2010 NATIONAL DROSOPHILA BOARD MEETING MINUTES

April 7, 2010, Marriott Wardman Park, Washington DC
Wilson A-C, Mezzanine Level
3:00-6:00 PM

AGENDA

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OTHER BUSINESS		
ADJOURN	6:00	

Present: Debbie Andrew, Michelle Arbeitman, Utpal Banerjee, Hugo Bellen, Giovanni Bosco, Michael Boutros, Suzy Brown, Sue Celniker, Kevin Cook, Janice Fisher, Mark Fortini, Liz Gavis, Bill Gelbart, Pam Geyer, Leslie Griffith, Karen Hales, Scott Hawley, Steve Hou, Thom Kaufman, Krystyna Keleman, A. Javier Lopez, Trudy MacKay, Helen McNeill, Teri Markow, Sherry Marts, Kathy Matthews, Stephanie Mohr, Denise Montell, Terry Orr-Weaver, Liz Perkins, Norbert Perrimon, Leslie Pick, Helena Richardson, Juan Riesgo Escovar, Hannele Ruohola-Baker, Jeff Sekelsky, Allan Spradling, Henry Sun, Jim Thompson.

Note: The reports listed above follow this section of the minutes that highlights the discussions that occurred during the board meeting.

Key Discussions during Board Meeting:

1. Suggestions from 2010 Meeting organizers:

The attached Report 1 provides detailed information about the meeting organization. The meeting organizers praised the assistance provided by Suzy Brown of the GSA. They stated that it is important to decide how to distribute topic assignments for the concurrent sessions to provide the needed distribution reflecting the areas in which abstracts are submitted. They recommended that future organizers decide on session topics early in the organization process. This year the talks were chosen by the session chairs, and the chairs reviewed all the abstracts, regardless of whether a talk was requested. This led to several instances of researchers being asked to give talks when they wanted to present a poster. In future years, only abstracts from researchers who designate they want to give a talk should be screened for talks. The final suggestion was that the instructions for abstract submission should state that the first author needs to be the presenter.

2. Report of the GSA Meeting Coordinator (Suzy Brown)

The key issue raised by Suzy was funds for events during the meeting. She recommended that we raise registration fees by 10% so that coffee and beverage breaks could continue to be provided during the meeting. The board discussed this at length and was not supportive of raising the registration costs for the 2011 meeting. Suzy pointed out that a survey would be conducted of the attendees at the 2010 meeting to determine what issues about the meeting were most important to them and what expectations regarding food and beverages at breaks were. The survey also would determine what registration costs could be afforded by participants. It was decided that following the survey Suzy would make a recommendation about an increase for registration costs and the board would vote about the increase electronically.

One point of clarification about the registration fees for the annual meeting is that the fees were raised in 2009 to pay for tee shirts, and at that time the board voted to keep this increased fee as the registration fee for future years. Mistakenly the old pricing was used for 2010, so the pricing for 2011 will be the 2009 amount.

Suzy also proposes to bring in additional support for the annual meeting by more advertising, more sponsor and vendor support, and more synergy on vendor support with other GSA sponsored meetings.

3. Treasurer's Report

Pam Geyer reported that we are in sound financial state. The GSA requests that there be a reserve fund of 30% of the meeting cost. Pam submitted the following amendment to her initial report.

Amendment to Treasurer's report

Following clarification of the budget expectations of GSA requirement, the following amendment is submitted. Based on projected registration numbers for the 2010 Washington DC meeting, the community will have made a small profit of $4, 790, resulting in a total surplus of $229,487. Based on the average cost for the last three conferences (corrected for the networking luncheon estimated to cost ~$17,000), our meeting expenses are ~$332,206. As such, we have a cushion of ~$130,000 over the minimal GSA requirement of 30% of the meeting costs.

Based on these calculations, I propose the following:

1. That registration fees not be increased for the San Diego, but should be instituted in at Chicago 2012 meeting. Chicago has been historically more expensive, as illustrated in 2009 when we lost ~$50,000.

2. Our surplus is large enough to provide Suzy more flexibility to increase spending associated with coffee breaks etc. that she feels we have stripped to the minimum to keep costs low.

3. We should consider the possibility of offering travel awards through the Drosophila community to support travel to the meeting, perhaps at the level of undergraduate, graduate and post-doctoral fellow.

Finally, I would like to support the proposal of Dan Barbash to support Igor Zhimulev to travel to give a plenary talk. I believe that this is a special case and we do have funds. While it sets a precedent, I believe that the Board or Organizing Committee should be given the authority to consider cases on an individual basis.

4. Scott Hawley's comments on GSA sponsorship of the Drosophila meeting

Scott Hawley is the current president of the GSA. He brought two issues to our attention. The first is that each year the organizers of the national meeting could be vulnerable to litigation and currently would not be covered by GSA insurance. To surmount this potential problem, the board supports the proposal that each year the meeting organizers be appointed as GSA officers to provide them legal protection for any litigation that could ensue from the meeting. Scott also made us aware that to date the Drosophila meeting has been billed solely for the time that GSA staff devote to it, not for the relevant fraction of the staff members' benefits. The GSA gradually will begin to bill us for these costs, but it will be transparent exactly what the charges are.

Scott reported that there will be an increase in the number of DeLill Nasser memorial awards provided to students and postdocs to attend meetings. There will be two deadlines per year rather than one.

5. Drosophila Board Election Report

Utpal Banerjee summarized the results of the election. His concern is to increase the number of Drosophila researchers who are voting in the election. The board suggested coupling the election with the announcement for abstract submission for the annual meeting to provide the election greater visibility. The regional representatives were requested to advertise the election in their areas.

6. Drosophila Image Awards

Michelle Arbeitman reported on the image awards, as summarized in the attached report. David Bilder is happy to continue to chair this award committee. He raised the possibility of making the submitted images available for commercial uses, as he has received solicitations about this. Terry Orr-Weaver will contact him to discuss this possibility.

7. Undergraduate Education Initiatives

Karen Hales, the newly elected representative for Primarily Undergraduate Institutions, attended the meeting and presented several ideas gathered from researchers who work largely with undergraduates. There were three proposals:

1) To add a plenary talk geared for undergraduates and to follow this with a reception. This reception could possibly be linked to an information/recruitment session for graduate schools.
2) To provide travel grants for undergraduates to attend the meeting
3) To flag posters from undergraduates. This already is in place in one sense, because posters are marked by whether the presenting author is an undergraduate, graduate student or postdoctoral fellow. An additional part of this proposal was to have a specific undergraduate poster session for part of the time.

Board members stressed the importance of including undergraduates from major research universities, not limiting these initiatives to liberal arts colleges. One suggestion was to have day passes to the national meeting for undergraduates from local universities and colleges.

Specific decisions about these proposals were not made at the meeting, but it was noted that the GSA has an education director, Beth Rudy, who is focused on undergraduate education and will be able to help implement these proposals.

8. Bloomington Stock Center

In addition to the enclosed report, there was a discussion about space availability in Bloomington. Kathy Matthews and Kevin Cook reported that funds are available for 35,000 stocks but it would be possible to increase this to 60,000 by renovating space with cushion funds. They will send a proposal to NIST (the National Institute of Standards and Technology) for space for 100,000 stocks.

9. Harvard Transgenic RNAi project

The details of the transgenic vectors are provided in the enclosed report, but Liz Perkins and Norbert Perrimon noted that the Bloomington Stock Center has agreed to maintain 7000 Transgenic RNAi lines. The TRiP project has provided 1600 stocks to Bloomington in the VALIUM 10 vector.

10.Discussion with Vijay Raghavan about a possible Indian stock center

Vijay Raghavan joined the board meeting by phone to discuss his proposal for a stock center in Bangalore. Vijay is raising Indian National funding from a five year grant program that would permit expansion of space in Bangalore to house a large collection of stocks. The proposal would be to house a large collection of transgenic RNAi lines there. Vijay is considering two possibilities. The first would be to provide a screening center where researchers could go, be housed, and conduct screens with RNAi lines, deletion strains, or mutants housed there. The second is to serve as a stock center.

The board discussed these two possibilities. Norbert Perrimon and Krystyna Keleman discussed their experience with visiting researchers at Harvard and Vienna to screen their collections. They both agreed that researchers wanted and needed the stocks shipped to their labs, that a model of researchers trying to go and complete a screen in a short time at a center had not proven to be effective or desired by researchers.

The second possibility of Bangalore becoming another stock center was discussed at length. A key issue is that it needs to be tested that Fed Ex will work effectively and consistently for shipping stocks. Several board members stressed that what would be most useful to the community is if a Bangalore stock center had additional stocks that cannot be contained at Bloomington, rather than duplicating the Bloomington stock collection. These additional stocks could include additional RNAi transgenic lines from the TRiP project beyond the 7000 that Bloomington can house and the complete Exelixis insertion collection. It would be crucial, however, that information on these stocks be added to Flybase so that personnel to handle the information side would be needed as well as stock

keepers. This requires someone to devote his/her career to this to provide expertise and stability as is the case for the Bloomington stock center.

