not changed much in the last 10 years, averaging ~1,540

individuals (the low was San Diego in 2008 with 1,447; the high was DC in 2010). In the next five years, we are scheduled for Chicago (2 times), San Diego, DC and Philadelphia. Of these venues, Chicago may lose revenues. Based on the previous data, it is likely that the other venues will be make gains that offset the Chicago loss.

Sandler Lecture Fund: The lecture fund is $30,345, which is slightly below last year's balance. In the last five years, cost for travel expenses for the speaker averaged ~$730. This is likely to increase in the upcoming years, as air fares continue to rise. At the present time, the investment gains may stay equal to the travel costs.

Recommendation: I do not think that there is a need to raise registration fees. Further, I think For example, we could afford 20 competitive $1,000 travel awards to post-doc and students.

Table 1: Summary of expenses: 2008-2011

	San Diego* 2008 Actual	Chicago* 2009 Actual	Wash., DC 2010 Actual	San Diego 2011 Budget	San Diego 2011 Estimate
REVENUE					
Registration Fees	$281,093	$294,266	$306,393	$291,740	$275,000
Sponsorships/Ads	$ 3,800	$ 6,100	$3,000	$6,600	$5,500
Exhibit Fees	$ 25,620	$ 25,650	$31,750	$30,000	$35,000
Miscellaneous (t-shirts, etc.)	$ 1,086	$ 4,170	$3,815	$5,800	$5,900
TOTAL REVENUE	**$ 311,599**	**$ 330,186**	**$344,958**	**$334,140**	**$321,400**
EXPENSE					
Salary, Payroll Tax and Benefit	$ 76,109	$ 79,502	$66,747	$80,850	$70,000
Printing/Mailing/Promotion	$ 26,715	$ 17,140	$14,662	$22,500	$14,500
Receptions and Catered Events	$ 118,942	$ 148,370	$110,848	$119,500	110,000
Posters/Exhibits	$ 18,919	$ 19,004	$20,701	$21,500	$20,000
Supplies/Duplicating/Signs	$ 1,211	$ 791	$1,452	$3,500	$2,000
Hotel and Travel	$ 4,607	$ 3,758	$2,835	$6,500	$5,000
Audio Visual Services	$ 53,125	$ 86,901	$54,458	$62,500	$62,000

Other Contracted Services	$ 3,096	$ 3,604	$4,371	$5,000	$3,500
Telephone/Internet/Fax	$ 4,905	$ 1,447	0	$5,000	$5,000
Credit Card Fees	$ 9,124	$ 7,672	$9,422	$9,000	$9,000
Miscellaneous (t-shirts, etc.)	$ 256	$ 9,929	$3,773	$4,000	$3,000
Overhead			$28,606	$24,255	$21,000
TOTAL EXPENSE	**$ 317,009**	**$ 378,118**	**$317,876**	**$364,105**	**325,000**
NET GAIN (LOSS)	**$ (5,410)**	**$ (47,932)**	**$27,082**	**$(29,965)**	**$(3,600)**

***Luncheon added without registration price increase.**

B. MEETING ATTENDANCE

Pre-registration 2011 (San Diego, CA):	1,328	$243,004
Total registration 2011 (est):	**1,500**	**$275,000**
Pre-registration 2010 (Washington, DC):	1,529	$261,246
Total registration 2010:	**1,668**	**$306,393**
Pre-registration 2009 (Chicago):	1,383	$256,800
Total registration 2009:	**1,506**	**$294,266**
Pre-registration 2008 (San Diego) :	1,343	$214,856
Total registration 2008:	**1,447**	**$281,093**
Pre-registration 2007 (Philadelphia):	1,345	$234,000
Total registration 2007:	**1,507**	**$288,067**
Pre-registration 2006 (Houston):	1,241	$222,165
Total registration 2006:	**1,402**	**$274,350**
Pre-registration 2005 (San Diego):	1,451	$264,440
Total registration 2005:	**1,515**	**$297,750**
Pre-registration 2004 (Wash DC)	1,470	$266,110
Total registration 2004:	**1,617**	**$313,645**
Pre-registration 2003 (Chicago):	1,488	$256,130
Total registration 2003:	**1,603**	**$283,270**
Pre-registration 2002 (San Diego):	1,219	$211,000
Total registration 2002:	**1,552**	**$290,170**
Pre-registration 2001 (Wash DC):	1,372	$240,240
Total registration 2001:	**1,627**	**$297,915**

C.ACCOUNT BALANCES

C.1. Drosophila Main Fund

Table 2: Summary of income and attendance since 1993

Meeting Year	Location	Net Income	Fund Balance*	# Meeting Attendees
1993	San Diego	$17,105	$ 25,146	1,165

1994	Chicago	2,800	27,946	1,222
1995	Atlanta	8,417	36,363	1,103
1996	San Diego	15,035	51,398	1,423
1997	Chicago	31,663	83,061	1,382
1998	Wash DC	21,522	104,583	1,378
1999	Seattle	(6,053)	98,530	1,366
2000	Pittsburgh	(56,060)	42,470	1,183
2001	Wash DC	71,656	114,126	1,627
2002	San Diego	60,661	174,787	1,552
2003	Chicago	(22,993)	151,794	1,603
2004	Wash DC	23,026	174,820	1,617
2005	San Diego	89,943	264,763	1,515
2006	Houston	6,196	270,959	1,402
2007	Philadelphia	16,663	287,622	1,507
2008	San Diego	(5,410)	282,212	1,447
2009	Chicago	(47,935)	234,277	1.506
2010	Washington, DC	27,082	261,359	1,668

***** The GSA Board (Sept. 2003 meeting) established a required ~$150,000 *minimum* reserve fund (one-half of meeting expenses). No cap figure stated

C. 2. Sandler Lecture Fund

Table 3: Summary of Sandler fund expenses

Year	Investment Gain	Travel expenses	Supplies/ Mailing expenses	Net Income	**Balance**
1993				1417	25,964
1994				(451)	25,513
1995				1,595	27,108
1996				1,142	28,250
1997				1,119	29,369
1998				1,385	30,754
1999				877	31,631
2000				257	31,888
2001				(234)	31,654
2002				(846)	30,808
2003				(2,431)	28,377
2004				432	28,809
2005	1076	1,208	37	(169)	28,640
2006	1963	469	15	1,479	30,119
2007	2187	501	15	1,671	31,790
2008	-859	441	20	(1,320)	30,470
2009	1198	768		430	30,900
2010	947	1,482		(555)	30,345

DROSOPHILA BOARD ELECTION REPORT (Carl Thummel)

The Elections Committee consisted of Carl Thummel (Chair), Jay Hirsh, Barry Ganetzky, and two new members, Debbie Andrew and Susan Parkhurst. We collected suggestions from outgoing representatives and the committee members, and then ranked them based on previous involvement in the fly community and our perception of their ability to perform the job. The chair contacted the individuals selected by the committee to construct the final ballot. The website surveymonkey was used to make voting and vote counting easier. 397 people voted this year, roughly the same as last year (356), which is only about 13% of the ~3000 people contacted. This year short statements of research interests and links to the candidates' home pages were provided in the e-mail to the voters, in response to the Board's 2008 suggestion. Linda Restifo asked the Election Committee if Regional groupings can be reevaluated, questioning, for example, the inclusion of Arizona, Utah, and Colorado in the Heartland region.

The following letter was emailed to Drosophila researchers by Flybase to solicit votes.

Dear Drosophila researcher,
It is time to cast your vote for new members of the National Drosophila Board of Directors. As you are likely aware, the Board plays an important role for the Drosophila research community, so please take a few seconds to learn about the Board and participate in this election. The Board's duties include: overseeing community resource centers and addressing other research and resource issues that affect the Drosophila research community. The Board also administers the finances for the annual North America Drosophila Research Conference and its associated awards, and it chooses the organizers and the site of the annual meeting. The Board consists of nine regional representatives, eight from the U.S. and one from Canada, who serve 3-year terms, as well as a representative for primarily undergraduate institutions. It also has three elected officers including a President, a President-Elect and a Treasurer. In addition, the Board has ex officio members, who represent Drosophila community resource centers or international Drosophila communities. For more information about the Board and the summaries of the annual Board meetings see: http://flybase.bio.indiana.edu/static_pages/news/board.html

This year we are electing the President-elect, who will serve as President starting with the fly meeting in 2012. We are also electing representatives for the Great Lakes, Northwest, Southeast, and New England regions, who will serve 3-year terms starting with the fly meeting in 2011.

Please participate in this election. It is your opportunity to choose the individuals who will help set priorities and garner support for community resources. In order to record your vote please go to the following URL and follow the instructions on that page.

<<>>

Please remember you may vote for candidates in ALL categories even though you do not reside in the region represented by the candidates. Balloting will end December 6, 2010.

Thank you,
Drosophila Board Election Committee
Carl Thummel (Chair)
Debbie Andrew
Barry Ganetzky

Jay Hirsh
Susan Parkhurst

The surveymonkey ballot listed the following candidates:

President-elect (Vote for ONE)

John Carlson
http://pantheon.yale.edu/~jcarlso/
Department of Molecular, Cellular, and Developmental Biology, Yale University
Research Interests: Molecular mechanisms of olfaction

Michael O'Connor
http://www.oconnor.umn.edu/
Department of Genetics, Cell Biology, and Development, University of Minnesota
Research Interests: Molecular genetics of signal transduction and developmental timing

Great Lakes (Vote for ONE)

Helen Salz
http://genetics.case.edu/?page_id=5&LN=Salz&FN=Helen
Department of Genetics, Case Western Reserve University
Research Interests: Regulation of RNA splicing

Michael Welte
http://www.rochester.edu/college/bio/labs/Welte/research/index.html
Department of Biology, University of Rochester
Research Interests: Mechanisms of transport by microtubule motors

Northwest (Vote for ONE)

Sarah Certel
http://dbs.umt.edu/people/facultyDetails.php?id=1576
Division of Biological Sciences, University of Montana
Research Interests: Control of social behavior by genetic and neural networks

Leo Pallanck
Pallanck Lab Home Page
Department of Genome Sciences, University of Washington
Research Interests: Studies of neurodegenerative disorders in *Drosophila*

Southeast (Vote for ONE)

Stephen Crews
http://www.unc.edu/~crews/
Department of Biochemistry and Biophysics, University of N. Carolina, Chapel Hill
Research Interests: Nervous system development

Andrea Page-McCaw
https://medschool.mc.vanderbilt.edu/facultydata/php_files/show_faculty.php?id3=18406
Department of Cell and Developmental Biology, Vanderbilt Univ. School of Medicine

Research Interests: Tissue remodeling by matrix metalloproteinases

New England (Vote for ONE)

Eric Baehrecke
http://www.umassmed.edu/faculty/show.cfm?faculty=1246
Department of Cancer Biology, University of Massachusetts Medical School
Research Interests: Regulation of autophagy, cell survival, and programmed cell death

Kim McCall
http://people.bu.edu/kmccall/
Department of Biology, Boston University
Research Interests: Molecular mechanisms of programmed cell death

The votes were tallied by Thom Kaufman using Surveymonkey, and the winners were:

Michael O'Connor for President-Elect
Helen Salz for Great Lakes regional representative
Leo Pallanck for Northwest regional representative
Steve Crews for Southeast regional representative
Eric Baehrecke for New England regional representative

The next Election Committee chair is Terry Orr-Weaver. The President, Liz Gavis, should remind her to start the process in September.

Drosophila Board Master List (Spring 2011-2012)
General contact: flyboardmorgan.harvard.edu
Year indicates the last Fly Meeting through which Board Members will serve as Officers or Regional Reps. Past-Presidents serve as members-at-large until the end of the indicated term.

Officers
Denise Montell President 2014 dmontell@jhmi.edu
Michael O'Connor President-elect 2016 moconnor@umn.edu
Elizabeth Gavis President-elect 2015 gavis@princeton.edu
Terry Orr-Weaver Past-President & Elections Chair 2013 weaver@wi.mit.edu
Carl Thummel Past-President 2012 carl.thummel@genetics.utah.edu
Pam Geyer Treasurer 2012 pamela-geyer@uiowa.edu

Regional Representatives
Helen McNeill Canada 2012 mcneill@mshri.on.ca
Helen Salz Great Lakes 2014 hks@po.cwru.edu
Leo Pallanck Northwest 2014 pallanck@u.washington.edu
Steve Crews Southeast 2014 steve_crews@unc.edu
Michelle Arbeitman California 2013 arbeitma@email.usc.edu
Janice Fischer Heartland 2012 jaf@mail.utexas.edu
Eric Baehrecke New England 2014 Eric.Baehrecke@umassmed.edu
Nancy Bonini Mid-Atlantic 2013 nbonini@sas.upenn.edu
Tom Neufeld Midwest 2012 neufeld@med.umn.edu

Primarily Undergraduate Institution Representative
Karen Hales 2013 kahales@davidson.edu

International Representatives
Helena Richardson Australia/Oceania 2013 h.richardson@pmci.unimelb.edu.au
Henry Sun Asia 2013 mbyhsun@ccvax.sinica.edu.tw
Michael Boutros Europe 2013 m.boutros@dkfz.de
Juan Riesgo-Escovar Latin America 2013 riesgo@inb.unam.mx

Ex Officio
Bill Gelbart FlyBase gelbart@morgan.harvard.edu
Susan Celniker BDGP celniker@fruitfly.org
Thom Kaufman Bl'ton S.C.& FlyBase kaufman@bio.indiana.edu
Kathy Matthews Bl'ton S.C.& FlyBase matthewk@indiana.edu
Kevin Cook Bl'ton S.C. & Nomenclature Comm. kcook@bio.indiana.edu
Teri Markow UC San Diego S.C. tmarkow@ucsd.edu

IMAGE AWARD (Michelle Arbeitman)

This year's competition received 50 submissions, including 7 videos. Both video and still submission are now of consistently excellent quality; comparing the two can be like comparing apples and oranges and we want to ensure that one type does not dominate the other in the competition. The committee has therefore decided to henceforth award an annual winner in both the still and the video categories. The 2011 winners are:

Video: Mollie Manier, for her video displaying fluorescently-labeled sperm in the seminal receptacle.

Still: Jai Yu, for his image depicting cellular organization of a neural circuit that drives Drosophila courtship behavior

This year's runners-up are:

-Ho Lam Tang, for his composition depicting ovarian organogenesis

-Chun Han, for his image depicting light-avoidance-mediating photoreceptors tile the Drosophila larval body wall

Michelle Arbeitman will make the Award presentation at the meeting.