Vijay expressed his interest in coordinating with the Bloomington stock center and the need for support and oversight from the Drosophila board. Denise Montell and Terry Orr-Weaver will establish a subcommittee of the board to investigate this possibility for a Bangalore stock center to augment the collection at Bloomington.

11. Sue Celniker-Proteomic resources from the Berkeley Drosophila genome project and modENCODE

Sue Celniker reported on the progress in producing C and N-terminal fusion proteins from the gold cDNA clones, as detailed in her report. In addition, Vijay is generating transgenic lines expressing these fusions, and community members can obtain these from him. The need for this information to be clearer and more accessible to the community was discussed. The availability of these clones will be made more prominent on the DGRC website, and announcements will be posted on Flybase. Additionally, it would be helpful to have these reagents listed on each specific gene page on Flybase under the clones section. It was proposed to send email alerts to the community about these new resources.

Sue noted that the PIs heading projects on modENCODE have prepared a vision statement in anticipation of requesting a four-year extension of the project. This vision statement was sent to the board to solicit suggestions.

Hugo Bellen commented as well on the need to update community members on progress on the gene disruption project. One proposal was to email everyone who subscribes to the website with updates, but this was generally not felt to be a good idea. Rather the consensus to post update announcements on Flybase. Representatives were encouraged to make researchers in their areas aware to look to Flybase for these updates about resources.

12. Flybase

Bill Gelbart provided a detailed report from Flybase (see attached). Flybase has incorporated the high throughput data from the modENCODE projects, they will have the protein-protein interaction screen data from Artavanis-Tsakonas by summer, and information from the MacKay 190 inbred lines will be included.

Bill stressed the need for metrics of the value of Flybase to the community and the importance of providing funding agencies, particularly NIH, of the use and value of this effort. Tom Kaufman echoed this for the Bloomington stock center. Both emphasized that users need to acknowledge and cite these resources in their publications. All board members were encouraged to make the importance of this clearer to researchers, and an announcement was made during the plenary session of the meeting.

1. MINUTES OF 2009 DROSOPHILA BOARD MEETING

The meeting was held March 4, 2009 at the Sheraton Chicago Hotel and Towers, Chicago Illinois. The minutes were prepared by Carl Thummel and posted on Flybase.

2. REPORT OF THE 2010 FLY MEETING ORGANIZING COMMITTEE (Debbie Andrew, Mark Fortini, Steve Hou, and Leslie Pick)

The formation of this year's organizing committee started in October 2007, when Steve Hou approached Mark Fortini, Leslie Pick and Debbie Andrew to explore the possibility of the four of us organizing the 2010 meeting in Washington DC. The Drosophila Board approved the organizing team for the 51st annual meeting by email shortly thereafter. As a first step toward learning what is involved in this process, Steve Hou and Leslie Pick attended the informal informational meeting on the Saturday of the 2008 meeting in San Diego and Leslie attended the same informal meeting at the 2009 meeting in Chicago.

Overall, the meeting organization went relatively smoothly, a feat nearly entirely attributable to Suzy Brown's organizational skills. In March 2009, she presented us with a timeline for all of our activities, which we largely followed. We both shared and split the major duties: Choice of plenary speakers and historical session was a group effort and, although there were one or two people assigned to each major activity, every decision was made with group consensus. Steve organized the plenary speaker selection process. Leslie took charge of the historical event. Leslie took care of the design cover art for the website, program book, and the tee-shirt. Jola Glotzer was the artist who did the program book cover design. Steve also made the final selections for the platform sessions. Debbie organized the workshop selections. Mark organized the selection of the poster prizes. Debbie was the media interface, and Debbie and Mark did the initial preparation of this report, with corrections provided by the entire group. EVERYTHING was done by email.

Program Book & Registration:

As directed by the discussion at last year's Board meeting, we printed only the schedule and lists of talks and posters 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. 1,516 people had registered for the meeting as of Feb. 20, 2010, suggesting we will break the all time attendance record set in Washington DC in 2004, which had a FINAL registration of 1,617. For comparison, pre-registration numbers for several recent years are as follows: 1,383 (2009), 1,343 (2008), 1,345 (2007), 1,241 (2006), 1,451 (2005), and 1,470 (2004).

The meeting organizers, plenary speakers, and panelists for the historical lecture were given a free conference registration. 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.

Invited Speakers:

During May, the organizing committee compiled a list of possible Plenary Speakers. Our criteria were representation of the breadth of research done with Drosophila, EQUAL gender representation, and a mix of junior and senior investigators. We eliminated people who had given Plenary talks for as long as records were available (see below) and then voted by email based on the research blurbs and short publication lists provided by whichever organizer nominated a given speaker. We had only one negative response from a potential speaker who felt he no longer did enough Drosophila research to warrant his participation. The list of speakers was completed by the end of May 2009.

2010 Plenary Speakers: Elizabeth Chen, Elisabeth Knust, Antonia Monteiro, Ken Irvine, Duojia Pan, Chiara Cirelli, Eric Baehrecke, Sharyn Endow, Ting Xie, Craig Montell, Larry Zipursky, and

Lynn Cooley. (*It should be noted that although three of the speakers are from Johns Hopkins, Debbie only nominated one speaker from that institution.*) We sent email invitations to the speakers by the end of May and heard back from everyone by early June. We did have the plenary speakers submit abstracts this year. One suggestion for future organizing committees would be to emphasize the requirement of a written abstract when inviting the Plenary Speakers, as many of the speakers waited until the last minute to provide this material as the printed book was going to press. We also need to emphasize that speakers make their own travel and accommodation arrangements.

The Organizing Committee agreed that the panel discussion format from last year was refreshing after many years of historical speakers, so we decided on the theme of "100 years of fly genetics and 10 year of the fly genome, what have we learned and what does the future hold?" We recruited Hugo Bellen, who has made enormous contributions supporting genome-wide efforts for gene disruption, to help select the speakers and monitor the event. As moderator of the event, Hugo Bellen was in charge of communicating with the speakers and arranging the order of their short (~10-15 minutes each) presentations. The speakers include Thom Kaufman (on the discovery of the *white* gene), Gerry Rubin (on the cloning of the *white* gene), Bill Gelbart (development of Flybase), Norbert Perrimon (RNAi-based screens and genomics/proteomics applied to Drosophila) and Susan Celniker (genome project, Flybase, fly tools, etc).

Sessions:

We had many discussions regarding the Platform Session Topics. Based on the primary topics selected with the abstract submissions, we initially combined several “low popularity” sessions into a single platform sessions and expanded “high popularity” session topics into two platform sessions. However, when we discovered we had time for three more platform sessions than initially thought, we re-expanded most of the low popularity topics into separate platform sessions. The result is that, depending on the topic, the chance of giving a talk on a given topic varied from 29% to over 61.5% (**Table 1**). We hope that the range in percentages of talks chosen for different topics does not mean that the quality of talks will vary too enormously from session to session. Finally, we did opt for two techniques sessions because of their high popularity (independent of abstracts) but many of the talks in those sessions were taken from abstracts for which “techniques” was the second choice for a speaker’s session in order to select for higher quality presentations. Based on our experiences as well as comments in recent meeting reports, it appears to be rather difficult to anticipate in advance which sessions will receive the most abstracts and presentation requests (e.g. relative popularity). We recommend analyzing these numbers and making adjustments to the session schedule as soon as possible to enhance the equal representation of abstracts and talks over the different sessions (see Table 1 below).

In late May, we began the task of selecting session chairs. The list was completed by the end of May/early June. In general, we found everyone we invited enthusiastic about participating in the meeting. **This year's chairs**: Andreas Jenny (Cell Biology and Signal Transduction), Lisa Nagy (Evolution and Quantitative Genetics I and II [Leslie Pick]), Eric Rulifson (Physiology and Aging), Rick Fehon (Cell Biology and Cytoskeleton), Wei Xie and Yi Rao (Neurogenetics and Neural Development), Mark Van Doren (Gametogenesis and Organogenesis I and II [Debbie Andrew]), Ilaria Rebay (Regulation of Gene Expression), Tian Xu (Cell Division and Growth Control), Yikang Rong (Techniques and Functional Genetics I and II [Steve Hou]), Francois Karch (Chromatin and Epigenetics), Rolf Bodmer/Karen Ocorr (Drosophila Models of Human Disease I and II [Mark Fortini]), Haifin Lin (Stem Cells), Paul Adler (Pattern Formation), Richard Carthew (RNA Biology), Laura Johnston (Cell Cycle and Cell Death), Jay Hirsh (Neural Physiology and Behavior), Ylva Engstrom (Immunity and Pathogenesis). Note that all four members of the organizing committee are stepping in to help the session leaders on the sessions that were split in two, due to the difficulty in lining up additional outside session chairs on short notice (brackets above).