SANDLER AWARD (Claude Desplan)

- Chair, Claude Desplan (NYU)
- Richard Mann (Columbia)
- Allison Bardin (Curie, Paris)
- Marek Modzik (Sinai)

We had only five applicants who were nevertheless quite good. The lectureship went to Daniel Babcock from Michael J. Galko's lab at UT Houston (MD Anderson). He is currently a postdoc with Barry Ganetsky at Madison.

Runner ups were Leah Sabin from Sarah Cherry's lab at U Penn and Ricardo Miguel Neto da Silva from Laura Johnston's lab.

Allison Bardin, a young group leader at Curie (Intestinal stem cells) will present the award at the fly meeting as she was the strongest supporter.

We absolutely need to do something to advertize this lecture that has seen so many great burgeoning scientists, and it is such great exposure.

Sending repeat emails several weeks before the deadline would do, but we also need to tell our friends to nominate their best students. It is really a minimum amount of work as the PI has already a letter when the PhD student applies for postdoc.
Cordially,
Claude

Undergraduate Educational Initiatives (Karen G. Hales)

A Primarily Undergraduate Institutions (PUI) representative was added to the Fly Board in 2010. The goal was to facilitate enhancements to the conference program to make the experience more productive for undergraduate students and their professors. The annual PUI workshop, held since 2001, was previously the only organized event. This workshop will continue, as will the reduced registration fees for undergraduates that were instituted last year.

Additions to this year's program have been implemented and in part conceived by Beth Ruedi, the GSA Education Programs Manager, with the help of Suzy Brown.
The following new events will occur:

- Undergraduate Student Mixer, Wednesday evening
- "Undergraduate Experience" program for invited students from local institutions and their professors, Thursday morning
- Education Special Interest Group Mixer for faculty interested in pedagogy, Thursday evening
- Undergraduate Plenary, for undergraduate researchers attending the meeting, Friday afternoon.

Furthermore, posters presented by undergraduates will be reliably identifiable for judging in a separate undergraduate poster contest category.

Goals that we hope to meet in future years include identifying a mechanism and funding source for travel awards for undergraduates, as well as establishing a pedagogy workshop.

Upcoming White Paper (Denise Montell)

I received the following email correspondence and would like to discuss it in the context of the White Paper that we will write this year.

March 13, 2011

Dear Denise,
Many thanks for your prompt reply. I will not be attending the fly meeting, so it would be great if you could simply read my letter to the Board to ask if it could be incorporated into a future white paper. According to Adam Felsenfeld, it hurt my grant application that Sciara had not been listed in the previous Drosophila white paper as that would have underscored the usefulness of the Sciara sequence to the Drosophila community had it been listed.

Here are a few ideas on how the Sciara genome sequence would blend in with the currently existing (2009) Drosophila white paper:

(1) In addition to high quality finishing of the 11 other Drosophila species, it would be useful to have a somewhat more divergent fly for evolutionary and comparative analyses --- the lower dipteran fly Sciara would be an excellent choice. Besides the usefulness of the Sciara sequence to the Drosophila community, having the sequence of the Sciara genome would allow the community to explore the fascinating biology offered by this fly.

(2) The genomic sequence from Sciara could assist in expanding our knowledge of the organization of sequences in Drosophila. My lab maintains translocation stocks set up by Helen Crouse several decades ago that have break points within the heterochromatin at the end of the X chromsome. These translocations subdivide the tandem repeats of ribosomal RNA genes and also separate the rDNA from the centromere. The translocation break points demarcate the "controlling element" that regulates X chromosome nondisjunction in male meiosis II and X elimination in early embryonic cleavage (part of the sex determination system). This controlling element is situated within the tandem array of rDNA repeats.

In addition, a paper has recently been submitted to *Chromosoma* by the Madrid group (Goday and Villasante labs) who have cloned and sequenced X heterochromatin DNA derived by microdissection of Sciara polytene chromosomes. In situ hybridization was used for a preliminary map of the various repeat sequences they cloned, but needs to be refined by further studies. Comparison of the organization of DNA in the heterochromatin of Sciara to Drosophila could help to elucidate basic underlying principles that are conserved.

Finally, I forgot to mention in my last E-mail that we have succeeded in developing a transformation system in Sciara and are in the final stages of refining this further. Transformation coupled with the genomic sequence will make Sciara a powerful model system for experiments. It is interesting to note that in our last NIH grant application we had listed Peter de Jong as a collaborator to create a
P[acman] BAC library but the study section shot down that specific aim.

Many thanks! I look forward to hearing the outcome from you.
Sincerely,
Susan

BLOOMINGTON STOCK CENTER
(Kevin Cook, Annette Parks)

Bloomington Drosophila Stock Center Report to the Drosophila Board, March 17, 2011. Prepared by Kathy Matthews, Kevin Cook, Annette Parks and Thom Kaufman, with figures as of 3/3/11.

- Stocks held: 31,620
- Registered user groups: 2,386
- Registered users: 5,160
- Shipped in 2010: 196,930 subcultures in 14,647 shipments
- **Funding**: We are in year 2 of a 5 year grant from NSF+NIH, ~$410,000 direct costs this year. We expect to raise approximately $650,000 (excluding postage/courier costs) through cost-recovery in 2011. Increased income from user fees is paying for the growth of the collection.
- **Growth**: HHMI awarded the BDSC $364,000 for renovations that will allow us to expand the collection to 60,000 – 70,000 stocks.
- **Costs**:
    - Accession and maintenance account for ~70% of costs
        - Average cost per stock to accession: ~$28
        - Average cost per stock for annual maintenance: ~$24
    - Distribution accounts for ~30% of costs
- **Cost recovery**: We are transitioning to a more traditional business model for user accounts. The goal is to essentially eliminate unpaid accounts and to reduce the large amount of redundant paperwork and follow-up that the old system required.
- **New stocks**: We expect to add ~8,800–9,800 new stocks in 2011.
    - 4,400 GAL4 drivers reflecting enhancer expression from the Rubin lab
    - 2,900 insertions of RNAi constructs from the TRiP
    - 1,000–1,900 insertions via the GDP pipeline
    - 400–500 stocks in all categories from the community at large
    - 100 interchromosomal duplications from the Bloomington Duplication Project
    - 51 human disease model stocks from Vitruvean, Inc.
    - 28 InSITE stocks for in vivo exchange of transgene components from the Clandinin lab
- **Pruning**: We will continue to remove obsolete, redundant and selected low-use stocks from the collection. We did not make the progress we'd hoped in 2010, but we expect to remove 500—1,000, possibly more, stocks from the collection in 2011.

Possible Indian Stock Center

Dear Utpal,
I realized that I have not got back on this. I hope this silence is not misunderstood by the fly board.
Briefly, we will have our new space ready April 2011.
Beginning April 2012 we will be have funds to keep stocks in a reasonable way. These

will for sure be collections we generate in our Transgenic facilty.
In addition, we will be happy to have agreements with Hughes/NIH or both to fund and manage collections for periods such as 5 years or 10 years. In reality a 5 year renewable agreement is likely to work.
One may ask what happens if NCBS or the Indian government wants to shut things down. I think a 5 year notice is one possibility. Any other suggestion??
I hope this helps.
cheers

Vijay
PS. We will have the UAS-HA-Tagged lines all done by next summer, we are halfway there. We are starting a couple of other genome wide generation of lines, so we are moving

Berkeley Drosophila Genome Project (Susan Celniker, Joseph Carlson, Ken Wan, Erwin Frise and Roger Hoskins)

A. Introduction

The BDGP was started in 1992 to sequence the *Drosophila melanogaster* genome. We are currently in our nineteenth year and have continued to expand activities. Since the sequencing of the euchromatic portion of the genome we have continued to work on the heterochromatin and moved into functional genomics. Specifically, we are characterizing the transcriptome using next generation sequencing; capturing cDNAs to validate gene and transcript models and to use as resources for proteomics studies; and determining embryonic spatial gene expression patterns.

B. Clone Resources

To date we have submitted DNA sequence for 255,362 cDNA clones, of which 20,325 were fully sequenced and 16,078 fully support a Flybase release 5.32 gene model. Our Gold Collection, cDNA's whose amino acid translation exactly matches the Flybase model with 100% identity, now contains 10,465 clones. From the Gold Collection, we produced 7,841 expression-ready donor clones lacking the native stop codon (for making C-terminal fusion constructs) and 7,508 expression-ready donor clones containing the native stop codon (for making N-terminal fusion constructs). Using the donor clones, we generated sets of expression clones in different vectors with a variety of tags, as summarized in Table 1.

Table 1. Summary of Expression Clones.

Collection	Vector	Promoter	N-term Tag	C-term Tag	ORF Stop Codon?	System	Past year (3/10-3/11)	Total
XO	pDNR-Dual	T7	--	6XHN	No	*E. coli*	1905	7841

XS	pDNR-Dual	T7	--	--	Yes	*E. coli*	2060	7508
MXO	pMK33-CTAP-BD	Metallothionein	--	TAP	No	Cell culture	0	1961
FMO	pMK33-CFH-BD	Metallothionein	--	Flag-HA	No	Cell culture	0	7103
UFO	pUAST-CFLAGHA-BD-PHI	UAS	--	Flag-HA	No	Gal4-UAS	0	3891
URO	pUAST-C-mCherry-BDatt	UAS	--	mCherry	No	Gal4-UAS	257	257
UGO	pUAST-C-eGFP-BDatt	UAS	--	eGFP	No	Gal4-UAS	248	248
URS	pUAST-N-mCherry-BDatt	UAS	mCherry	--	Yes	Gal4-UAS	250	250
UGS	pUAST-N-eGFP-BDatt	UAS	eGFP	--	Yes	Gal4-UAS	242	242

Table 2. Summary of Clones at the DGRC for distribution:

Collection	Past year (2010Mar-2011Mar)	Cumulative
AU (Gold)	1002	9066
XO	1536	7715
XS	192	5077
MXO	0	1961
FMO	1545	7103
UFO	0	3891

C. Embryonic Gene Expression

We continue to collect embryonic spatial gene expression data from high throughput *in situ* hybridizations using the BDGP gold clones as templates for RNA probes. In the coming year, we plan to add expression patterns for CRM driven reporter constructs. In 2010, we redesigned our gene expression patterns database to facilitate the transfer of expression pattern images and controlled vocabulary annotations from our production pipeline to the public database (http://insitu.fruitfly.org) and to add new search and discovery tools based on computational image analysis. We are active participants in the development of the open source image analysis platform Fiji (fiji.lbl.gov). To date we have examined 7986 genes and documented their expression patterns with over 100,000 images.

D. User Resources

1. In an effort to improve the quality of our web-based user support, we have made changes to our website (http://www.fruitfly.org) including: updated FAQs, updated protocols and updated the design to make it easier for users to navigate to the relevant information. We have also added

software for the users to generate complete plasmid maps for the proteomic clones. In addition we have added a user search function so that individual users can identify all expression clones for a particular gene or transcripts.

2. We have worked and continue to work with FlyBase to improve gene and transcript annotations. We continually submit clones to the DGRC molecular stock center for distribution to the community.

E. TECHNOLOGIES

cDNA and proteomic resource sequencing continues to rely heavily on the ABI3730. Characterization of the transcriptome via modENCODE has primarily been on the Illumina GAII. We have two from our project and one from the division.

F. FUNDING

The BDGP is funded solely by NIH grants (NHGRI and NIGMS). The P41 (SEC) should be funded as of April 1 to continue to generate proteomics resources for three years. An R01 (SEC) funds the spatial expression for two more years. Informatics support is currently weak and a BISTI grant (15th percentile) will either be funded or resubmitted.

modENCODE Project (Susan Celniker, Steven Henikoff, Gary Karpen, Manolis Kellis, Eric Lai, David MacAlpine, Brian Oliver and Kevin White)

A. Introduction

The modENCODE project grew from a White Paper written in 2006. Grants were solicited and awards made in April of 2007. Six research proposals were funded in addition to a data distribution center (Lincoln Stein) and more recently a data analysis center (Manolis Kellis). A marker paper was published in Nature in 2009 and a series of publications in Science, Nature, NSMB and Genome Research in 2010 and 2011. We were given a fifth year of funding to complete proposed studies and to expand studies within the limits of the original aims to determine the function of every base in the genome. The project has been very successful and NHGRI is considering a second round of RFAs to be discussed at Council in May. Community support will greatly facilitate moving forward with modENCODE II.

B. Transcription

The Celniker group has continued to fulfill their goals of generating a complete characterization of the Drosophila melanogaster transcriptome by sequencing polyA+ RNA samples from a variety of cell lines, tissues and perturbations, for a total of 74 new stranded samples and a total of ~9 Billion mapped reads. This is more than four times as much data as published (Graveley et al., 2011) that led to the discovery of thousands of new transcribed elements, tens of thousands of new spliced junctions and ten times the number of editing sites. In addition, we studied RNA binding proteins involved in splicing (Brooks et al., 2011) promoter elements using RACE and CAGE (Hoskins et al., 2011) and transcriptionally profiled 25 cell lines using microrrays (Cherbas et al., 2011).

The Oliver group worked with the Celniker group on the production and analysis of polyA+RNA sequence and has brought comparative analysis to the modENCODE project. They isolated and

sequenced polyA+ RNAs from adult male and female heads from D. pseudoobscura and D. mojavensis. They have a complete developmental profile in process.

The Lai group has continued to sequence many small RNA libraries that cover new cell/tissue sources and combination of mutant backgrounds and Ago immunoprecipitations. These data fueled insights into the sorting of endo-siRNAs (Okamura MCB 2011), discovery of many new mirtrons (Chung Gen Research 2011) and allowed a major reannotation of canonical miRNAs, their variants and their modifications (Berezikov Gen Research 2011).

C. Chromatin

The Karpen group has published three papers describing 1) the basic mapping of histone modifications and chromosomal proteins and an analysis of combinatorial chromatin states (Kharchenko et al., Nature 2010), 2) analysis of the plasticity of epigenetic marks in heterochromatin (Riddle et al., Genome Research 2011, and 3) a comprehensive analysis of the specificity of commercially available histone modification antibodies with an accompanying web site for public access to the data and opportunities to upload information from other labs (in collaboration with the Lieb and Ren groups), in addition to contributing chromatin data and analyses to the integrative paper (modENCODE consortium et al., Science 2010). We are currently completing the mapping and analysis of chromatin 'landscapes' for 75 proteins and marks in five tissue sources (early and late embryos, Kc, S2 and BG3 cell lines, which we expect to complete by the end of year 5.

The Henikoff group has previously demonstrated cell-type-specific epigenomic profiling by expression a nuclear envelope protein under control of a tissue-specific promoter and isolation of tagged nuclei using affinity purification on magnetic beads. This was done in Arabidopsis, and for modENCODE, we have been adapting this strategy to flies and worms, with promising preliminary results. Our project has also used RNAi knockdowns of chromatin regulators to catalog changes in chromatin properties using salt-fractionation of chromatin. We have found that single-base-pair resolution of nucleosomal and sub-nucleosomal landscapes can be achieved for low-salt-soluble classical active chromatin. Combining these technologies to obtain a single base pair resolution map of the entire Drosophila and worm epigenome for selected cell types is the current goal of our modENCODE project.

D. Replication

The MacAlpine group has characterized the DNA replication program using multiple genomic approaches which include replication timing, origin mapping and binding sites of essential replication initiation factors (MacAlpine et al., 2010, Eaton et al., 2011). A key finding of these studies was that chromatin environment was predictive of origin function. The Orr-Weaver group examined the differential replication of multiple polytene tissues and identified tissue specific regions of differential replication including amplicons and under-replicated regions that are coupled to transcriptional regulation in some but not all of the tissues (Nordman et al., 2011).

E. Cis-regulation

The White group has continued to perform ChIP seq experiments, prioritizing factors requested by the community on the modENCODE web pages or through direct contact. To date, over 350 datasets have been produced by this project and are publicly available. Analyses of these data have revealed the organization of insulators, dynamic chromatin markings during development, more than 150,000 transcription factor binding sites representing over 35,000 unique locations, signatures of enhancers and promoters (Negre PLoS Genetics 2010; Negre Nature 2011). More than 1,500 novel promoter predictions have been validated in cell culture and by comparing to CAGE data from the Celniker group and Hoskins et al. 2011, as well as dozens of predicted enhancers (Hoskins Gen Research 2011; Negre Nature 2011). Working with Hugo Bellen's group, a community BAC resource was developed and epitope tagging applied to ChIP and imaging, and strains are released to the Drosophila stock center as they are validated

(Venken et al. Nat Methods 2009). Future work will continue to focus on producing ChIP seq data to provide tissue-specific maps of the regulatory architecture of the genome.

F. Funding

modENCODE is funded solely by NHGRI U01 grants.

Drosophila Gene Disruption Project (GDP) (Hoskins, Spradling, Bellen)

The Drosophila Gene Disruption Project (GDP) has created a widely used, publicly available collection of transposon insertion mutants. We will continue to expand the collection using new tools that will dramatically increase its utility. Koen Venken developed a versatile *Minos* transposon, named Mi{MIC}, that contains two phage φC31 *attP* sites for site-specific recombination flanking a gene-trap cassette. Mi{MIC} inserts in coding introns, allowing Recombination Mediated Cassette Exchange (RMCE) to swap the gene-trap cassette with any other DNA cassette to create genes expressing custom tagged fusion proteins. We have developed a battery of such cassettes for protein tagging to visualize expression patterns in fixed or live animals, chromatin immunoprecipitation-sequencing for transcription factor binding studies, and immunoprecipitation-mass spectrometry for analysis of protein complexes.

The most valuable aspect of Mi{MIC} technology extends beyond insertion mutants and fusion genes. Mi{MIC} allows the integration of specific segments of DNA at specific locations in the genome. Yikang Rong and colleagues have developed a technique called SIRT that combines site-directed insertion of large DNA segments with homologous recombination to create targeted mutations within 80 kb of an integrated *attP* site (Gao et al. 2008). Thus, a large collection of Mi{MIC} insertions and the SIRT technique will allow precision engineering of the genomic landscape to manipulate genes, regulatory regions, chromatin boundary elements, origins of replication, and other genomic elements for functional analysis of essentially all euchromatic regions.

To utilize the power of Mi{MIC} technology, a pre-existing insertion in or near the gene or genomic region of interest is required. We will expand our collection of Mi{MIC} insertion stocks and bring the approaches outlined above to bear on more than 95% of Drosophila genes and euchromatic regions. We will create a collection of 6,500 new Mi{MIC} lines that will tile the genome with insertions spaced no more than about 40 kb apart. Moreover, the lines will be directly associated with an estimated 5,500 genes, of which an estimated 2,800 genes will have an insertion in a coding intron.

We will utilize newly generated Mi{MIC} lines with intronic insertions to produce strains with functional protein trap (gene-reporter) fusions in at least 1,000 of the highest priority genes for immediate use by the community. These lines will more than double the current number of tagged fusion genes. In sum, the proposed collection of Mi{MIC} insertions spaced throughout the genome will move virtually every aspect of Drosophila genetics to a higher plateau unmatched by any other metazoan model organism.

Currently 757 Mi{MIC} insertion lines are in the BDSC and 492 are being balanced.

A manuscript updating the status of the GDP should appear in Genetics.

Bellen HJ, Levis RW, He Y, Carlson JW, Evans-Holm M, Bae E, Kim J, Metaxakis A, Savakis C, Schulze KL, Hoskins RA, Spradling AC (2011) The Drosophila gene disruption project: progress using transposons with distinctive site-specificities. Genetics, submitted.

A manuscript by Venken KJT et al. describing the Mi{MIC} and its versatile applications is in preparation.

The X chromosome duplication project (Kaufman, Hoskins, and Bellen)

The goal of this proposal was to use the P[acman] technology to create a defined chromosomal duplication set for the X chromosome. Duplication mapping is an alternative to deficiency mapping, which is efficient on the autosomes but of limited utility on the X chromosome, especially in the absence of duplications. These defined duplications would also allow rescue of mutant phenotypes ascertaining that a phenotype is indeed due to a mutation in a specific gene. In addition, the rescue constructs can easily be tagged to determine where a gene is expressed and where the protein is localized.

Two existing P[acman] BAC libraries, the 20 kb CHORI-322 and the 80 kb CHORI-321, were end sequenced as part of this project (Venken et al., 2009). The sequences were submitted to GenBank and the alignments were used to tile the clones on the genome. We end sequenced 80,000 clones so that we could essentially cover all fly genes. This work has been published as a resource paper in Nature Methods in 2009. All the mapped clones can be searched at a web site (http://pacmanfly.org/) and ordered from BACPAC Resources (http://bacpac.chori.org/).

We then created an 80 kb tiling path for the entire X chromosome euchromatin. 408 clones of an average length of 88 kb were hand selected from the CHORI-321 P[acman] library in the context of the gene annotation, resulting in an optimized tiling path. The end sequences were verified, and the DNAs were injected to create transgenic flies. We had a good success rate in obtaining transformants. We recovered correctly inserted clones in 66% of cases during our first injection, whereas re-injections yielded 80% transformants. In total we obtained 382 correctly inserted clones (94%), and these 382 resultant targeted duplications cover 96% of the euchromatic portion of the X chromosome and extend into the pericentric heterochromatin. We further demonstrated that the lines can successfully rescue mutations in the genes that they cover. The lines have been deposited to the Bloomington Drosophila Stock Center (http://flystocks.bio.indiana.edu/) and are available to the fly community. This work was published in Genetics in 2010. All the stocks are in the BDSC.

Publications:

Venken KJT, Carlson JW, Schulze KL, Pan H, He Y, Spokony R, Wan KH, Koriabine M, de Jong PJ, White KP, Bellen HJ, Hoskins RA (2009) Versatile P[acman] BAC Libraries for transgenesis studies in Drosophila melanogaster. Nature Methods 6:431-434. PMID: 19465919.

Venken KJ, Popodi E, Holtzman SL, Schulze KL, Park S, Carlson JW, Hoskins RA, Bellen HJ, Kaufman TC (2010) A molecularly defined duplication set for the X chromosome of Drosophila melanogaster. Genetics 186:1111-1125. PMID: 20876565.

Mapping 400 EMS induced complementation groups on the X chromosome (Rui, Kaufman, Bellen)

The X chromosome in Drosophila poses specific genetic challenges because of the difficulty of carrying out complementation tests with essential genes. Males can only be used for complementation testing if the corresponding mutation in an essential gene is rescued by a duplication that carries the gene on another chromosome. Hence, many fly labs have avoided screening the X chromosome for essential genes. Although the X chromosome carries approximately 2,400 genes (Adam et al., 2000), the number of essential genes has been estimated at 820 (Ashburner et al., 1999). Yet a detailed analysis of the X chromosome shows that less than 150 genes are represented by mutations established to be lethal and available from the Bloomington Drosophila Stock Center (BDSC). These mutations, combined with *P* element insertions that have been mapped and are homozygous lethal, still only account for less than 30% of all of the estimated essential genes on the X chromosome (Peter et al., 2002; Bellen et al., 2004; unpublished data). Hence, we estimate that lethal mutations in more than 70% of the essential genes are unavailable to the fly community after 100 years of fly genetics.

The goal of this work is to more than double the collection of mutations in essential genes on the X chromosome, i.e., to bring the number of essential genes that can be immediately studied to more than 400. In addition, the point mutations in these genes will be identified and rescued, and thus be valuable to the community. Moreover, their presence on FRT-carrying chromosomes will allow for mosaic analysis in most tissues. Hence, we will provide a collection of EMS (ethylmethane sulfonate)-induced and molecularly identified mutations in ¯400 different essential genes on the Drosophila X chromosome, including mutations in more than 250 essential genes that are currently not available. We will identify the molecular lesions, and document the rescue with defined 80 kb and 20 kb P[acman] duplications. We will deposit this collection of mutations with the corresponding rescuing duplications in the BDSC for distribution to the Drosophila research community.

To accomplish this we generated 35,000 stocks (low EMS), and isolated 6,000 mutations that cause homozygous lethality on an FRT-containing X chromosome. Approximately 2,100 mutations cause interesting phenotypes based on two FRT mosaic screens in eye and thorax. About 1,600 mutations have already been mapped using

large duplications to about ¯1 Mb using 20 large X chromosome duplications. So far, 110 different complementation groups have been identified in which the molecular lesions has been identified. We are using whole genome sequencing technologies to identify the point mutations. We then confirm mutation identification by Sanger sequencing and by rescuing the lethal mutation using 80 kb genomic P[acman] clones that we have generated.

Harvard Drosophila RNAi Screening Center (DRSC; N. Perrimon, PI)

The *Drosophila* RNAi Screening Center (DRSC; www.flyrnai.org) at Harvard Medical School is an NIH grant-funded center that supports full-genome and smaller cell-based RNAi screens by the community through RNAi reagent library production; support of on-site and off-site screening; a database and website of protocols, information and screen results; and more. This is a critical grant renewal year for the DRSC. Early in March, we turned in a revised application for funding. We are grateful to the community—in particular, the *Drosophila* Board, our advisory board, and recent screeners—for their strong letters of support. In response to NIGMS request, our application includes a plan for cost-recovery of a larger proportion of our budget. Our fee for the genome-wide screening library (one set in duplicate) will go from $5,000.00 to $6,500.00, and other library fees will similarly go up by noticeable but not excessive amounts. Also in response to grant review input, we recently began migrating screen results data to PubChem BioAssay. Screen results data continue to be available from our own website, as well as FLIGHT, GenomeRNAi, and FlyMine, and as external links to our pages from FlyBase gene results pages. Last year, we implemented a policy change and will now distribute any reagent libraries (including the full-genome library) for off-site screening at another institution or center, in addition to continuing to host assay development visits and screens on-site. Moreover, we are offering a popular new service, custom production of small dsRNA libraries (*e.g.* ~100-300 genes), which makes excellent use of our collection of more than 30,000 high-quality amplicons, and saves time and costs for the researcher.

Recent Screens. Focusing specifically on the science ongoing at the DRSC, we are extremely pleased with recent happenings. Anyone is welcomed to apply to the DRSC, and in the past few years, we have hosted screens from several US states, Europe and South America. The screens focused on topics such as cytokinesis, host-pathogen interactions, organelle morphology, stress responses, transcriptional responses, and metabolite sensing. These included full-genome, sub-library and over-expression screens performed on site at the DRSC, as well as two full-genome and several smaller screens performed off site using our reagent libraries. The specificity and sophistication of screen assays continues to increase. We are able to support a very wide range of assays, from simple plate-reader assays to laser scanning cytometry, epifluorescence, and fluorescence confocal imaging. About a dozen publications based on DRSC screens were published in the last year, bringing the total number of publications based on screens, meta-analyses, protocols, *etc.* to more than 70, with many additional manuscripts based on screen data currently in preparation.

At the Fly Meeting. The DRSC Director, Stephanie Mohr, will be talking about full-genome immunofluorescence-based screens performed at the DRSC by three different groups in the Techniques & Genomics session (Mohr *et al.* Platform 133). Each of these screens was aimed at studying a different aspect of the nucleus and utilized our instrumentation for automated confocal imaging. Eric Joyce of the Wu Lab at HMS will be presenting a poster on yet another full-genome DRSC screen that used our confocal imaging platform to look at a nuclear feature, in this case using fluorescence *in situ* hybridization (Poster 384C). In addition, DRSC bioinformatician Claire Hu will be presenting an integrated approach to identification of orthologs and linking fly genes to human diseases (Hu *et al*. Poster 452B).

What's Next. Looking forward, in addition to facilitating screens with existing libraries, we will also continue to expand our library collection and services, such as by continuing to rapidly transfer technologies developed in the Perrimon lab and elsewhere for general use by the community. We are currently completing production on two new RNAi libraries, an autophagy-related library and a G-protein coupled receptor (GPCR) library, each of which will have three independent reagents per gene coverage. We are also planning to complement our miRNA over-expression library (E. Lai, Sloan Kettering) with a miRNA "sponge" collection for reduction of miRNA function (Perrimon & D. Van Vactor, HMS). Additional technologies we expect to transfer to general use by the community in the future include a genome-wide shRNA plasmid collection (with G. Hannon, Cold Spring Harbor Labs), a reagent collection for double knockdowns (with S. Kondo, Japan), and newly derived cell lines (with A. Simcox, Ohio State University).

Concluding Remarks. Cell-based screening continues to be a powerful method for gene discovery and for functional validation of gene lists resulting from other high-throughput approaches. We feel that cell-based screening by the community is well supported by the DRSC but as always, we welcome feedback on how we can continue to improve.