In late December the session chairs were each sent a link to the list of abstract submissions for their respective topic. They were asked to rank order their selections for talks, with one or two

alternates. The organizers took these lists to assign platform presentations for each session. We compiled a master list to determine whether any lab had excessive representation, limiting total talks from a given lab to two platform presentations. We did have a small problem with this approach. At least five of the session chairs selected presentations from those who indicated they only wanted to give a poster. We did not catch this mistake when we put together the final platform schedules. In the end, it involves only nine presentations, but it would have been better if it had not happened. NEXT YEAR'S ORGANIZERS NEED TO BE AWARE THAT THIS COULD BE A PROBLEM, although so far, we have not received any complaints. We were also not pleased with the first name on several of the abstracts being the lab PI and not the speaker. This could be viewed as subtle ploy to persuade the person selecting the platform talks to choose their abstract. **In the future, the organizing committee needs to be clear in the instructions that the actual speaker should be the first author on the abstract.**

It was recommended to next year's organizers that they instruct those selecting the talks to choose only those submissions requesting to give a talk, not those requesting a poster.

Table 1. Data on selected platform selections from the abstracts

Primary Session / Topic Title	# abstracts submitted	# platform session requests	# platform sessions given	% of total abstracts submitted	% of total platform requests
Topic 01. Cell biology and signal transduction	126	51	15	11.9%	29.4%
Topic 02./03. Cell cycle and checkpoints/Cell death	23 + 25	10 +10	5 + 2	14.5%	35.0%
Topic 04. Cell division and growth control	47	27	7 (2 NR)	14.9%	25.9%
Topic 05. Chromatin and epigenetics	60	25	8	13.3%	32.0%
Topic 06. Drosophila models of human disease	74	37	14 (2 NR)	18.9%	37.8%
Topic 07. Evolution and quantitative genetics	88	43	18	20.4%	41.9%
Topic 08. Gametogenesis and organogenesis	99	36	15	15.2%	41.7%
Topic 09. Immunity and pathogenesis	36	15	8 (1 NR)	22.2%	53.3%
Topic 10. Neural physiology and behavior	50	17	8	16.0%	47.0%
Topic 11. Neurogenetics and neural development	59	32	7	11.9%	21.9%
Topic 12. Pattern formation	45	17	7 (2 NR)	15.5%	41.2%
Topic 13. Physiology and aging	37	17	8	21.%	47.0%
Topic 14. Regulation of gene expression	75	29	10	13.3%	34.5%
Topic 15. RNA biology	30	17	7	23.3%	41.1%
Topic 16. Stem cells	26	13	8 (2NR)	30.8%	61.5%
Topic 17. Techniques and functional genetics	39	23	9	23.1%	39.1%
Topic 18. Educational initiatives (no platform session)	7	0	0	--	--
Total	946	419	156	16.5%	37.2%

NR – chosen speaker did not request a talk – communication problem with the plenary session leaders

Abstract Submission:
Abstracts were solicited in 18 topics with associated keywords (see table above). We received 946 abstracts by the early deadline, and 100 late abstracts for a total of 1046 abstracts. Totals in recent years were: 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 419 requests for platform presentations for 156 available slots, allowing accommodation of (on average) 37.2% of the requests, close to that of recent years.

Workshops:

The web-based form on the meeting web site worked wonderfully well in terms of having all of the information in place for prioritizing the requests for workshops. We received 15 workshop applications, which we initially ranked, not knowing what the room availability would be (**Table 2**). In the end, two were declined because of space limitations and the view that they overlapped significantly with existing platform sessions. We decided to keep the late Saturday night workshop timeslots in order to accommodate more of the workshop requests. Having been to late Saturday night workshops, it is clear that they can be well attended and are therefore worthwhile. We did assign most of the workshops that ranked lower on our list to late Saturday, but because of the room configurations (needing a large versus small room), this was not a strict assignment.

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.

Table 2. Workshop requests / workshops granted

Workshop	Organizers	Rank in list	Attendance estimate	Workshop accepted
The modENCODE project	Susan Celniker Gary Karpen Kevin White David MacAlpine	1	200	**Friday, April 9 1:45 – 3:45 pm**
Image analysis for Drosophila research	Pavel Tomancak Uwe Ohler	2	100	**Saturday, April 10 6:45 – 8:45 pm**
RNAi Screening in cells and Flies	Stephanie Mohr Bichael Boutros Krystyna Keleman Liz Perkins	3	50-100	**Friday, April 9 1:45 – 3:45 pm**
Chemical Genetics and Drug Screening in	Tin Tin Su	4	25	**Friday, April 9 1:45 – 3:45 pm**

Drosophila				
Everything you ever wanted to know about sex	Michelle Arbeitman Artyom Kopp Mark Siegal Mark Van Doren	5	100	**Saturday, April 10 6:45 – 8:45 pm**
Drosophila Research and Pedagogy at Primarily Undergraduate Institutions (PUI)	Alexis Nagengast Janet Rollins Thomas Onorato	6	50	**Saturday, April 10 6:45 – 8:45 pm**
Insect evo-devo	Markus Friedrich	7 - tie	50-100	**Saturday, April 10 9:30 – 11:30 pm**
Drosophotoxicology: the growing potential for flies in toxicology research	Matthew Rand	7 - tie	200	**Friday, April 9 1:45 – 3:45 pm**
Ecdysone Workshop	Deborah Hoshizaki Christen Mirth	8	200	**Wed, April 7 12 – 6 pm**
Apoptosis, Autophagy and other cell death mechanisms	Andreas Bergmann Michael Brodsky	9	150	**Saturday, April 10 6:45 – 8:45 pm**
Automated Tracking of Drosophila Behavior	Tim Lebestky Andrew Straw Kristin Branson	10	100-200	**Saturday, April 10 9:30 – 11:30 pm**
Neurodegenerative diseases in flies: reflecting back and looking ahead	Pedro Fernandez-Funez	11	200	**No**
Chromosome Structure and Function	Giovanni Bosco	12	100	**No**
Gases in Drosophila Physiology and Development	Dan Zhou Greg Beitel	13	50-100	**Saturday, April 10 9:30 – 11:30 pm**
Developmental regulation of cell proliferation	Wu-Min Deng	14	100	**Saturday, April 10 9:30 – 11:30 pm**

Poster awards:
The Society of Developmental Biology (SDB) made a very generous gift for a poster travel award (up to $1,000). This award will be given for the best Drosophila developmental biology poster to help defray travel and meeting expenses for presentation of this best poster at the SDB 69th Annual Meeting.

The award committee consists of all the platform session chairs for the initial judging, and the meeting organizing committee (Debbie Andrew, Leslie Pick, Steve Hou, and Mark Fortini) for the final selection. The session chairs are responsible for examining all the posters in their sessions and nominating one per session via e-mail to Mark Fortini 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 (1st, 2nd, 3rd 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).

The poster number signs indicate whether the author is an undergraduate, graduate student or postdoc to help the award committee judge each of these categories of authors.

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 answers every question. The GSA staff was also very helpful in finalizing the graphic design for the program book and the design of the anniversary tee shirt.

INFORMATION USEFUL FOR PLANNING FUTURE MEETINGS:

PLENARY SPEAKERS, FROM 1995 THROUGH 2010:

Susan Abmayr	1995
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
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
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
Ulrike Gaul	2007
Elizabeth R. Gavis	2002
Pam Geyer	1996
Richard Gibbs	2003
David Glover	2000
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
Chuck Langley	2006
Paul Lasko	1999
Cathy Laurie	1997
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
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
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
Rachel Wilson	2008
Mariana Wolfner	2009
Ting Wu	1997
Ting Xie	2010
Tian Xu	1997
Jennifer Zallen	2009
Philip Zamore	2003
Larry Zipursky	2010
Susan Zusman	1998

SESSION TOPICS & KEYWORDS 2010

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 2010 WASHINGTON DC

Cell Biology & Cytoskeleton
2009 Elizabeth Chen
2010 Rick Fehon

Cell Biology & Signal Transduction
2009 Henry Chang
2010 Andreas Jenny

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

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

Cell Division & Growth Control, Cell Death
2010 Laura Johnston

Chromatin & Gene Expression
2008 Elissa Lei

Chromatin & Epigenetics
2009 Ting Wu
2010 Francois Karch

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)

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

Gametogenesis & 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

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

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

Neurophysiology & Behavior
2003 Smith / Taylor
2004 Gabrielle Boulianne
2005 Krantz
2006 Troy Littleton
2007 Blau
2008 Clandinin

2009 Ravi Allada
2010 Jay Hirsh

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

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

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

RNA Biology
2008 Lopez
2009 Andrew Simmonds
2010 Richard Carthew

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

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

HISTORICAL SPEAKERS, THROUGH 2010 WASHINGTON DC

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

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

3. 2011 FLY MEETING ORGANIZERS

The organizers for the 2011 Drosophila meeting in San Diego, March 30-April 3, will be Giovanni Bosco (University of Arizona), Dan Barbash (Cornell University), Leslie Griffith (Brandeis University).