TRiP Summary for the Fly Board Meeting, March 30, 2011

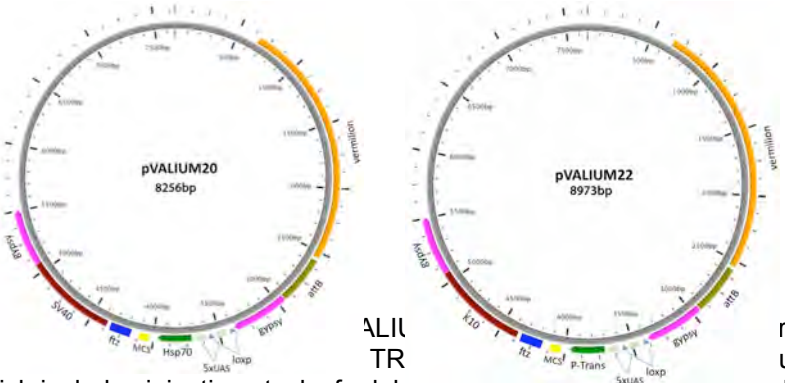
Prepared by Liz Perkins

The goal of the **Transgenic RNAi Project** (the TRiP: supported by NIGMS, R01-GM08494; N. Perrimon, PI), which enters its final year of funding this June 2011, is to generate 6,250 transgenic RNAi lines and to make them immediately and openly available to the community. The TRiP facility was established at Harvard Medical School in September 2008, and to date approximately 6,000 stocks have been generated or are in production. The stocks are then annotated on the TRiP website (http://www.flyrnai.org/TRiP-HOME.html) and on FlyBase, and transferred to BDSC for distribution to the community.

The first generation TRiP stocks contain long dsRNA hairpins in either VALIUM1 or VALIUM10: Our first vector for introducing RNAi into the genome was VALIUM1 (Vermilion-AttB-Loxp-Intron-UAS-MCS) (Ni et al, 2008). We targeted long dsRNAi constructs to the 3rd chromosome at 68A4, using the phiC31 site-specific integration method (Groth et al, 2004). All the hairpins were about 500bp and designed head-to-head utilizing Matt Booker's "Snapdragon" algorithm at the DRSC. VALIUM1was an effective vector for targeted transgenic RNAi. The RNAi phenotypes are expected, specific, and reproducible. There are 668 RNAi lines generated using VALIUM1. However, the strength of RNA knock-down with VALIUM1 was not satisfactory and higher temperature and UAS-Dicer 2 are needed to achieve maximum knock down. VALIUM10 was the best performing vector among our first generation of vectors,

which were generated in the effort to optimize the various features of VALIUM1. (Ni et al, 2009). There are 1,640 long dsRNA stocks generated in VALIUM10.

The second generation TRiP stocks contain short shRNA hairpins in either VALIUM20 or VALIUM22 (variant: VALIUM21). Both VALIUM1 and VALIUM10 have proved to be effective for RNAi in somatic tissues, however, they do not work in the female germline. In the endeavor to get RNAi to work in the female germline, we have generated VALIUM20, which combines the optimized expression features of VALIUM10 with a modified scaffold of the microRNA *miR-1,* which delivers short hairpin RNA into the genome. Our data shows that VALIUM20 works well in the germline and is stronger than VALIUM10 in the soma. VALIUM22 (and variant VALIUM21) the newest vector at the TRiP, features a P-transposase promoter instead of the hsp70 basal promoter. Data shows that VALIUM22 is stronger than VALIUM20 in the germline, but not in the soma (Ni et al, Nature Methods*, in press*). New TRiP-Soma lines are generated in VALIUM20. To date, there are 1,510 shRNA stocks generated in VALIUM20, and 438 stocks in VALIUM22. These stocks are now becoming available through the BDSC.



The TRiP a ALI rotocols to labs wishing to generate TR ugh the BDSC, the "TRiP Toolbox", which includes injection stocks for labs wishing to generate their own RNAi lines, and commonly used GAL4 lines with UAS-Dcr2 to enhance message knockdown.

The future of the TRiP is uncertain due to the precarious funding situation. The quality of the shRNA approach has led us to realize that the community would greatly benefit from a genomic scale collection of shRNA lines.

For the soma: the best is to have a single shRNA line in VALIUM20. We ultimately need one line in VALIUM20 against every gene in the genome: 15,000 lines. Since we already have ~1,500 lines we need to generate 13,500 additional lines.

For the female germline: we need two lines against all germline expressed genes. We propose to have one of the lines in VALIUM20 as these work well for the germline (these are already part of the collection above). In addition, as VALIUM22 is usually more potent, we will generate the second line in VALIUM22 (on a different chromosome). Altogether we are talking about 6,000 VALIUM22 lines to cover all genes expressed in the female germline and early embryos. Right now there are 438 VALIUM22 lines.

To prepare for the TRiP's next phase, we have generated with Greg Hannon a library of DNAs that are described in our shRNA paper that will soon appear in Nature Methods. Target coverage goals were set to at least three shRNAs per gene in the construct library, all of which could be used for the production of transgenic animals. Toward this end, we predicted shRNA sequences for all genes using DSIR12, an algorithm trained on effective siRNAs (http://biodev.extra.cea.fr/DSIR/DSIR.html). DSIR has proven quite reliable for the prediction of shRNAs for effective knockdown in transgenic flies, and the vast majority of the shRNAs described in this paper were designed using the DSIR algorithm of Vert et al. A total of 83,256 unique shRNA oligonucleotides were synthesized *in situ* on four custom glass slide microarrays13. These were amplified as pools, and inserted into VALIUM20 and VALIUM22. Approximately 160,000 individual clones are analyzed per vector. Accurate clones are identified through a two-step process. The first involves a DNA Sudoku14 compression followed by Illumina sequencing. Candidates nominated via that process are verified by conventional capillary sequencing, and resulting constructs are deposited into the TRiP for distribution and transgenic fly production.

Our issue now is how do we get this done and who will keep and distribute eventually the 21,000 lines. To raise more money for the project, we have submitted two grants in the past year. An R01 for the germline project and a smaller R24 for the Human disease TRiP project. Our germline R01 did well but was borderline for funding and we are appealing this decision. We will hear about the R24 grant in 6 months or so but this is a small grant. A competing continuation of the current TRiP RO1 will be submitted this coming July, 2011.

Because of the uncertainties of our ability to continue producing lines, we have encouraged the community to participate in the production of TRiP lines but only with the condition that these lines will end up in Bloomington. Thus, Brian Oliver has paid for injection of 268 lines and Ruth Lehmann for about 435 lines. Recently, two former Perrimon postdocs took positions in China (Jianquan Ni at Tsingua) and in Japan (Shu Kondo at the National Institute of Genetics). Both have funds to generate some of the lines with China promising to deliver about 4,000 lines a year and Japan 2,000 lines per year. In exchange for the DNAs that we will provide them, the lines will be sent back to us for quality control and if Bloomington is able to accept them, we will forward them to the BDSC.

Overall, our strategy to achieve the 21,000 stock goal, 15,000 TRiP-Soma lines and 6,000 TRiP-Germline lines, is to: 1. Keep trying to raise money for the TRiP; and 2. make available the DNAs to anyone who wants to make 100 or more lines and who will make the lines freely available to anyone as soon as they are available. Most important to us is that they agree to send the lines to the TRiP and we will send them to the BDSC (if possible). **In essence, the TRiP at HMS will serve as a "clearing house", ensuring quality control, distribution and maintaining the "official TRiP website and database".** For some of these lines there will be some redundancy but, considering how popular the TRiP stocks are, this should not be too much of an issue. We feel that we have no choice but to expand the project abroad as it has been so difficult to raise money in the US for this. If all goes well, within four years the entire collection, 15,000 TRiP-Soma lines and 6,000 TRiP-Germline lines, may be put together.

Publications:

Ni, J-Q., Markstein, M., Binari, R., Pfeiffer, B., Liu, L-P., Villalta, C., Booker, M., Perkins, L. A., and Perrimon, N. (2008) Vector and Parameters for Targeted Transgenic RNAi in Drosophila melanogaster. Nature Methods 5, 49-51.

Ni J-Q, Liu L-P, Binari R, Hardy R, Shim H-S, Cavallaro A, Booker M, Pfeiffer B, Markstein M, Wang H, Villalta C, Laverty T, Perkins L, and Perrimon N. A Drosophila resource of transgenic RNAi lines for neurogenetics. Genetics 2009, 182(4): 1089-1100.

Ni J-Q, Zhou R, Czech B, Liu L-P, Holderbaum L, Yang-Zhou D, Kim H-S, Tao, R., Handler D, Karpowicz P, Binari R, Booker M, Brennecke J, Perkins LA, Hannon GJ and Perrimon N. A genome-scale shmiR resource for *Drosophila* transgenic RNAi in both the germline and soma. Nature Methods 2011, *in press*.

Vienna Drosophila RNAi Center (VDRC) (Krystyna Keleman)

The VDRC was established in April 2007 as non-profit research infrastructure by the IMP and IMBA research institutes in Vienna, Austria. Its mandate is to maintain and distribute the transgenic RNAi stocks constructed by Dickson group at the IMP. In addition to the original P-element based library, a second genomewide collection of phiC31-based transgenes was made available to the Drosophila community in April 2009. The VDRC currently has 1703 registered users world-wide and has delivered a total of 611,278 RNAi lines to the Drosophila community.
Currently, the VDRC maintains and makes available 31,920 Drosophila lines, consisting of:
• 21,152 lines in the GD RNAi collection, constructed by P element mediated transgenesis
• 10,740 lines in the KK RNAi collection, constructed by phiC31 mediated transgenesis into preselected single genomic locus, VIE260b, on chromosome II.
• 33 miscellaneous stocks used for the construction of both collections
Additionally, the VDRC provides:
• 13,848 DNA constructs used for the generation of the GD collection
Collectively, the GD and KK libraries cover a total 13,264 Drosophila genes (93.1%), with GD collection covering 11,972 genes (84.6%) and KK collection covering 9502 genes (71.49%). For most of the genes, more than one independent RNAi line is available through the VDRC.
The VDRC is staffed with 17.5 employees:
0.5 VDRC head (Krystyna Keleman)
1 stock maintenance and shipping head (Reinhard Klug)
1 software developer (Thomas Micheler)
0.5 administrative assistant (Virginia Salva)
14.5 technicians for maintenance and shipping
Administratively, the VDRC was initially operated jointly by the IMP and IMBA. From March 1, 2011, the VDRC formally becomes independent of IMP and IMBA and joins the Vienna Biocenter Campus Support Facility (CSF), an infrastructure project funded jointly by the Austrian government and the city of Vienna. This administrative move should not effect any of the operating procedures of the VDRC, but should provide for more secure long-term funding.
The VDRC running costs are currently 1,223,000 euros per annum. Depending on the demand for lines, approximately 700,000 euros is recovered from the users fees. The remainder is provided by the CSF.

DIS REPORT (Jim Thompson)

Volume 93 (2010) of Drosophila Information Service was published on schedule just after the end of the calendar year. At 269 pages, the issue is significantly larger than in

the last several years. It was uploaded onto the DIS web site for free access within a few days of its completion, and printed copies are being mailed as orders are received. As in the recent past, most printed copies are ordered by libraries. Our traditional annual "Call for Papers" stimulates a large number of submissions. Indeed, most contributions are received between mid-November and the end of December. But this year we have started uploading "prepublication" files of articles that are received well before the deadline. For example, we already have two technique articles prepared for Volume 94 and uploaded onto the DIS web site in prepublication form (www.ou.edu/journals/dis).

We are also making very good progress in preparing past volumes for electronic access, and most previous volumes are now available on-line or nearing completion for free on-line access. I also continue to provide free pdf copies of older articles in response to email requests with very short turn-around time. Several requests are received each week, so there is still a need for information published in the older volumes.

Since most printed copies are ordered for libraries and the costs of printing, binding, and mailing continue to rise, we will charge $25.00 per copy (including shipping and handling) for orders after 1 January 2011. We hope to keep the cost at this level for the foreseeable future. Submissions are accepted at any time. Manuscripts and orders can be sent to James N. Thompson, jr., Department of Zoology, University of Oklahoma, Norman, OK 73019; jthompson@ou.edu.

DROSOPHILA SPECIES STOCK CENTER

(Therese Markow)

University of California at San Diego --- Therese Markow

The Drosophila Species Stock Center (DSSC) collection currently consists of 1599 living stocks, representing 227 species. In 2010, the DSSC acquired 77 new stocks from 35 species. Twenty-six of the new stocks were additional transgenic strains of 4 species created and provided by Thom Kaufman's lab, which we started making available to the community in September 2009. The rest of 51 new stocks represented 31 species, with several new species additions from Dr. Masayoshi Watada (Ehime University, Japan) such as *D. asahinai*, *S. bocki*, *D. lacertosa*, and *D. rufa*. We also decommissioned 19 stocks that were not frequently ordered from species with strong representation in the collection. There were 7 additional stocks lost in 2010. Genomic DNA is available for all 12 sequenced species, as well as for 5 commonly ordered stocks: *D. santomea*, *D. miranda*, *D. teissieri*, *D. orena*, and *D. eugracilis*. We have also created three genomic DNA packs for 1) the *D. virilis* group, 2) a global representation of *D. melanogaster*, and 3) the *D. mojavensis* species cluster.

The DSSC always has consisted of a permanent collection of both ethanol-stored and living stocks. As of March 22nd 2011, the 1599 cultures in the living collection consist of 1076 wild-type stocks (both multi-female and isofemale lines), 372 mutant

allele stocks, and 151 transgenic stocks. The living collection represents a diversity of 227 species. On the other hand, the 502 stocks in the ethanol-stored collection contain 418 wild type, 39 mutant, and 45 transgenic stocks. We periodically offer, on a temporary basis, a varying number of recently caught isofemale wild-type cultures. These isofemale collections are subsequently made "permanently available" by storing adults in ethanol or in the -80°C freezer.

In 2010, the Drosophila Species Stock Center provided the *Drosophila* research community with 1,172 stocks in 254 shipments representing 60% of species in the Stock Center. 32% of the orders came from international institutions. The genome-sequenced species' cultures presented approximately 15% of stocks sold. The top 20 species requested represent 56% of the total stocks sold by the DSSC. Details of the stock sales in 2009 and 2010 are presented in the tables below.

As a means of instituting new quality control methods in the Stock Center, we have initiated collaboration with Paul Hebert and the Barcode of Life project at the University of Guelph (Canada) to barcode all wild-type stocks in the Stock Center. In addition, this project establishes a record for each stock that includes an image and geographic data from all known collections of the species. We are in the process of linking each record in the Stock Center database to the records established in the Barcode of Life Database (BOLD).

Last year, we were operating on a six-month, bare-bones supplement from NSF and thus were unable to hold the annual Drosophila Species Workshop last October. There have been numerous inquiries about the next workshop and we are planning to hold one at UCSD in October 2011.

Table 1. Transgenic stocks added and ordered in 2010.

Species	**Number Transgenic strains**	**Number strains ordered**	**Times ordered**
D. simulans	17	4	1 twice, 3 once
D. yakuba	26	2	1
D. erecta	16	1	1
D. sechellia	2	2	1
D. pseudoobscura	29	4	1
D. willistoni	13	2	1
D. mojavensis	1		
D. mercatorum	8		
D. virilis	33	3	1
Total orders of transgenic stocks = 19			

Table 2: Shipment totals

	2009	**2010**
# Orders		

USA	165	173
INT	71	81
Total	**236**	**254**
# Stocks		
USA	883	799
INT	360	373
Total	**1243**	**1172**

Table 3: Top 20 stocks ordered 2009.

Rank	Species	2009
1st	*D. melanogaster*	119
2nd	*D. virilis*	106
3rd	*D. simulans*	101
4th	*D. sechellia*	90
5th	*D. pseudoobscura*	69
6th	*D. ananassae*	64
7th	*D. mauritiana*	59
8th	*D. yakuba*	55
9th	*D. persimilis*	50
10th	*D. erecta*	45
11th	*D. mojavensis*	36
12th	*D. willistoni*	30
13th	*D. serrata*	22
14th	*D. mercatorum*	19
15th	*D. hydei*	11
16th	*D. subobscura*	11
17th	*D. americana*	10
18th	*D. takahashii*	10
19th	*D. bipectinata*	9
20th	*D. miranda*	8

Table 4: Top 20 stocks ordered 2010

Rank	Species	2010
1st	*D. simulans*	109
2nd	*D. sechellia*	68
3rd	*D. melanogaster*	66
4th	*D. pseudoobscura*	62
5th	*D. ananassae*	41
6th	*D. yakuba*	41
7th	*D. virilis*	39
8th	*D. willistoni*	38
9th	*D. mojavensis*	36
10th	*D. mauritiana*	29
11th	*D. persimilis*	28
12th	*D. erecta*	24
13th	*D. teissieri*	15
14th	*D. santomea*	14
15th	*D. mercatorum*	13
16th	*D. arizonae*	9
17th	*D. immigrans*	8
18th	*D. novamexicana*	8
19th	*D. montana*	7
20th	*D. orena*	7

FlyBase Report to the North American Drosophila Board
March 08, 2011

We are pleased to present our 2011 report to the Fly Board.

In this report, we will highlight new features in FlyBase, some parts of FlyBase that the Fly Board should be aware of, and our future plans and issues we are grappling with. We make extensive use of screenshots to highlight important new features.

Respectfully submitted,

Bill Gelbart, Nick Brown, Thom Kaufman, Kathy Matthews & Maggie Werner-Washburne

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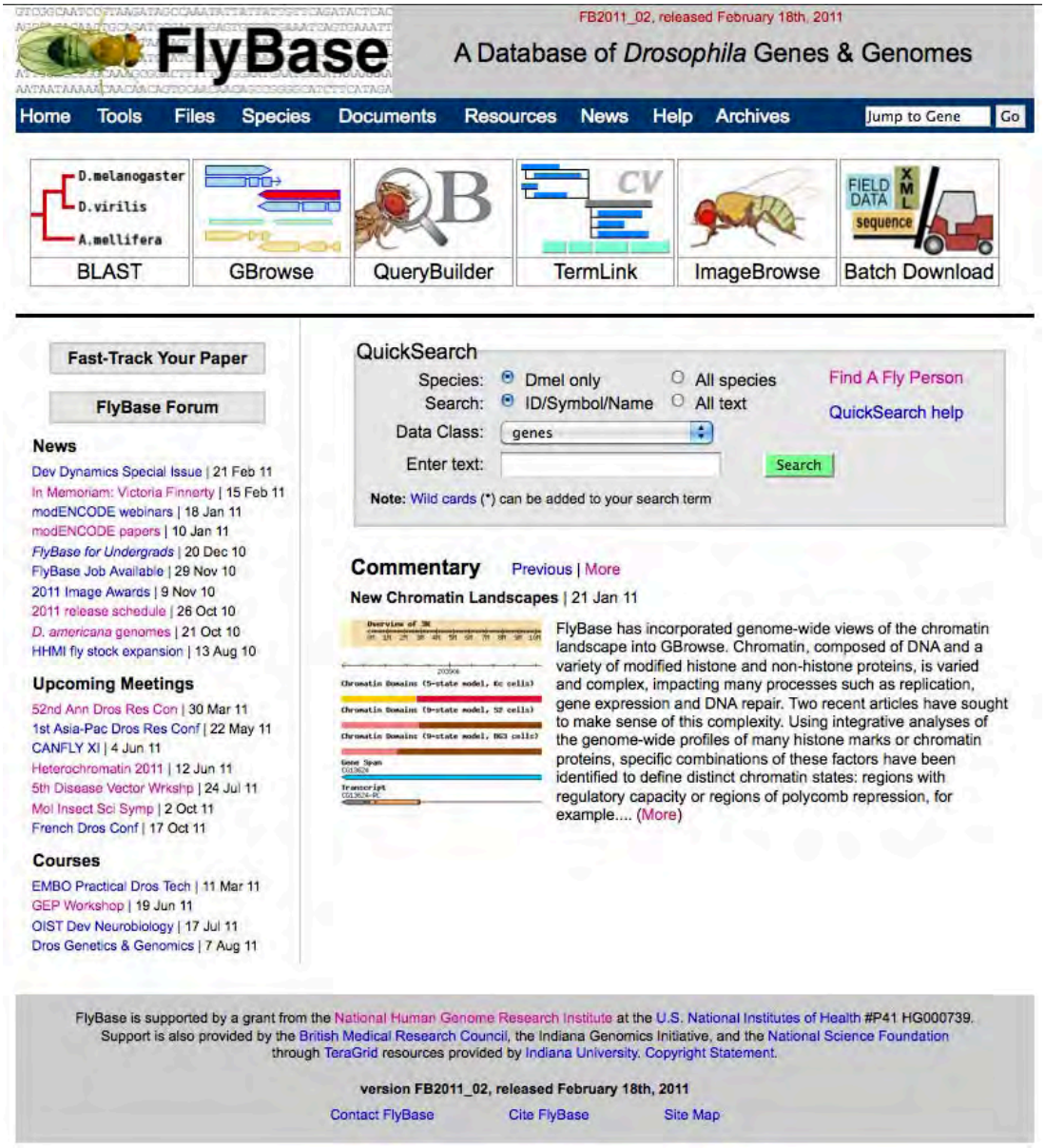
The Current FlyBase Home Page: FB2011_02: February 18th, 2011



FLYBASE REPORT – EXECUTIVE SUMMARY

We are pleased to report that 2010 was another excellent year for FlyBase. Our plans have largely moved forward as anticipated. We are most appreciative of the steady level of funding from our NHGRI grant (we are about midway through our 5 year renewal which runs through 12/31/2013).

Some highlights of our progress are:

Production statistics

- Nine public site releases in 2010; ten releases scheduled for 2011 (Table 1).
- Steady progress on literature curation and gene model annotation (exemplified by the data class statistics in Tables 2 and 3).

Community outreach:

- We continue to have extensive community outreach through direct communication with users who have emailed to us, through News and Fly Board postings, FAQ sheets, documentation, a Community Forum and the FlyBase demo room at each ADRC.
- **We invite the Fly Board to take advantage of the Commentary space on the FlyBase home page to post notices of interest to the Drosophila research community**.
- We have taken advantage of our excellent relationship with the community to ask authors to do initial high level paper curation (Fast Tracking). We have had 681 submissions in the last year. Beginning in Oct. 2010, we now email requests to corresponding authors of newly published papers requesting that they Fast Track them; this is an important aid to us in prioritizing our curation effort. To date, we have made 1319 such email requests with a 37.7% success rate. In general, false positive and false negative rates are tolerable for many data classes, and where they are high, we are using these observations to clarify the data types that we are looking for.

New data types and data enhancements

- Additional high-throughput data sets / data displays, including RNA-Seq exon-exon junctions, gene-by-gene temporal and tissue expression patterns, chromatin domains and protein-protein interactions (exemplified in screen-shots below).
- Addition of Recent Updates listing to flag new information in FlyBase gene reports.

GENETICS to FlyBase hyperlinks

- FlyBase is pleased to report on a successful collaboration with WormBase and the journal GENETICS to produce PDFs of research articles with genetic elements hyperlinked to their respective FlyBase report page. The hyperlinked elements include existing genes, alleles, aberrations, transgenes and transgene insertions (as long as they are italicized and use the current FlyBase symbol/name) . At present we are not able to hyperlink new genetic elements that are not yet in FlyBase, nor do we hyperlink non-D. melanogaster genetic entities. The first hyperlinked GENETICS articles will be in the April 2011 issue, and we hope that readers will benefit from being able to link directly to the relevant FlyBase page for more information.

On-going areas of focus

- Literature curation:
    - Data capture prioritization necessitated by the increase in the amount, scope and depth of the primary scientific literature (including supplementary data).
    - Expand options for author assistance with literature curation.
    - Developing natural language processing (NLP, aka text-mining) approaches for automatic first-pass curation and/or in-depth curation.
- Incorporating data and developing web reports and GBrowse views of data from numerous large-scale data production projects, with particular focus on modENCODE DNA feature datasets, protein-protein interactions, cell-based RNAi screens, genome-scale *D. melanogaster* re-sequencing projects and new *Drosophila* species' genomes.
- NextGen sequencing-based large-scale data contributed by individual laboratories.
- Evaluation of different approaches including InterMine for managing and querying complex data sets, especially large-scale datasets (subject of an NHGRI ARRA supplement to FlyBase).
- Improving our ability to assess what FlyBase data are of most value to the community.
- Making FlyBase more accessible to broader biomedical community, especially vis-à-vis medical relevance of Drosophila data and concepts.
- Developing quantitative metrics on the value of FlyBase to the scientific community.

FLYBASE WEB SITE UPDATE SCHEDULE

- Our goal is to have 10 web site releases per year. In 2010, we had to drop one release in order to buy the developer time to focus on some long overdue backend development tasks. We expect to return to our goal of 10 releases for 2011. The dates of actual and planned releases are shown in this table, along with the list of major datasets introduced in various releases.

TABLE 1: FLYBASE PRODUCTION REPORT TO FLYBOARD – 2011 MARCH 30			
FlyBase – Schedule of Future 2011 Releases			
Release Date	*Release ID*	*Dmel annotation version*	*Notable Events*
2011 November 11	FB2011_10	Dmel Release 5.42	
2011 October 07	FB2011_09	Dmel Release 5.41	
2011 September 02	FB2011_08	Dmel Release 5.40	
2011 July 22	FB2011_07	Dmel Release 5.39	
2011 June 24	FB2011_06	Dmel Release 5.38	
2011 May 27	FB2011_05	Dmel Release 5.37	
2011 April 22	FB2011_04	Dmel Release 5.36	NEW: Additional modENCODE datasets
2011 March 18	FB2011_03	Dmel Release 5.35	
FlyBase – Actual Releases			
Release Date	*Release ID*	*Dmel annotation version*	*Notable Events*
2011 February 18	FB2011_02	Dmel Release 5.34	NEW: RNA-Seq Junctions & DPiM data
2011 January 21	FB2011_01	Dmel Release 5.33	NEW: Chromatin Landscapes
2010 November 19	FB2010_09	Dmel Release 5.32	NEW: Recent Update Tags
2010 October 13	FB2010_08	Dmel Release 5.31	NEW: Fast-Track Community Curation
2010 September 03	FB2010_07	Dmel Release 5.30	NEW: Gene Level Transcript Data
2010 June 25	FB2010_06	Dmel Release 5.29	Update: Expression Pattern Data
2010 May 28	FB2010_05	Dmel Release 5.28	
2010 April 23	FB2010_04	Dmel Release 5.27	
2010 March 19	FB2010_03	Dmel Release 5.26	NEW: RNA-Seq Profiles, Insulators
2010 February 19	FB2010_02	Dmel Release 5.25	
2010 January 22	FB2010_01	Dmel Release 5.24	
2009 November 20	FB2009_10	Dmel Release 5.23	NEW: QueryBuilder Enhancements
2009 October 16	FB2009_09	Dmel Release 5.22	Dmel 5.22 submitted to GenBank
2009 September 11	FB2009_08	Dmel Release 5.21	
2009 August 10	FB2009_07	Dmel Release 5.20	NEW: GBrowse of BDSC Deficiency kit
2009 July 07	FB2009_06	Dmel Release 5.19	NEW: Cell line reports
2009 May 29	FB2009_05	Dmel Release 5.18	NEW: Seq. feature & library reports
2009 April 27	FB2009_04	Dmel Release 5.17	
2009 March 20	FB2009_03	Dmel Release 5.16	NEW: User data submission tool
2009 February 20	FB2009_02	Dmel Release 5.15	
2009 January 23	FB2009_01	Dmel Release 5.14	NEW: GBrowse view of aberrations
2008 November 19	FB2008_10	Dmel Release 5.13	
2008 October 17	FB2008_09	Dmel Release 5.12	
2008 September 12	FB2008_08	Dmel Release 5.11	11 seq. D. spp. submitted to GenBank Dmel 5.10 submitted to GenBank
2008 August 08	FB2008_07	Dmel Release 5.10	
2008 July 03	FB2008_06	Dmel Release 5.9	
2008 May 05	FB2008_05	Dmel Release 5.8	
2008 April 28	FB2008_04	Dmel Release 5.7	
2008 March 21	FB2008_03	Dmel Release 5.6	NEW: Annotated dozen fly genomes
2008 February 20	FB2008_02	Dmel Release 5.5	
2008 January 23	FB2008_01	Dmel Release 5.5	NEW: 10/year web site releases begun
2007 November 01	FB2007_03	Dmel Release 5.4	
2007 September 12	FB2007_02	Dmel Release 5.3	NEW: 11 D. spp. genomes in FlyBase Dmel 5.2 submitted to GenBank
2007 August 02	FB2007_01	Dmel Release 5.2	
2006 December 08	FB2006_01	Dmel Release 5.1	NEW: Totally New Web Site Introduced