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

51st ANNUAL DROSOPHILA RESEARCH CONFERENCE
As you can see from the information in the treasurer's report, while I budgeted for a loss of $9,430, it looks like we will be able to turn that loss into a modest gain thanks to strong registration numbers and tight controls on expenses.

Registration:
The total registration number for 2010 as of March 28 is 1,631. This number is up 13% from last year at this time. The registration cut-off is March 30 so we may see a few more come in before we close out advanced registration.

Registration income at this point is about $11,000 below the total budgeted registration income of $301,270 (increased by 2.5% this year). The number of individuals registering as GSA members is up another 2% over last year. Currently over 65% of the people attending the conference are GSA

members. I anticipate the revenue from late and on-site registrations will help us meet our budgeted revenue numbers for registration income.

Hotel Rates and Pick-up:
The single/double sleeping room rate is $215 ($2 LESS than in 2004 when we last met at this property) and represents less than a 3% increase over last year. The hotel cut-off date was March 16 and we have sold out our block. The hotel will continue to accommodate reservations as space allows. Generally we experience about a 5% slippage (rooms cancelled after cut-off) but we have met our commitment of 85% of the block which is important because it directly ties into complimentary space, reduced coffee prices and other contractual obligations. It also strengthens our relationship with the hotel which is very important as that has enabled us to receive further discounts in areas that hotels have now started to charge for because of the impact the weakened economy has had on their business.

Exhibitors/Sponsorship/Advertising:
We sold twenty booths this year which is up from last year. In addition, we also sold more print ads and have added a web advertising option of which one company took advantage. Last year we had two sponsors for refreshment breaks. One of the companies that did it last year had been purchased and wanted the additional exposure. This year we only have one sponsor. In the future I think it would be beneficial to offer overall conference sponsorships as all of the other GSA meetings do. Members of those other communities have approached people that they deal with for lab needs, etc. and have been very successful in collecting donations for the meeting in exchange for their logo being displayed on the website and in printed materials. These companies are willing to provide some funding because of the relationship they have with the customer and for the additional exposure. Overall revenue for exhibits/ads/sponsorship is up 7% .

Promotion:
This year we significantly ramped up our marketing efforts. Among other things, we purchased an ad in Nature Magazine as well as had a series of informative e-mails regarding the conference with more specific program information. Washington, DC historically has been a good draw and I think that this year is no different. Based on data collected, the main way that people learned about the meeting was through a colleague or had been a previous attendee (nearly 82%). Approximately 10% of meeting registrants learned of the meeting through a promotional e-mail.

New This Year:
We've added the option of printing posters on site so that poster presenters don't have to carry them on the plane. The cost per poster is $60 and they can pick up their posters from the Fedex/Kinkos office that is located in the hotel.

Although full text of the abstracts has always been available online, last year we eliminated the printing of the full abstracts in the program book. We received very few complaints about the new process and, since many other conferences are doing the same thing, we anticipate no problems this year. However, if an attendee would like to print the full abstracts in book format, we have now made that available for sale to to them through a third party vendor. 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.

We introduced website advertising this year to try and generate additional funds. It is off to a slow start but we do have one paying vendor and we offered a complimentary placement to one of our large exhibitors to guage traffic to their site.

Through PSAV we are using a content management system for our live presentations this year. In the past we have tried to "build" this with our existing a/v company due to the cost associated with such a system. However, PSAV has a system in place that has been used with great success and were able to work within our budget for the most part. One very important component is that all

speakers must upload their presentations in advance or in the speaker ready room prior to their session. Since the speakers have a vested interest in having their presentation run smoothly, I don't see that this should cause too much anxst. ASHG moved to this system years ago with a much larger group of speakers and are successful in getting all speakers to upload their presentations in advance so I'm hopeful that we will have the same experience.

An undergraduate registration category was added this year and 86 students have taken advantage of this discounted registration. The majority of them have joined GSA to get the greatly discounted rate of $25 for registration.

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. It is significant to note that we were able to negotiate a 10% rate decrease with the Sheraton Chicago for 2012. We will start looking at 2017 and beyond later this year. Detailed below is the schedule for the next five years:

2010 – 51st Annual Drosophila Conference: April 7-11, Marriott Wardman Park Hotel, Washington, DC. $215 ($2 LESS than 2004). All guest rooms and meeting space will have been renovated by 2010.

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 - 2010

	Number	Amount
Faculty/Lab Tech Members	452	$88,055
Faculty/Lab Tech NonMembers	93	$63,020
Postdoc Members	233	$40,891

Postdoc Nonmembers	125	$36,840
Grad Student Members	308	$26,080
Grad Student Nonmembers	212	$31,550
Undergrad Members	61	$1,525
Undergrad Nonmembers	25	$2,500
Complimentary	22	0
Early/Regular	**1,631**	**$290,461.00**

Registrants by Country

United States	1275
Canada	58
United Kingdom	36
France	34
Germany	32
Japan	30
Taiwan	22
Israel	20
Spain	20
Switzerland	16
Australia	13
China	11
Korea	11
Italy	8
Sweden	6
Mexico	5
Singapore	5
Belgium	4
Czech Republic	4
Portugal	4
Russian Federation	4
Austria	3
Netherlands	3
Brazil	2
India	2
Chile	1
Malta	1
New Zealand	1

Total Number of Registrants: 1631
Total Number of Countries: 28

5. TREASURER'S REPORT (Pam Geyer)

A. ANNUAL DROSOPHILA CONFERENCE INCOME/EXPENSE

(Data are from the GSA [Chuck Windle, Suzy Brown], 3/23/10)

		Philadelphia 2007 Actual	San Diego* 2008 Actual	Chicago 2009 Actual	Washington 2010 Budget	Washington 2010 Estimate
	REVENUE					
1	Registration Fees	$288,067	$281,093	$294,266	$301,270	$305,350
2	Contributions and Sponsorships	0	3,800	6,100	7,500	4,000
3	Exhibit Fees	19,600	25,620	25,650	25,000	28,000
4	Advertising/Mail Lists/Other	3,760	1,086	4,170	3,000	3,290
5	Revenue	311,427	311,599	330,186	336,770	340,290
	EXPENSE					
6	Salary, Payroll Tax and Benefits	82,027	76,109	79,502	83,500	86,000
7	Printing and Mailing	24,815	26,715	17,140	17,200	15,000
8	Receptions and Catered Events (Note 1)	83,758	118,942	148,370	121,000	123,000
9	Posters and Exhibits	34,832	18,919	19,004	21,500	20,000
10	Supplies and Duplicating	1,798	1,211	791	9,500	3,000
11	Hotel and Travel	3,640	4,607	3,758	3,500	2,000
12	Audiovisual Services (Note 2)	45,535	53,125	86,901	63,000	65,000
13	Other Contracted Services	3,221	3,096	3,604	5,500	5,000
14	Telephone and fax	2,541	4,905	1,447	10,500	3,000
15	Credit Card Fees	7,641	9,124	7,672	9,000	9,500
16	Miscellaneous	373	256	9,929	2,000	4,000
17	Expense	290,181	317,009	378,118	346,200	335,500
18						
19	Net Revenue Over (Under) Expense	$21,246	($5,410)	($47,932)	($9,430)	$4,790

* Luncheon added without increase in registration cost.

B. MEETING ATTENDANCE

Pre-registration 2010 (Washington, DC):	1,529	$261,246
Total registration 2010 (est):	**1,675**	**$305,000**
Pre-registration 2009 (Chicago):	1,383	$256,800
Total registration 2009:	**1,506**	**$316,000**
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)	1470	$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**
Pre-registration 2000 (Pittsburgh):	1,083	$131,075
Total registration 2000:	**1,183**	**$167,005**
Pre-registration 1999 (Seattle):	1,142	$156,350
Total registration 1999:	**1,366**	**$191,425**

C.ACCOUNT BALANCES

C.1. Drosophila Main Fund

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	4,790	229,487	1,675

* The GSA Board (Sept. 2003 meeting) established a required ~$150,000 *minimum* reserve fund (one-half of meeting expenses). It should be noted that as the meetings are increasing in expense, the amount of the minimum reserve might need to be increased. No cap figure stated.

C. 2. Sandler Lecture Fund

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

D. SUMMARY AND REMARKS

The **2009** meeting in Chicago resulted in a loss of **$47,850**, exceeding the projected loss by **~$10,100**. Attendance at the Chicago meeting was slightly higher than the 2009 San Diego meeting. Factors that contributed to the larger deficit included 1) retention of the networking lunch without a corresponding increase in registration fees and 2) higher union prices that increased the cost of audio visual services by ~40%.

The **2010** Washington meeting has an early registration number of 1,529 (an increase from 2009). Based on past records, a total of 1,675 attendees are projected, representing a record number of participants. To keep costs down, the networking luncheon has been eliminated. Even so, at the current registration, we are projected to run a deficit of **$9,430**, which would bring the Drosophila main fund to **~$224,847,** a sum that is **~$75,000** over the historical minimum required by GSA. If the projected registration is reached, the meeting should run a small surplus of **$4,790**.

The Sandler lecture endowment fund showed decrease in the past year, but maintains a healthy balance of **~$31,000**. These are enough funds to continue its function of providing sufficient income to cover travel expenses for the Sandler lecturer.

Issues to discuss:

1. Changing the registration fees:
    a. Last change was in 2004
    b. Current surplus is expected to be $224,847

c. Historical minimum balance is $150,000, but with increased meeting cost, should this be increased?
d. Concern that meeting costs have been cut to the core, impacting the overall impression of quality of the meeting. The continental breakfast and reception are sparse.
e. Concern for an additional costs for the meeting: inclusion of GSA overhead charges

6. DROSOPHILA BOARD ELECTION REPORT (Utpal Banerjee)

The Elections Committee consisted of Utpal Banerjee (Chair), Ken Burtis, Barry Ganetzky, Jay Hirsh, and Jessica Treisman. We collected suggestions from outgoing representatives and the committee members, and then ranked them based on previous involvement in the fly community or our perception of their ability to perform the job. The chair contacted the individuals selected by the committee to construct the final ballot. This year the website surveymonkey was used for the third time to make voting and vote counting easier, replacing the e-mail response system with manual vote count used in previous years. 346 people voted this year, roughly the same as last year (397), which is only about 12% of the ~3000 people contacted.

The following letter was e-mailed to Drosophila researchers by Flybase to solicit votes.

Dear Drosophila researcher,

The time has come again 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 cast your vote. The Board's duties include: overseeing community resource centers and addressing other research and resource issues that affect the entire 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 9 regional representatives, 8 from the U.S. and 1 from Canada, who serve 3-year terms. It also has 3 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.org/static_pages/news/board.html

This year we are electing the President-elect, who will serve as President starting with the fly meeting in 2010. We are also electing representatives for the California, Mid-Atlantic regions, and for Primarily Undergraduate Institutions who will serve 3-year terms starting with the fly meeting, April 2010**. [NOTE: THE ELECTED PRESIDENT AND BOARD MEMBERS ACTUALLY BEGIN WITH THE DROSOPHILA MEETING IN 2011 NOT 2010.]**

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.

http://www.surveymonkey.com/s.aspx?sm=jzMLcT2A_2fh6SX1TxIp5MOQ_3d_3d

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 November 12, 2009.

Thank you,

Drosophila Board Election Committee

Utpal Banerjee, Chair
Ken Burtis
Barry Ganetzky
Jessica Treisman
Jay Hirsh

The surveymonkey ballot listed the following candidates:

President Elect (Vote for ONE)

Welcome Bender (Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School)
Research Interests: The chromosomal structure of the bithorax complex is different in different body segments; we hope to understand how those different structures are established and maintained.

Elizabeth Gavis (Department of Molecular Biology, Princeton University)
Research Interests: mRNA localization and translational control in the generation of cellular and developmental polarity.

California (Vote for ONE)

Michelle Arbeitman (Department of Biological Sciences, University of Southern California)
Research Interests: Identifying genes and neural circuits that underlie animal behaviors, using genomic and molecular- genetic approaches.

Thomas Clandinin (Department of Neurobiology, Stanford University)
Research interests: Understanding circuit development and function in the visual system.

Mid-Atlantic (vote for ONE)

Nancy Bonini (Department of Biology, University of Pennsylvania)
Research interests: Molecular genetics of neurodegenerative disease.

Mark Van Doren (Department of Biology, Johns Hopkins University)
Research interests: Germ cell development, gonad formation and sexual dimorphism.

Primarily Undergraduate Institution (Vote for ONE)

Karen Hales (Department of Biology, Davidson College)
Research interests: Genetic dissection of mitochondrial morphogenesis during Drosophila spermatogenesis.

Mark Hiller (Department of Biology, Goucher College)
Research interests: Drosophila genetics and developmental biology, regulation of gene expression, and reproductive biology.

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

Elizabeth Gavis for President-Elect March 2010 – March 2011
Michelle Arbeitman for California regional representative
Nancy Bonini for Mid-Atlantic regional representative
Karen Hales for Primarily Undergraduate Institution representative

International Representatives are not voted on but selected by consensus. These new representatives were chosen this year:

Helena Richardson Australia/Oceania international representative
Henry Sun Asia international representative
Michael Boutros Europe international representative
Juan Riesgo-Escovar Latin America international representative

The next Election Committee chair is Carl Thummel. The President, Denise Montell, should remind him to start the process in the fall.

Drosophila Board Master List (Spring 2010-2011)
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
Elizabeth Gavis President-elect 2015 gavis@princeton.edu
Terry Orr-Weaver Past-President 2013 weaver@wi.mit.edu
Carl Thummel Past-President & Elections Chair 2012 carl.thummel@genetics.utah.edu
Utpal Banerjee Past-President 2011 banerjee@mbi.ucla.edu
Pam Geyer Treasurer 2012 pamela-geyer@uiowa.edu

Regional Representatives
Helen McNeill Canada 2012 mcneill@mshri.on.ca
A. Javier Lopez Great Lakes 2011 jlaa@andrew.cmu.edu
Hannele Rhohola-Baker Northwest 2011 hannele@u.washington.edu
Jeff Sekelsky Southeast 2011 sekelsky@unc.edu

Michelle Arbeitman California 2013 arbeitma@email.usc.edu
Janice Fischer Heartland 2012 jaf@mail.utexas.edu
Leslie Griffith New England 2011 griffith@brandeis.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
Masa Toshi Yamamoto DGRC, Kyoto yamamoto@kit.jp
Jim Thompson DIS jthompson@ou.edu
Michael Ashburner Europe ma11@gen.cam.ac.uk
Hugo Bellen Bl'ton S.C. Adv. Comm. & P element project hbellen@bcm.tmc.edu
Allan Spradling P-element project spradling@ciwemb.edu
Helen Salz Sandler Comm. hks@po.cwru.edu
Scott Hawley Nomenclature Comm rsh@stowers-institute.org
David Bilder Image competition bilder@socrates.berkeley.edu
Chuck Langley At large chlangley@ucdavis.edu

2010 Meeting Organizers
Debbie Andrew dandrew@jhmi.edu
Mark Fortini fortinincifcrf.gov Steve Hou shou@mail.ncifcrf.gov
Leslie Pick lpick@umd.edu

7. DROSOPHILA BOARD WHITE PAPER (Carl Thummel)

The first White Paper was written in 1999 by a Fly Board subcommittee led by Bill Gelbart. It was modified by a group that Laurie Tompkins organized for an NIH workshop in March 2000, and posted on the FlyBase Web site as the White Paper 2001. In 2002, the Fly Board decided that we should update the White Paper every two years, focusing on project goals and not individual projects. The White Paper was updated in 2009, following this tradition.

On January 22, 2009, I sent an email to the Drosophila Board, and on January 26, 2009 I sent an email to all members of the fly community, both requesting feedback and ideas on how best to update the White Paper. These responses were passed along to the Fly

Board and used as discussion points at the Board meeting in 2009, addressing the following possible changes:

1. Update list of recent achievements listed in White Paper 2007

2. Continue or modify three "resources that must continue":

- Stock centers that provide a comprehensive range of genetically defined stocks at affordable costs are essential.
- Expanded and improved electronic databases to capture and organize *Drosophila* data, and integrate the information with other databases used by the research community.
- Continued support for a molecular stock center that provides the community with fair and equal access to an expanding set of key molecular resources at affordable costs.

3. Continue or modify five "high priority projects":

- Functional analysis of the *Drosophila* genome. The most powerful advantage of *Drosophila* as a model system lies in the wide repertoire of genetic manipulations possible
- Capturing temporal and spatial expression patterns for all *Drosophila* genes and proteins.
- Production of comprehensive cDNA resources.
- Functional annotation of *Drosophila* genomes.
- Completion of the mapping, sequencing, and annotation of *Drosophila melanogaster* heterochromatin.

4. Delete or update "high priority needs that may best be met by R01 support":

- Development of new methodologies that broaden the scope of the use of RNAi in *Drosophila* cells and whole animals.
- Development of new cell lines and molecular characterization of existing cell lines.
- Development of methods to understand the evolution of gene function.
- Generation of a well-characterized collection of conditional (ts lethal) mutants.
- Developing an efficient means of cryopreservation of *Drosophila* at any stage of development.

There was general agreement at the Board meeting that it was time for a major revision to the overall format of the White Paper, which has stayed fairly constant since 2003. The updated version should consist of two main sections: **(1) Basic Resources that Serve the *Drosophila* Community** and **(2) Research Support for Functional Analysis of the *Drosophila* Genome.** The third section in past White Papers ("high priority needs that may best be met by R01 support") was discontinued. The three resources listed in section 1 – fly stock centers, electronic databases, and molecular stock center – were all continued and updated. Section 2, on functional analysis of the *Drosophila* genome, was subdivided into three sections: (1) Genetic resources (generating collections of loss-of-function mutations, RNAi screening *in vivo*, RNAi screening in cells, and cDNA resources) and (2) Functional annotation of *Drosophila* genomes (sequencing of additional genomes, resources for sequenced genomes, genome-wide variation in *D. melanogaster*, genome-scale analysis of DNA elements,

finish characterizing *D. melanogaster* heterochromatin), and (3) Capturing temporal and spatial expression patterns for all *Drosophila* genes and proteins (establishment of transgenic lines with tagged proteins, antibody resources, efforts to record expression patterns).