SELECTED FLYBASE DATA CAPTURE STATISTICS

TABLE 2: CURRENT FLYBASE STATISTICS COMPARED W/ PREVIOUS YEAR (ALL DATA ARE FROM FLYBASE WEB SITE RELEASE NOTES)		
Category	***March 20, 2009***	***February 18, 2010***
General Statistics	**FB2010_03**	**FB2011_02**
Number of References in FlyBase	194,014	196,696
----- Research papers	82,638	83,863
----- Personal Communications	4,841	5,107
Number of Fly Strains	100,692	108,284
Fly Workers Registered with FlyBase	7,614	5,604
***D. melanogaster* Genetic Object Statistics.**	**FB2010_03**	
Number of Gene records	31,129	30,169
----- Genes w/ Gene Models	14,824	15,147
----- Genes w/o Gene models	16,305	15,022
Number of Alleles	129,331	135,334
----- Alleles of genes w/ Gene Models	110,399	116,523
----- Alleles of genes w/o Gene Models	18,932	18,811
Number of Chromosomal Aberrations	18,889	19,668
----- Deficiencies	8,101	8,267
----- Deficiencies w/ Mapped Endpoints	2,044	2,089
Number of TE Insertions	117,466	121,430
----- TE Insertions Localized on Genome	57,245	58,843
***D. melanogaster* Annotation Statistics.**	**Dmel Rel_5.26**	**Dmel Rel_5.34**
-- Protein-Coding Genes		
Number of Genes	13,732	15,147
----- Mean Length Genes (bases)	5,638	5,674
Number of Transcripts	21,921	23,178
----- Mean Length Transcripts (bases)	2,475	2,585
Number of Exons	69,209	69,338
----- Mean Exon Size (bases)	485	492
Number of Introns	51,989	53,056
----- Mean Intron Length (bases)	1,414	1,468
-- Non-Protein-Coding Genes		
rRNA Genes	160	160
tRNA Genes	314	314
snRNA Genes	47	47
snoRNA Genes	249	249
miRNA Genes	90	171
Miscellaneous Non-Coding RNA Genes	129	165
Miscellaneous Non-Coding Transcripts	157	210
Pseudogenes	101	134
-- Repeat Features in Genome		
Natural Transposable Elements	5,620	5,600
Annotated Repeat Regions	10,159	10,159
***D. pseudoobscura* Annotation Statistics.**	**Dpse Rel_2.9**	**Dpse Rel_2.17**
Number Protein-Coding Genes	16,153	16,087
Number of Exons	58,358	57,927
Number of Introns	41,606	41,765

FLYBASE *D. MELANOGASTER* GENE MODEL ANNOTATION PROGRESS REPORT

- There has been a steady effort to update gene models, with ***major changes*** to about 633 gene models having taken place during the last calendar (see Table 3 below). These include:
    - ***Merges*** combine two or more existing gene models into one larger gene. All associated data must be merged as well. The process of merging is largely automatic and so can be implemented as such cases are encountered.
    - ***Splits*** separate one gene model into two or more new genes. All associated data need to be evaluated carefully so that each piece of data in these gene records can be reassigned correctly to one of the resulting new genes. For this reason, splits are only scheduled infrequently, with careful project-wide planning and coordination.
    - ***Complex*** changes (involving simultaneous merges and splits) also need careful evaluation and management and are only scheduled infrequently.
    - ***New*** gene models typically arise from the introduction of new supporting evidence.
    - ***Restored*** gene models are ones that were removed because of limited evidence but were resurrected based on new supporting evidence.
    - ***Deleted*** gene models arise typically when the original evidence for an annotation is deemed suspect.
- Another ~3,000 *D. melanogaster* gene models were examined and updates (additional isoforms, additions to UTRs) were made to a majority of these.
- Gene models are reviewed by FlyBase curators when triggers tell curators that new data inconsistent with current gene models are available within FlyBase.
    - When new cDNA alignment data (provided monthly by NCBI) predicts splicing patterns that are not present in the FlyBase transcript models for a given gene.
    - When curators encounter a publication that reports evidence for a new or changed gene model.
    - New genes and changes to CDS's (protein-coding regions of gene models) are given the highest priority for gene model review.
    - FlyBase periodically submits our then current annotation sets to GenBank; these sets are also used as the NCBI RefSeq gene sets for *D. melanogaster.* The most recent whole genome *melanogaster* GenBank submission, based on FlyBase annotation Release 5.30, became public on 14-JAN-2011.
- We continue to use data from the modENCODE project and from contributions from other members of the research community (e.g., Bryce Daines and Rui Chen, Baylor). We expect that many additional gene model changes will be motivated, particularly involving:
    - Additional isoforms of known protein-coding genes.
    - Extensions of 5' UTRs and 3' UTRs of known protein-coding genes.
    - Novel non-protein-coding genes.
- The new data sets that will be used to inform these gene model changes include:
    - RNA-Seq exon-exon junction and coverage developmental profiles.
    - Transcription start site data (5' RACE, TSS-associated chromatin marks).
    - Profiles of marks for actively transcribed chromatin.
    - New gene prediction sets.

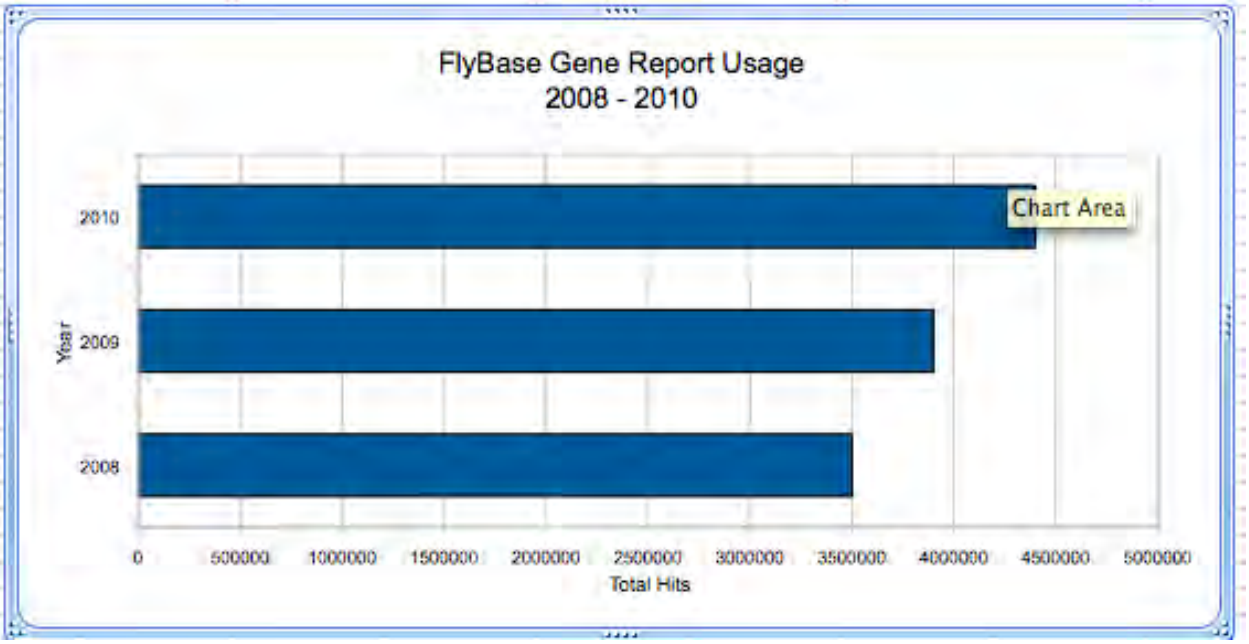
TABLE 3: MAJOR CHANGES TO D. MELANOGASTER GENE MODELS BY CATEGORY (ALL DATA FROM FLYBASE WEB SITE RELEASE NOTES)

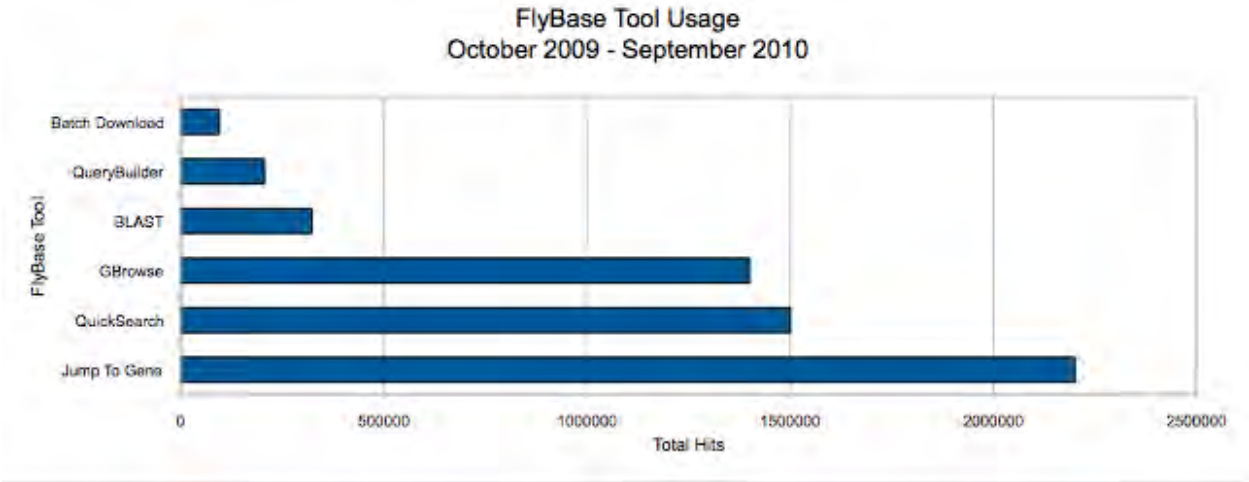
Dmel Release	PROTEIN-CODING GENE MODEL CHANGES FROM PREVIOUS RELEASE					
	NEW	RESTORED	DELETED	MERGED	SPLIT	COMPLEX
Rel_5.27	10	0	0	6->3	3->6	1
Rel_5.28	36	1	2	16->8	0	0
Rel_5.29	5	0	1	6->3	0	0
Rel_5.30	41	2	2	25->12	12->24	0
Rel_5.31	120	0	1	36->17	0	0
Rel_5.32	40	4	0	14->7	0	0
Rel_5.33	30	3	0	16->8	0	0
Rel_5.34	89	3	5	10->5	0	0
TOTALS	**371**	**13**	**11**	**129->63**	**15->30**	**1**

FLYBASE WEB SITE USAGE

FlyBase Web Usage

- To provide the Fly Board with a flavor of our current usage, we provide two simple histograms.
    - **Gene reports:** FlyBase Gene pages coalesce much of the pertinent information on gene structure, phenotype, interactions, gene function, gene expression, literature citations, etc. Thus, these pages are particularly popular with our users. Total hits to these pages was 4,400,000 through the first three-quarters of 2010, extrapolating to about 5,800,000 hits for all of 2010, as compared to 3,900,000 hits for all of 2009 ... a nearly 50% increase in Gene report page hits.
    - **FlyBase Querying and Browsing Tools:** Usage for a recent one year period (10/2009-09/2010) for various entry points to FlyBase gene/genome data was compiled. As expected, the QuickSearch and JumpToGene entry points were most popular (and most simple), combining for about 4,000,000 hits. The Genome Browser (GBrowse) was the next most popular utility, followed by BLAST and the advanced search query engine (QueryBuilder).

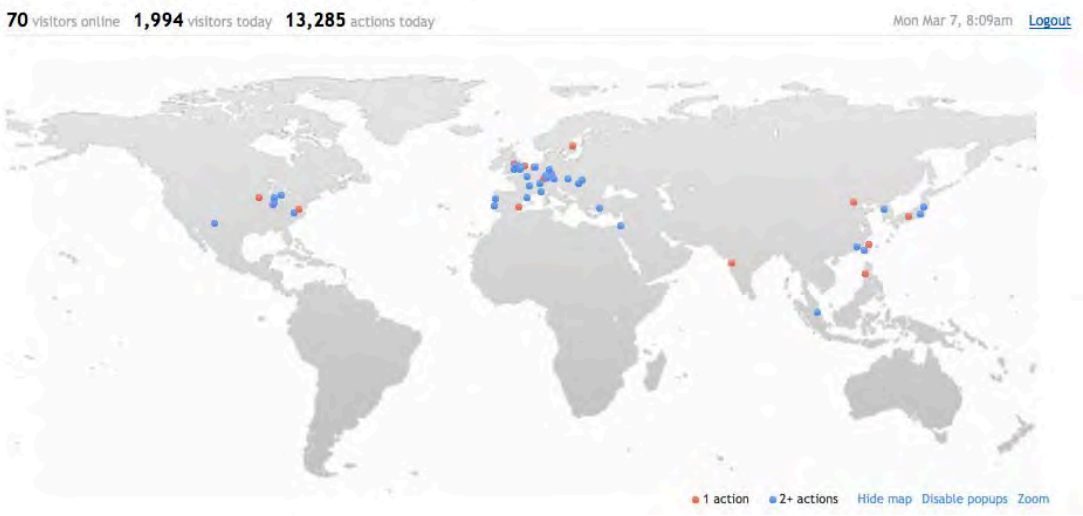


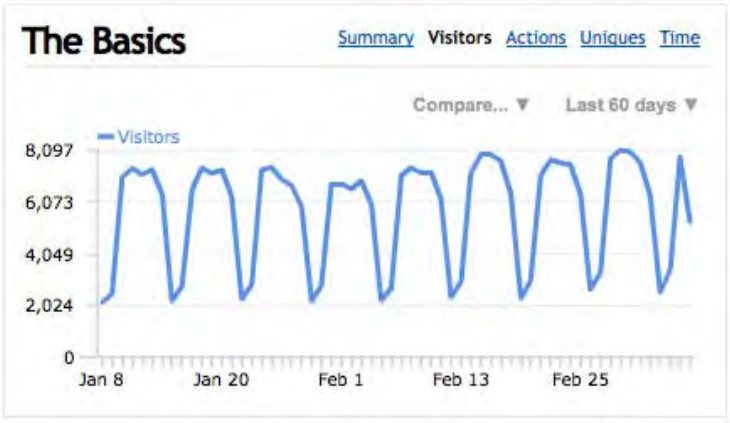


Clicky Web Analytics

We have begun to use other web analytical tools, including Clicky, to record much more detailed information about FlyBase usage. We can track usage geographically and temporally, and get a detailed sense of what kinds of queries and pages are interrogated during a session to better tune our web site structure and presentation.

Some clicky screenshots of geographic distributions of hits at two different time points on Monday, March 7, 2011 and a distribution of hits over the last 60 days (with weekly rhythms) exemplify information that can be culled from Clicky tools.