Drafts of the 2009 White Paper were sent to Kathy Matthews, Thom Kaufman, Kevin Cook, Teri Markow, Stephanie Mohr, Bill Gelbart, Allan Spradling, Hugo Bellen, Susan Celniker, Trudy MacKay, Norbert Perrimon, Justen Andrews, and Terry Orr-Weaver for multiple rounds of revision. The final draft of the White Paper was posted online at FlyBase and the following email was sent to the community on 10/14/09:

Dear Fly Person,
Every two years the Drosophila Board, together with extensive input from the fly community, revises and publishes the Drosophila Board White Paper. This document is extremely useful for informing NIH and other funding agencies of our top research priorities. Past White Papers have helped to justify support for valuable community resources such as insertion mutations, stock centers, cDNA collections, and FlyBase.

The White Paper has undergone extensive revision this year. We have discontinued the third section in the 2007 White Paper ("high priority needs that may best be met by R01 support") in an effort to emphasize community needs rather than attempting to predict which R01s should be supported. The current document has two main sections: (1) basic resources and (2) support for functional analysis of the *Drosophila* genome – with specific goals outlined in each section.

Please download and read the latest version of the White Paper:
http://flybase.org/static_pages/news/whitepapers/DrosBoardWP2009.pdf

Do you have any suggestions for improving this document? Your input to this process is essential for maintaining and expanding our research tools. Please take the time to send your comments and ideas so that our stated priorities accurately represent the fly community for the next few years. Respond to me, to your regional Representative on the Board, or to any member of the Board. Our email addresses can be found at: http://flybase.org/static_pages/news/board.html

Thank you for your help,
Carl Thummel
Past-President, Drosophila Board

There was some feedback from this message, leading to several modifications of the document. The final version of the 2009 White Paper was posted online at the beginning of November 2009.

8. SANDLER LECTURESHIP COMMITTEE (Janice Fisher, Robin Wharton)

The committee was composed of Robin Wharton (chair), John Carlson, Claude Desplan and Janice Fisher. The Committee initially reviewed 12 nominations, approximately half as many as received the previous year. Based on these reviews, we selected two finalists: Josh Bayes, whose thesis work in Harmit

Malik's lab focused on the role of heterochromatin in hybrid sterility as an underpinning of speciation; and Leonardo Koerich, whose thesis work in Bernardo de Carvalho's lab focused on the evolution of the Y chromosome. After careful reading of these two theses, the Committee selected Dr. Koerich for the Sandler prize. His conclusion that many of the Y chromosome genes are recent acquisitions rather than relics that have survived degeneration from an ancestral state has broad implications for the evolution of sex chromosomes.

The chair for the Sandler committee next year will be Claude Desplan.

9. IMAGE AWARD (David Bilder)

This year's competition received 50 submissions, including 4 videos, from the US, Europe, East and South Asia. The 2010 winner is:

Guy Blanchard, for his video displaying quantitative analysis of cell movements during gastrulation

This year's runners-up are:
-Maximillian Fürthauer, for his video illustrating directional transport of endocytosed Delta during asymmetric cell division

-Xiao-Yong Li, for his figure showing that quantitative differences in transcription factor occupancy determine different output expression patterns.

Brian Calvi will make the Award presentation at the meeting.

Seven other finalists are highlighted at the meeting and as always on the Award Website. I continue to receive positive feedback and inquiries about the archived images, including questions about purchasing prints for decorations, calendars, or clocks. I plead ignorance about copyright issues, but if GSA is feeling entrepreneurial…

10. BLOOMINGTON STOCK CENTER (Kathy Matthews, Kevin Cook Annette Parks Thom Kaufman)

- Stocks held: 27,972
- Registered user groups: 2,395
- Registered users: 4,867
- Shipped in 2009: 166,153 subcultures in 13,488 shipments
- **Staff:** Annette Parks, Ph.D., joined the center in September, 2009
- **Funding**: We are in year 1 of a 5 year grant from NSF+NIH, ~$400,000 direct costs this year. We expect to raise approximately $561,000 (excluding postage/courier costs) through cost-recovery in 2010. Increased income from user fees is paying for the growth of the collection.

- **Growth**: We applied for ARRA construction funds for a Drosophila resources building at IU, which would solve the space problem. We have not received a final funding decision, but our score of 27 was above the expected funding cut-off of 23. We are pursuing a funding opportunity through NIST and will pursue any other opportunities that arise. We are also in discussion with our department about additional space that could be renovated for BDSC use. We are reasonably confident that 60,000 stocks could be accommodated at IU even if a new building does not come to pass.
- **Costs**:
    - Accession and maintenance account for ~70% of costs
        - Average cost per stock to accession: ~$28
        - Average cost per stock for annual maintenance: ~$23
    - Distribution accounts for ~30% of costs
- **New stocks**: We expect to add ~3,620–4,890 new stocks in 2010.
    - 1,450–1,750 insertions via the GDP pipeline
    - 1,200–1,800 insertions of RNAi constructs from the TRiP
    - 20–30 Bloomington Deletion Project deficiencies
    - 150–200 Bloomington Duplication Project duplications
    - 300–450 molecularly defined X duplications from the DC consortium
    - 50–100 GAL4 lines with expression in the brain
    - 50–60 Q system lines (a tri-component expression system similar to GAL4/GAL80/UAS)
    - 400–500 stocks in all categories from the community at large
- **Pruning**: We will continue to remove obsolete, redundant and selected low-use stocks from the collection. This year we expect to target primarily:
    - Excess non-insertion alleles (mostly BXC and ANTC genes)
    - Excess or obsolete insertions

11. BERKELEY DROSOPHILA GENOME PROJECT (Sue Celniker)

I. Universal Clone Resources for Drosophila Proteomics (Celniker, NHGRI HG003487 2005-2011)

The goal of this community resource grant is to generate sequence-verified ORF clones for gene expression and proteomics studies. We generated 11,500 expression-ready constructs: 6,000 clones for making C-terminal fusion proteins and 5,500 clones for N-terminal fusion proteins. Using the Cre-lox site-specific recombination system, we generated three C-terminal fusion protein sets: 1,900 with a metallothionein-inducible promoter and TAP tag; 5,600 with a metallothionein-inducible promoter and FLAG-HA tag; and 3,800 with a Gal-4-inducible promoter and FLAG-HA tag. The FLAG-HA clones are being used successfully by the Spyros Artavanis-Tsakonas lab to generate a protein complex map of the *Drosophila* proteome. They have made over 2,000 transfected S2 cell lines expressing fusion constructs and isolated protein complexes for analysis using mass spectroscopy.

We scored well on a grant renewal to generate an additional 5,000 expression-ready clones and the cell-line and transgenic expression clones. We have the appropriate “gold” cDNA clones ready but were only funded for one additional year, because the review panel wanted additional documentation that the community is using this resource. A renewal will need to be submitted in May with additional letters of support from users of the resource.

II. Patterned Gene Expression in Drosophila Development (Celniker GM076655 2006 – present)

This grant renewal will go to Council in May. The proposal scored well, and we are hoping it will be renewed. We determined embryonic expression patterns for over 7500 genes, including 97% of the sequence-specific transcription factors (TFs), and now have in place a database that allows monthly updates to the public website (NEW SITE - URL: http://insitu.fruitfly.org/cgi-bin/ex/insitu.pl). For the renewal, we proposed to complete the embryonic expression survey of protein-coding genes not yet interrogated. In addition, with a complete set of expression patterns for TFs in hand, we proposed a new aim to characterize expression patterns driven by TF *cis*-regulatory regions using reporter construct in situ assays. The new database includes an image-based search tool that uses representations of the expression patterns in virtual embryos, or Triangulated Images (TIs), generated with a deformable, triangular mesh grid. All data, including the TIs, and image analysis software are available for download from the website.

III. Completion of the Drosophila Gene Collection (Celniker NHGRI HG002673, 2002-2010)

This grant has ended primarily because of significant overlap with the goals of the modENCODE project. The grant goals were to capture a cDNA for every annotated gene in the genome to improve the annotation and produce a cDNA clone resource for the fly community. This was extremely successful and resulted in thousands of changes in annotations at the 5' and 3' UTRs, alternative splice sites and CDS. In addition, we provided experimental evidence for hundreds of gene merges and splits. We have submitted sequences for over 19,052 clones to GenBank, and the clones are available from the DGRC. In addition, our collection includes 10,036 "gold" cDNA clones (which contain complete ORF sequences without point mutations) for functional genomics and proteomics.

IV. The Drosophila Heterochromatin Genome Project (Karpen NHGRI HG00747 1998-2010)

The DHGP reached the practical limits of current technologies for efficient high-throughput mapping and sequence finishing of repeat-rich regions of genomes. The project has been a success, and the grant ends in June 2010. In the coming months, we will generate and distribute the Release 6 version of the reference genome sequence. Compared to Release 5, this will include an additional 2 Mb of high-quality finished genomic sequences in centric heterochromatin. It will also include significantly improved and substantially complete mapping of sequence assemblies to chromosomal locations as a result of BAC-based FISH experiments on *y; cn bw sp* mitotic chromosomes and SuUR; *Su(var)3-9* polytene chromosomes. We have successfully captured, mapped and finished sequences of most single-copy and moderately repetitive transposon-rich regions of the genome in a high-quality assembly. Pending the availability of new technologies for very long sequence reads and very-high-resolution physical mapping, further progress on sequence assembly in *D. melanogaster* heterochromatin is an appropriate area for smaller-scale research projects.

12. modENCODE (Sue Celniker)

The modENCODE project to determine the function of every base in the *Drosophila* genome is entering its fourth year. The specific fly projects and lead PIs are listed below (I – VII). For the February data freeze there were a total of 722 Drosophila data submissions that are publicly available from the Data Distribution Center (DCC) administered by Lincoln Stein (http://www.modencode.org). and FlyBase. These datasets have been and will continue to be of great use to the community. In addition, a newly formed data analysis center led by Manolis Kellis (MIT), in collaboration with the analysis working group has undertaken data integration, with the goal of producing a project-wide manuscript by the fall. Our program directors, Elise Feingold and Peter Good (NHGRI) are conducting a mid-

course review. This review is assessing productivity, measuring saturation levels and identifying areas in need of further study, with a vision towards continuing the project to be presented to May council. The PIs are working on a vision document to be completed by April 7th that will propose a plan for going forward with modENCODE II for another four years. A workshop designed to update the Drosophila community on the progress of the project, and to encourage access and utilization of the data, will be given on Friday, April 9, 2010 1:45-3:45 pm (Marriot Ballroom Salon 2).

I. Comprehensive Characterization of the *Drosophila* Transcriptome (Sue Celniker, Lawrence Berkeley National Laboratory)

II. Genome-Wide Mapping of Chromosomal Proteins in *Drosophila* (Gary Karpen, Lawrence Berkeley National Laboratory and University of California at Berkeley)

III. A Cis-regulatory Map of the *Drosophila* Genome (Kevin White, University of Chicago and Argonne Natl. Laboratory)

IV. Genome-wide Profiling of Histone Variants in *Drosophila* and *Caenorhabditis* (Steven Henikoff, Fred Hutchinson Cancer Research Center)

V. The Systematic Identification and Analysis of Replication Origins in *Drosophila* (David MacAlpine Duke University)

VI. Annotation of the Small RNA/microRNA Component of the *Drosophila* genome (Eric Lai, Sloan-Kettering Institute)

VII. RNA-seq in the Drosophila Genus to Support Transcript Annotation in *Drosophila melanogaster* (Brian Oliver, NIDDK)

13. GENOME DISRUPTION PROJECT (Hugo Bellen)

The Gene Disruption Project (Spradling, Hoskins and Bellen)

The GDP has now shifted to the production of MIMIC insertions. The major features of the MIMIC (MI) vector are shown in Figure 1. MI is a modified *Minos* TE that supports recombination mediated cassette exchange (RMCE). RMCE allows the precise replacement the DNA present between the two *attP* sites present in MIMIC (Figure 1) with essentially any DNA sequence. GDP believes that a broad collection of MIMIC insertions will greatly expand the ability of the *Drosophila* community to manipulate the fly genome. One immediate application is the production of protein trap lines. Protein traps have proven to be useful and popular, but extensive random insertion projects have succeeded in tagging less than 1,000 genes. Once an MI insertion is recovered in an intron, however, one can directionally swap in an appropriate cassette to generate an in-frame fusion of the gene to any tag of choice.

So far, approximately 2,500 MI insertions have been generated, and 2,300 have had their insertion site sequenced. MI inserts randomly in the genome, and almost 30% of the insertions are in introns. The production of these lines is slower due to an intrinsically lower *Minos* transposition rate, but more lines that are valuable are still produced per unit time than with other vectors. Currently, plans call for the generation of 3,000 additional MIMIC lines this year and another 4,000 next year.

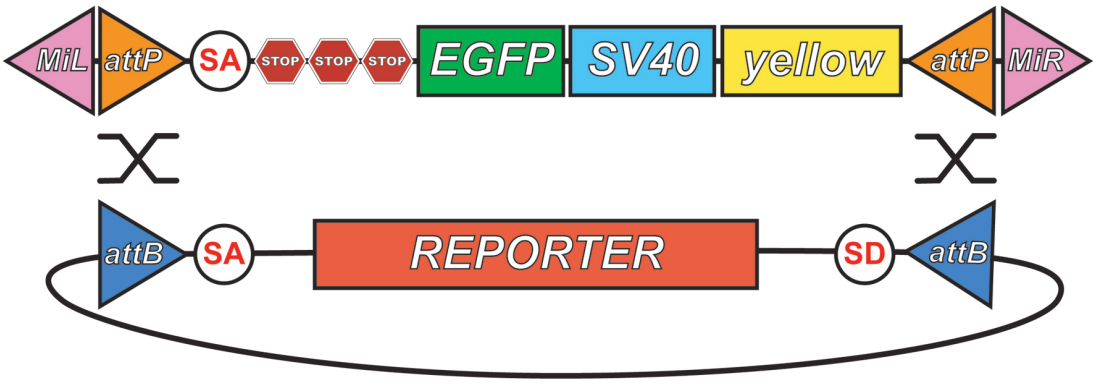

Figure 1. MIMIC and RMCE.

In parallel with the MIMIC scale-up, we have carried out experiments to ensure that the MIMIC technology is fully operational. A key issue is how frequently protein trap lines generated by RMCE from a MIMIC insertion in an intron produce an expression pattern that accurately reflects normal protein expression and subcellular distribution. Thus, it is necessary to compare protein trap patterns with antibody staining patterns for a series of MIMIC-tagged genes. Consequently, we inserted numerous different tags in ten test loci and analyzed their expression patterns. These tests showed that all the tags label the proteins of interest, and that all but one of the tags in a given gene show virtually identical expression patterns, and that some tagged inserts can be used in live or fixed animals without antibody staining. These results further support the view that a MIMIC collection will have a very major impact. We feel that it will truly transform how we do biology in flies.

GDP has continued to tag as many *Drosophila* genes as possible using both project-generated and donated *P*-element, *piggyBac* and *Minos* insertion lines. We finished a large "MB" screen using the *Minos* MiET transposable element. This project created and sequenced about 12,500 strains, 2,652 of which were added to the BDSC over the past few years. The MB collection tags ~2,000 genes, ~1,000 of which were previously not hit.

In addition, the phase-out of the Korean GenExel collection permitted us to add *P*-element insertions in a significant number of genes not previously hit by the GDP. We selected ~1,700 insertion stocks that would have added value to our collection. However, the GenExel stocks had never been balanced, some stocks had been lost, and sequence traces for the insertion site assignments were not available. Consequently, GDP undertook an extensive effort to bring these lines up to the standards of those generated

in-house. We balanced all the stocks that we received and sequenced all the insertions after balancing. This effort allowed us to add *P*-element insertions in about 550 genes that were previously not tagged, as well as other valuable lines, such as those with insertions in a location more likely to mutate a gene. This effort is nearly complete.

Finally, the Szeged *Drosophila* Stock Centre closed in 2009 because of lack of funding. Again, we have been rescuing the most valuable stocks to enhance the GDP collection. This effort will also result in the deposition of ~100 lines. We will finish this project in the coming months.

In conclusion, GDP now has transferred *P*-element, *piggyBac* or *Minos* insertions into the public domain that tag at least 62% of protein-coding fly genes. These insertions continue to be extensively used by hundreds of laboratories. More than 370,000 GDP stocks have been shipped from the BDSC to laboratories around the world. In the future, we are confident that MIMIC stocks will prove even more useful to the *Drosophila* community.

The P[acman] Libraries (Hoskins and Bellen)

We constructed two *Drosophila* melanogaster genomic BAC libraries with average insert sizes of 21 kb and 83 kb in a P[acman] transformation vector (Venken et al., 2009). We mapped clones representing more than 12X genome coverage by aligning paired end sequences to the reference genome. The mapped libraries provide transformation- and recombineering-ready clones for more than 95% of annotated genes. The clones can be integrated into the *Drosophila* genome using ΦC31 integrase or *P* transposase and can rescue mutations in small and large genes, including a heterochromatic gene. Recombineering allows manipulation of clones, including the incorporation of protein tags to reveal expression patterns. This new public resource is highly versatile, facilitating a broad range of experimental approaches in transgenic flies. Clones are available via BacPac resources and can be searched at FlyPush (http://flypush.imgen.bcm.tmc.edu/lab/index.html).