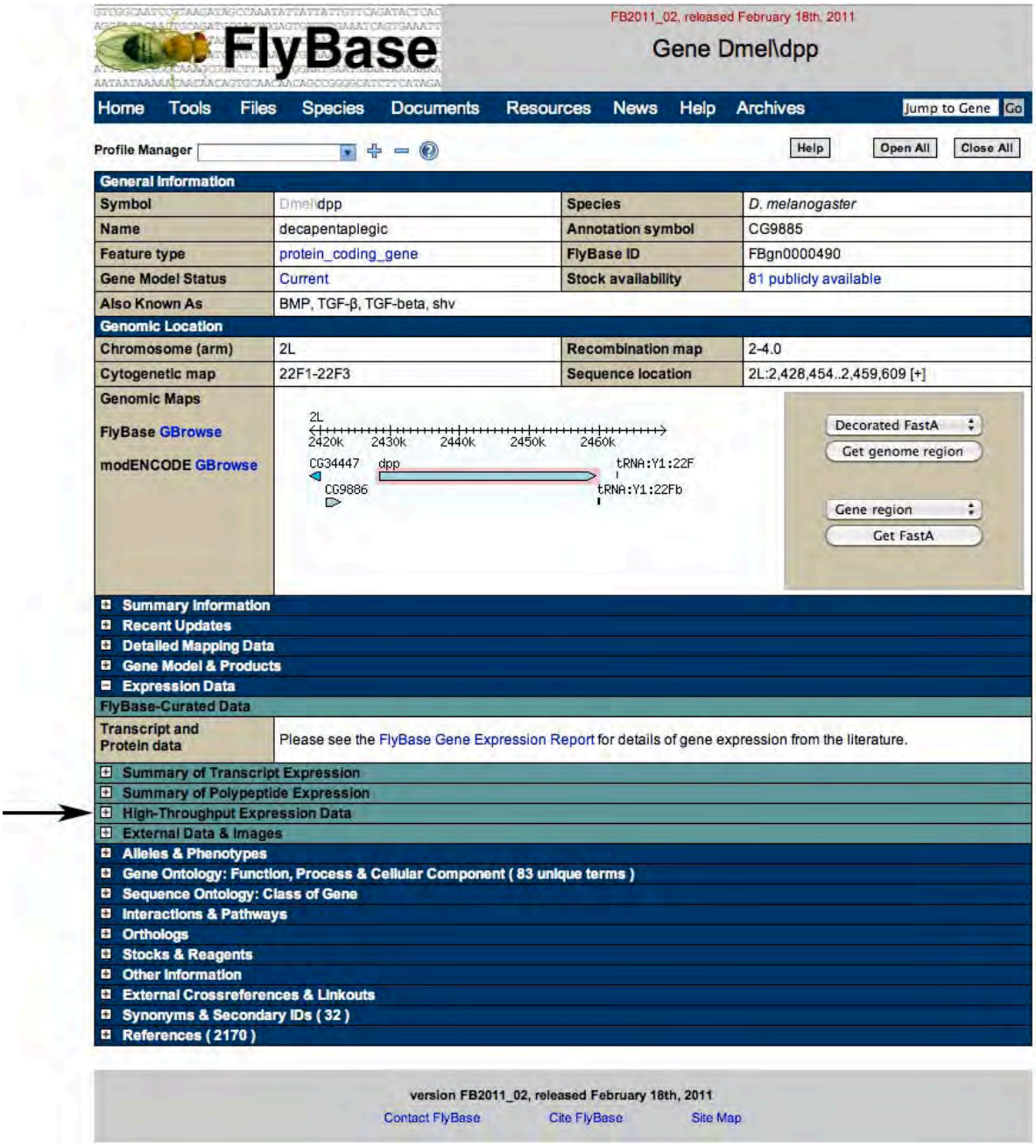




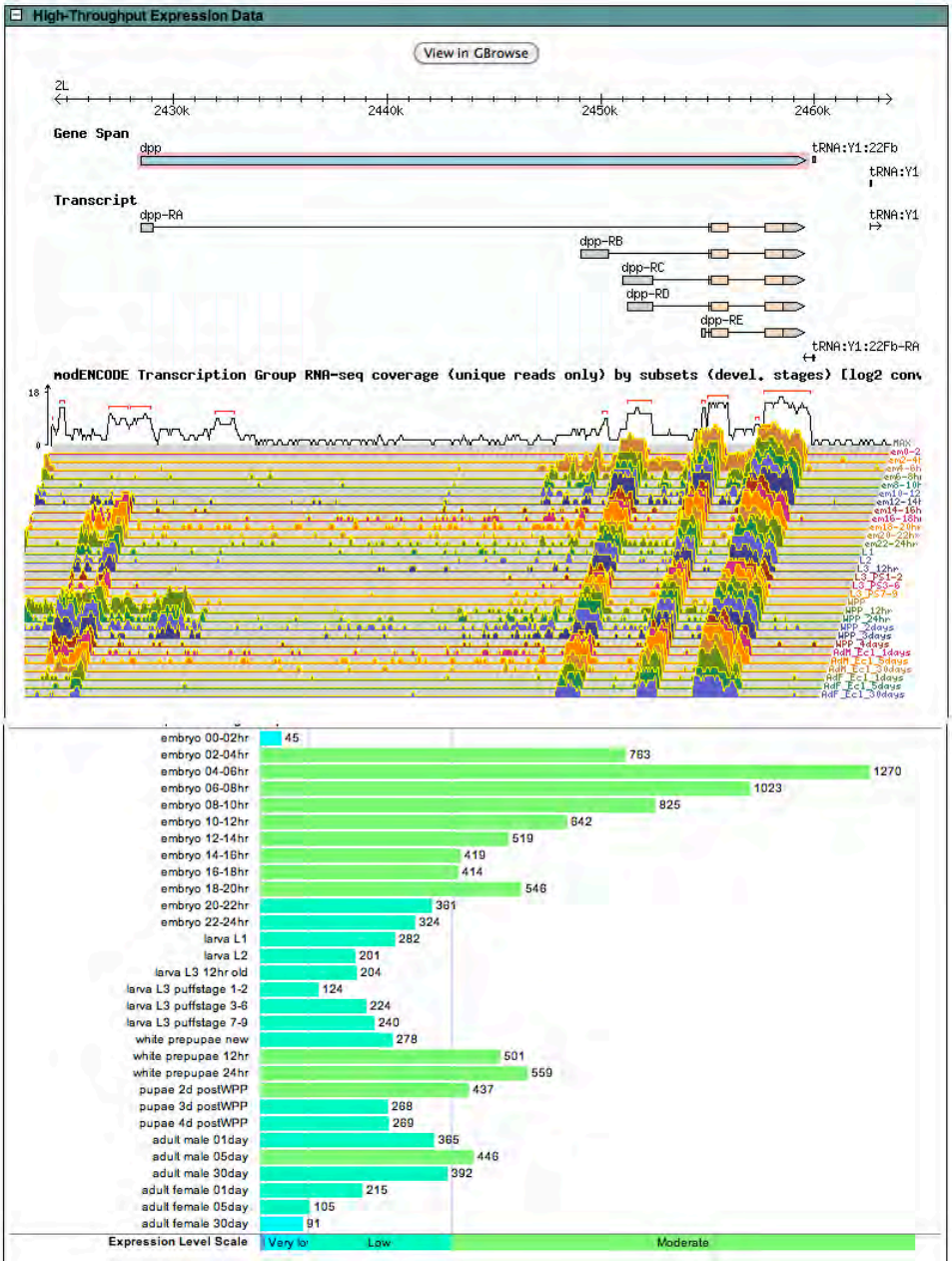
NEW FEATURES ON THE FLYBASE WEB SITE

New Features #1: FlyBase High Throughput expression data

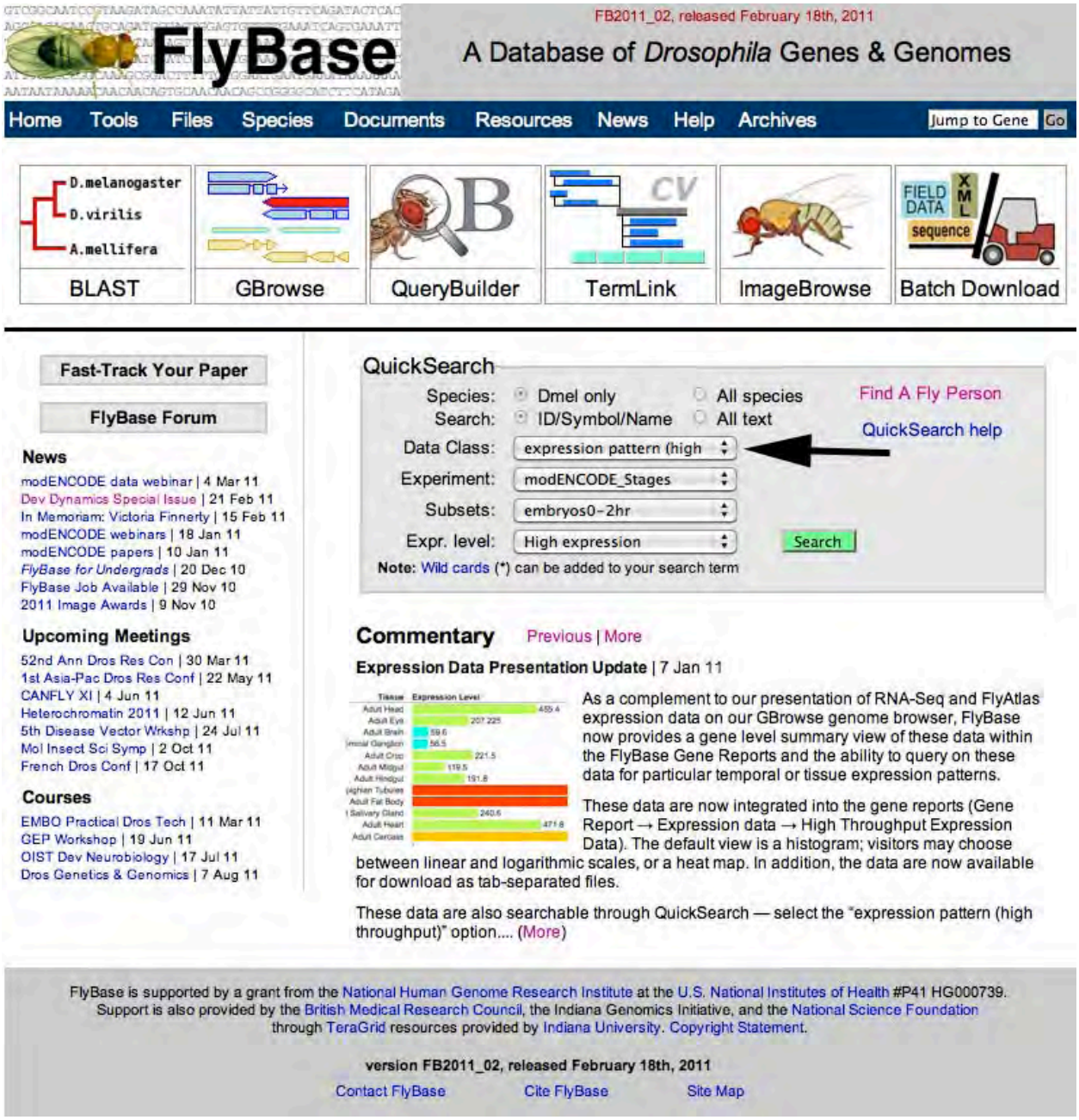
- As a complement to our presentation of RNA-Seq and FlyAtlas expression data on our GBrowse genome browser, FlyBase now provides a gene level summary view of these data within the FlyBase Gene Reports and the ability to query on these data for particular temporal or tissue expression patterns.
- These data are now integrated into the gene reports (Gene Report → Expression data → High Throughput Expression Data). Users now have the option to set the visualization parameters. The default view is a histogram with a scale set to the maximum expression level of the gene being viewed. Visitors may choose between linear and logarithmic scales, or a heat map. In addition, the data are now available for download as tab-separated files.
- These data are also searchable through QuickSearch — select the "expression pattern (high throughput)" option.
- The methods used to generate this data set can be found on the reference report for Gelbart and Emmert, 2010.
- The data can be found on the gene report page under <*Expression Data*> and the sub heading <*High-Throughput Expression Data*>.



- Clicking on the "High-Throughput Expression Data" section will open to a histogram summary of data from the modENCODE community transcriptome project and the FlyAtlas organ and body parts data.
- These data can be displayed to accentuate genes with varying levels of expression using the buttons at the top left of each display.



- These data can also be interrogated from the Home page using the Quick Search tool



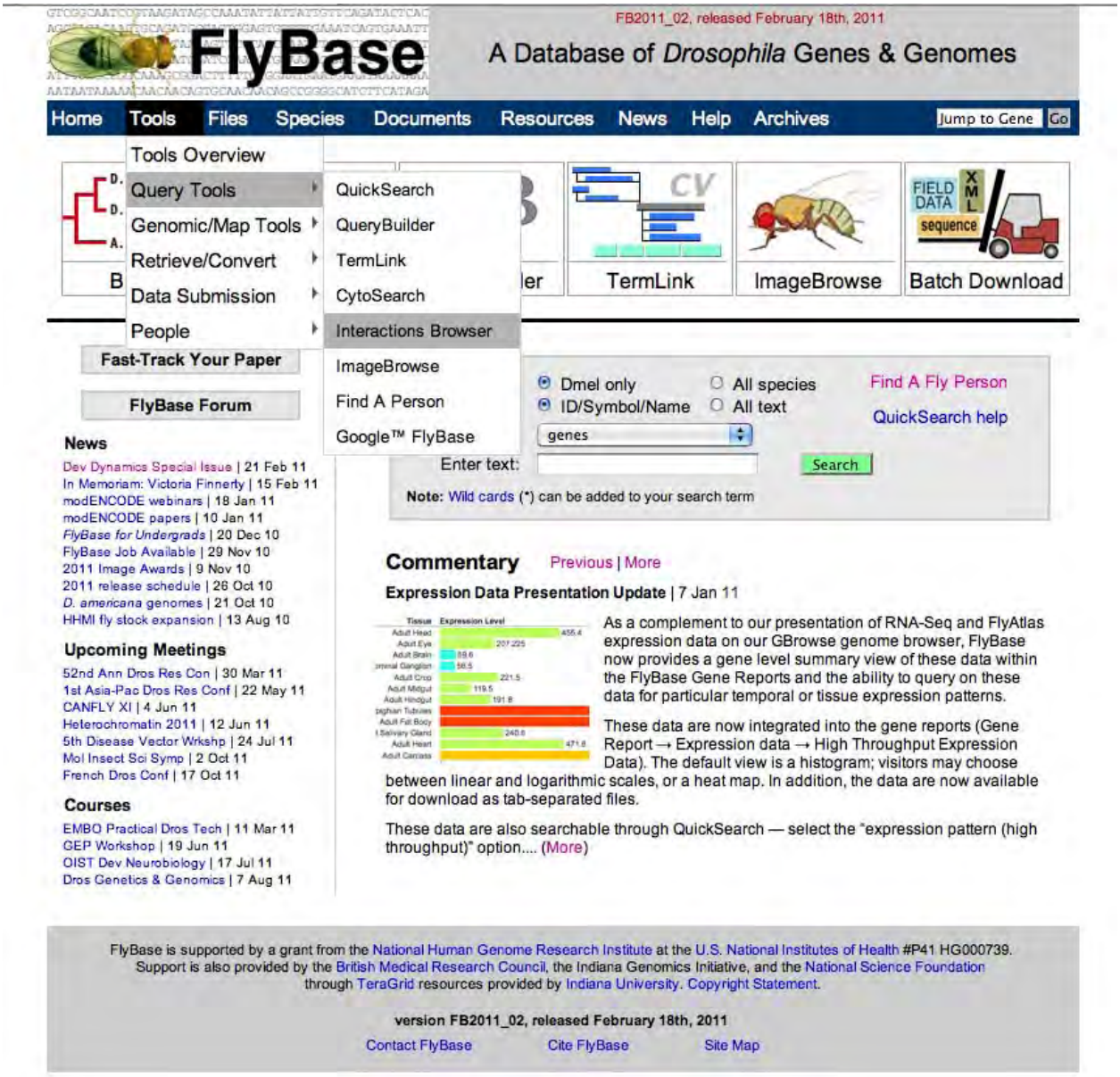
- The output of this type of search will be a table showing all of the genes expressed in the specified pattern.

New Features #2: FlyBase new gene/genome annotations: Splice Junctions, Insulators and Chromatin Domains

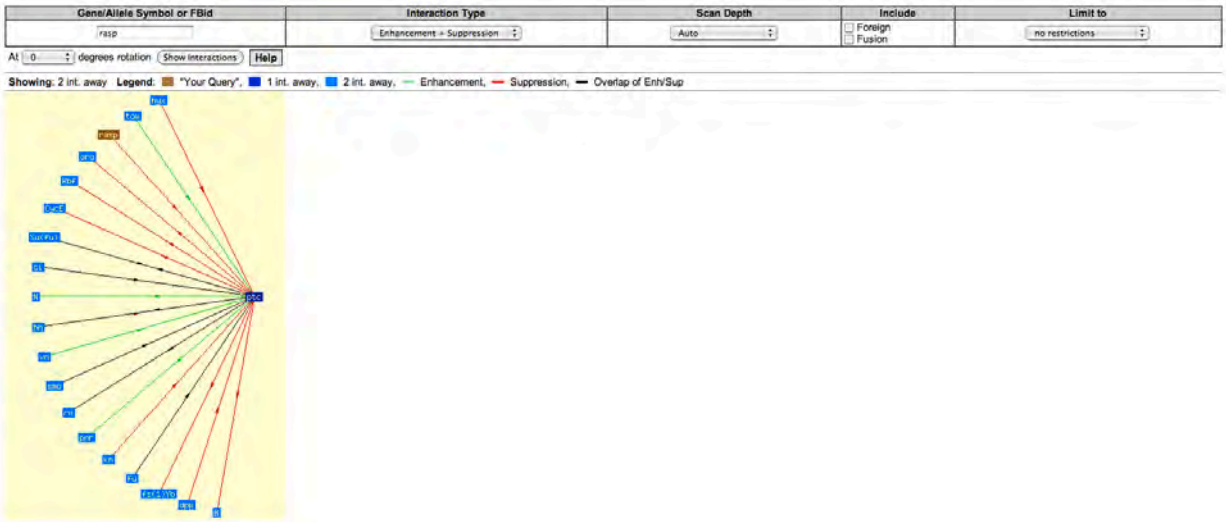
- FlyBase has incorporated genome-wide views of the chromatin landscape into GBrowse. Chromatin, composed of DNA and a variety of modified histone and non-histone proteins, is varied and complex, impacting many processes such as replication, gene expression and DNA repair. Two recent articles have sought to make sense of this complexity. Using integrative analyses of the genome-wide profiles of many histone marks or chromatin proteins, specific combinations of these factors have been identified to define distinct chromatin states: regions with regulatory capacity or regions of polycomb repression, for example.
- Filion et al. (2010) have identified five principal chromatin states from the analysis of 53 chromatin protein genome-binding profiles in Kc167 cells. As part of the modENCODE project, Kharchenko et al. (2010) profiled the genome-wide localization of 18 histone marks in S2-DRSC and ML-DmBG3-c2 ('BG3') cells and identified nine prevalent combinatorial patterns. The significance of Kharchenko's nine chromatin states is further explored in the modENCODE consortium's integrative paper. Together, these models identify various regions of functional significance, such as promoters, regulatory regions, regions of polycomb repression and classic heterochromatin in the cell lines assayed.
- FlyBase has incorporated these chromatin landscapes into GBrowse as color-coded tracks, each state represented by a different color. To view them, first go to **GBrowse** and select **[D. melanogaster RNA-seq Data]** in the **Data Source** pull down menu. Then scroll to the bottom of the page to the **Tracks** section, click on the desired 'Chromatin Domains' data sets, and hit the **Update Image** button (just under the GBrowse image display). Move the cursor over the color-coded track for a pop-up information window. The display of these and other GBrowse tracks can be customized using the **Configure Tracks** button.

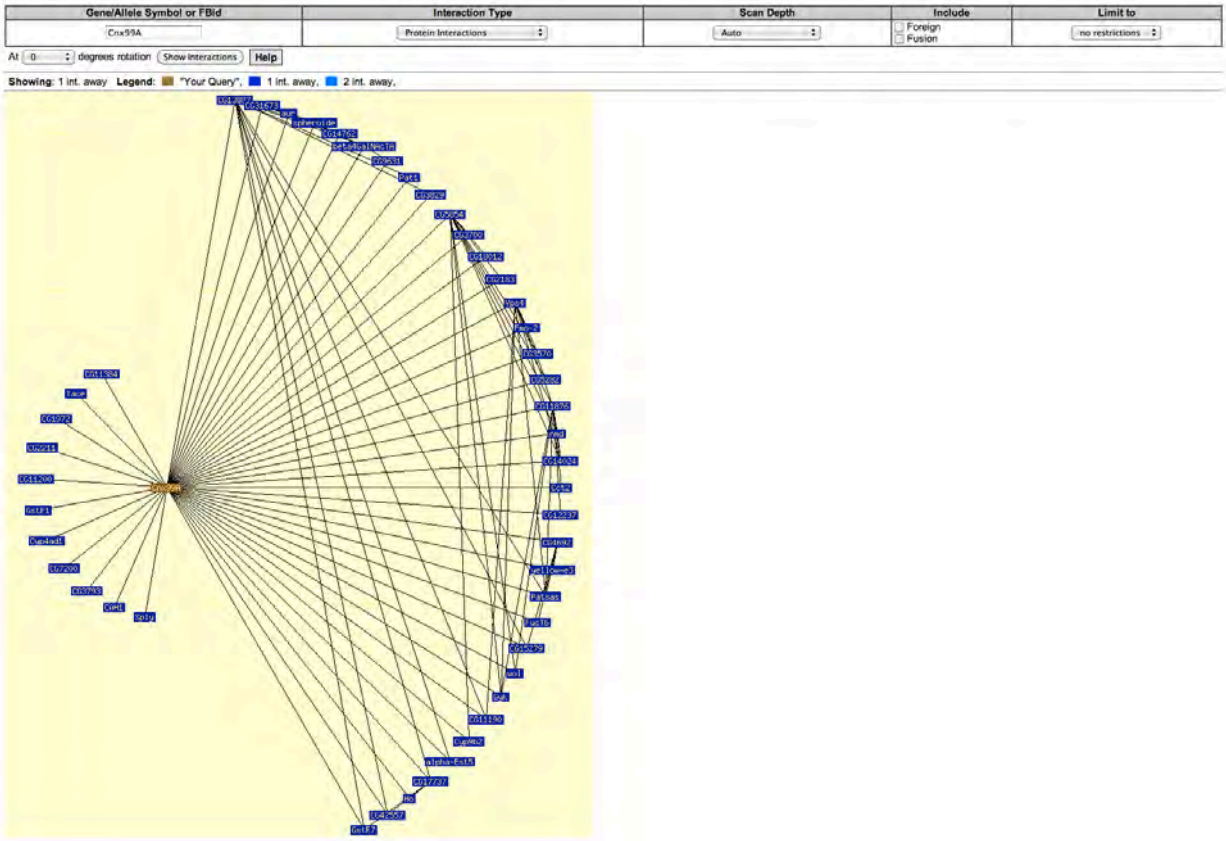
New Features #3: FlyBase Interactions Browser for Genetic & Protein::Protein interactions

- FlyBase now offers both genetic and protein::protein interaction data.
- Genetic interactions are derived from curation of the literature.
- The recently introduced protein::protein interaction data are provided by the DPiM (Drosophila Protein Interaction Map) project (https://interfly.med.harvard.edu/).
- The data can be accessed through the <*Interactions Browser*> found in the pull down Tools menu or in the interactions subsection of the Quick Search tool on the Home Page.



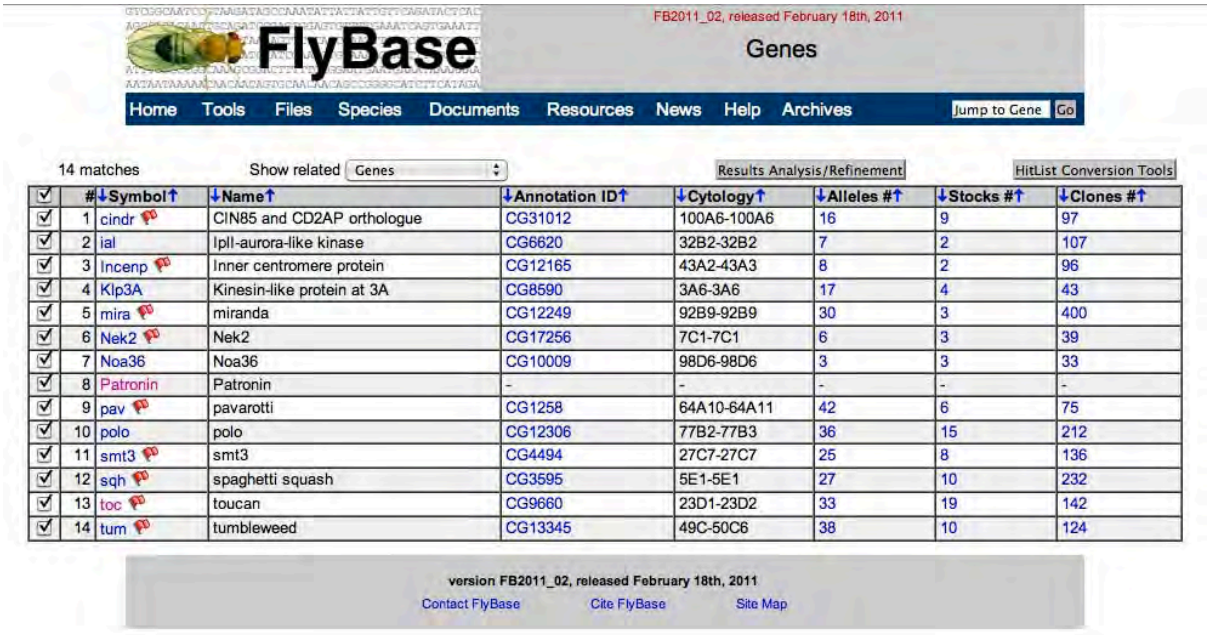
- The output of the interactions browser is in the form of a tree or web of identified interactions.
- The genetic interactions are characterized as either enhancing or suppressing.
- Selecting any of the identified interactors will take you to a new window showing the web for the selected gene.


Gene/Allele Symbol or FBid
rasp
Interaction Type
Enhancement + Suppression
Scan Depth
Auto
Include
Foreign
Fusion
Limit to
no restrictions
At 0 degrees rotation
Show Interactions
Help
Showing: 2 int. away Legend: "Your Query", 1 int. away, 2 int. away, Enhancement, Suppression, Overlap of Enh/Sup


Gene/Allele Symbol or FBid
Cnx99A
Interaction Type
Protein Interactions
Scan Depth
Auto
Include
Foreign
Fusion
Limit to
no restrictions
At 0 degrees rotation
Show Interactions
Help
Showing: 1 int. away Legend: "Your Query", 1 int. away, 2 int. away,

New Features #4: FlyBase Recent Updates

- At this time, the information we track for updates include new links between a FlyBase report and other FlyBase data classes (e.g. genes, references, stocks) or controlled vocabulary terms (e.g. GO, anatomy terms). We do not currently track gene model changes or links that have been removed. We do have plans to add the ability to track gene model changes in the near future. Update information is available starting with our FB2010_08 release and on.
- **Updates in FlyBase HitLists** The first place to find information about updates is on any FlyBase HitList. If your record has an update in the **current** FlyBase release it will have a small red flag located next to one of the fields (Symbol, Genotype, Author, etc.) in your list of search results. Holding your mouse over the flag for a few seconds will popup a window containing links to the newly added items. Records flagged with small green flags indicate a newly added record or one that is the result of a merge/split of existing FlyBase records.



#	Symbol	Name	Annotation ID	Cytology	Alleles #	Stocks #	Clones #
1	cindr	CIN85 and CD2AP orthologue	CG31012	100A6-100A6	16	9	97
2	ial	IpIl-aurora-like kinase	CG6620	32B2-32B2	7	2	107
3	Incenp	Inner centromere protein	CG12165	43A2-43A3	8	2	96
4	Klp3A	Kinesin-like protein at 3A	CG8590	3A6-3A6	17	4	43
5	mira	miranda	CG12249	92B9-92B9	30	3	400
6	Nek2	Nek2	CG17256	7C1-7C1	6	3	39
7	Noa36	Noa36	CG10009	98D6-98D6	3	3	33
8	Patronin	Patronin	-	-	-	-	-
9	pav	pavarotti	CG1258	64A10-64A11	42	6	75
10	polo	polo	CG12306	77B2-77B3	36	15	212
11	smt3	smt3	CG4494	27C7-27C7	25	8	136
12	sqh	spaghetti squash	CG3595	5E1-5E1	27	10	232
13	toc	toucan	CG9660	23D1-23D2	33	19	142
14	tum	tumbleweed	CG13345	49C-50C6	38	10	124

- **Updates in FlyBase Reports** Updates in FlyBase reports are displayed in two ways. First, we've added a new section called **Recent Updates** to our reports. This section contains a list of updates for the report spanning the 3 most recent FlyBase releases and a link to a page listing updates for all releases (from FB2010_08 and on). Second, updated items for the **current** release are highlighted in light green throughout the report page.
- **Update Feed** We have also started providing this update information in the form of an ATOM feed for each individual report. The links to the ATOM feed for any FlyBase report can be found in the **Recent Updates** section or in the location bar of your browser when viewing a report (your browser must support RSS/ATOM feeds). Using these links and your favorite news aggregator you can automatically be notified when your favorite gene, insertion, allele, etc. is updated. If you prefer to get updates in the form of an email then we suggest using a service such as Feed My Inbox to pull from our RSS/ATOM feeds and convert them into emails.