The X-Chromosome Duplication Project (Kaufman, Hoskins and Bellen)

The goal of this project is to create a series of small, molecularly defined duplications that will greatly facilitate X chromosome genetics in *Drosophila* and permit the rescue of thousands of genes. The X chromosome has been less studied because males only carry one X chromosome. This creates a hurdle, as complementation tests among lethal mutations can only be carried out when the male lethality is rescued with a duplication on another chromosome. Although a set of large duplications is available (Kevin Cook), we decided to create a library of small, molecularly defined 80 kb P[acman] duplications in specific *attP* docking sites on the autosomes to permit rapid fine mapping, rescue of essential and viable genes, and the definition of required structural features of genes such as enhancers. We selected a set of 440 P[acman] BACs with an average insert size of about 80 kb and average overlap of about 20 kb to create a tiled path that covers almost the entire *D. melanogaster* X chromosome. The majority of these clones were inserted in a specific docking site VK33 on chromosome 3L. Our current collection of 300

transgenic fly lines covers about 80% of the X chromosome and will be available at the end of April from the BDSC. The project will be completed in the coming 6 months, and all of the lines will be deposited in the BDSC.

A collection of EMS mutations in most essential genes on an FRT containing X-chromosome (Kaufman, Chen and Bellen)

It is now possible to create a molecularly characterized collection of EMS induced mutations in essential genes on FRT chromosomes. We mutagenized 8,000 males with low EMS concentrations (10-15 mM) to create 33,000 X chromosome balanced stocks. Of these, about 17% carried mutations in essential genes (6,000 stocks). The remainder of the stocks were discarded. These 6,000 stocks were screened with eyeless-FLP and Ubx-FLP, which allowed us to identify numerous mutations that cause overgrowth, eye loss, bristle loss, wing margin loss, ERG defects, neurodegenerative defects, and other phenotypes. We saved 2,100 homozygous lethal stocks and mapped 60% of them using large X-Y chromosome duplications to 300 kb to 1 Mb intervals. We have identified more than 90 complementation groups thus far and are currently using gene capturing sequencing technology to identify the molecular lesion in the most interesting mutations. We submitted a proposal (R01) to deliver molecularly characterized mutations (that are rescued by a P[acman] duplication) in about 380 essential genes on the X chromosome and that are not yet available from the BDSC. The proposal was not considered as the reviewers questioned whether the stocks would be used. They requested documentation of interest by the members of the community. We resubmitted and provided 23 letters of support.

14. HARVARD DROSOPHILA RNAi SCREENING CENTER AND TRANSGENIC RNAi PROJECT (Stephanie Mohr)

Update on the DRSC for the Fly Board Meeting April 2010
Prepared by Stephanie Mohr

The *Drosophila* RNAi Screening Center (DRSC; see www.flyrnai.org) at Harvard Medical School has provided dsRNA libraries and resources for on-site screening since 2003. Last year, the total number of screens hosted at the DRSC surpassed 100. We continue to host full-genome and smaller-scale RNAi screens in Drosophila cultured or primary cells interrogating diverse topics and performed by researchers visiting from across the U.S. and overseas. Recent studies have focused on the nucleus, host-pathogen interactions, signaling, and organelles. The trend toward increasingly sophisticated image-based assay readouts has continued and is well supported at the DRSC by state-of-the-art instruments and resources for image analysis. In response to community demand, we have expanded the number of RNAi reagents provided for off-site screening. Use of our bioinformatically grouped dsRNA sub-libraries (*e.g.* Kinases & Phosphatases) for on- and off-site screening continues to increase, and we recently provided customized small dsRNA libraries for a number of off-site screens.

We very recently completed production and sequence verification of a UAS-ORF library for over-expression screens that was based on a set of ORF 'master' clones provided by S. Celniker at the BDGP. The ORFs were moved to a pUAS-derived

expression vector in collaboration with the Broad Institute RNAi Platform. We also performed a pilot project introducing mCherry as an exon into cells via Minos transpoase (system from H. Bellen lab) and successfully isolated cells positive for mCherry in specific subcellular distributions. These cells may serve as excellent start-points for image-based RNAi screens and other studies. Improving the quality of high-throughput screen data remains a continuing focus, one that we address through availability of new reagents (*e.g*. non-*melanogaster* fosmids for rescue, and validation amplicons for re-test of primary screen results), software tools (*e.g*. cell line expression lookup tool based on modENCODE data), re-analysis of DRSC datasets, and more.

Our website and database are kept up-to-date with recently published papers (at least 13 reports based on data obtained at the DRSC were published in 2009), searchable screen data, useful protocols, *etc*. Our database will soon be expanded to allow for search and view of all DRSC and TRiP resources for a given gene (including how often the gene was a 'hit' in which screens and what we have in terms of dsRNA amplicons, UAS-ORF clones, and TRiP fly strains for a given gene). As part of our commitment to outreach and education, DRSC Director S. Mohr is co-organizing workshops at two GSA meetings in 2010, the ADRC (look for us Friday afternoon!) and the Model Organism to Human Biology (MOHB) meeting, which will be held in Boston this June.

Finally, the DRSC will be submitting a competitive renewal application this summer to NIGMS at NIH and would be very appreciative of Drosophila Board support for the application.

TRiP Summary for the Fly Board Meeting, April, 2010

Prepared by Liz Perkins

The goal of the **Transgenic RNAi Project** (the TRiP: supported by NIGMS, R01-GM08494; N. Perrimon, PI) 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 3,100 stocks have been generated. 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 TRiP targets genes based on the BDSC mandate of one mutation per gene and the needs of the *Drosophila* community for *in vivo* phenotypic analyses. From the time a nomination is received from the community it takes approximately 5 months before the transgenic RNAi stock becomes available at the BDSC. The TRiP stocks are extremely popular and as of March 15, 2010, 16,780 TRiP stocks had been shipped by the BDSC, and 12,647 had been shipped by the TRiP at HMS. In addition to the transgenic RNAi lines, we provide the community through 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. Maps and cloning protocols for the VALIUM vectors can be seen on the TRiP website and aliquots of these vectors are provided upon request. The TRiP at HMS also maintains the complete set of TRiP lines. For labs wishing to screen the entire collection the TRiP will either host and provide visiting scientists with all essential stocks, equipment and space to carry out their screens or the TRiP will send to labs discard TRiP stocks for screening. Finally, the TRiP maintains a database of all established transgenic stocks. This list, which includes amplicons used to generate the RNAi hairpins, is posted and updated regularly on the TRiP website. The TRiP also interfaces regularly with the BDSC and FlyBase to ensure up-to-date information at each

of these sites is available to the *Drosophila* community.

In the past year the TRiP has shifted from the use of long dsRNA hairpins to short 21bp hairpins flanked by microRNA cassettes (shmiRs), which utilizes the TRiP vector VALIUM20. Specifically, we found that shmiRs are more efficient at RNAi knock down in the soma than was achieved by the long dsRNA hairpins used previously in the vectors VALIUM1 and VALIUM10. All lines currently being generated in the TRiP for knockdown in the soma utilize shmirRs cloned into the vector VALIUM20.

Finally, the TRiP has recently developed a vector, VALIUM22, that expresses shmiRs in the female germ line. This advance in the field will allow, for the first time, researchers to interogate knockdown phenotypes throughout oogenesis and early embryogenesis.

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 et al. A genome-wide shmiRNA Resource for Drosophila Transgenic RNAi. In preparation.

15. VIENNA TRANSGENIC RNAi PROJECT (Krystyna Keleman and Barry Dickinson)

Report of the Vienna Drosophila RNAi Center, April 2010

Stock collection

The VDRC currently maintains two genome-wide RNAi libraries. The GD library was generated by the Dickson group and consists of a collection of GAL4/UAS-driven inverted repeat transgenes inserted into random chromosomal locations by P-element mediated transgenesis (Dietzl et al. 2007). The KK library is currently being generated by the Keleman and Dickson groups, and consists of an independent set of RNAi transgenes inserted into a common 2nd chromosomal site by phiC31-mediated transgenesis (Keleman et al., unpublished).

The GD library has been available from the opening of the VDRC in April 2007, prior to publication of the Dietzl et al paper. Lines of the KK library have been available since March 2009 and are continuously deposited as they are generated. A manuscript on the KK library is currently in preparation.

Stock numbers

GD stocks	21,379
KK stocks	10,402
Miscellaneous stocks	16
Total stocks	31,797

The VDRC does not presently have means to expand beyond its current capacity. However, it could conceivably decomission some of the GD lines if appropriate in order to take on other large-scale RNAi collections or other resources.

Funding

The VDRC is a non-profit research infrastructure, and operates according to similar principles as the Bloomington Stock Center. The VDRC currently employs 18 FTEs and has annual operating costs of approx. €1M. Funding is primarily obtained through user fees. From April 2007-March 2009, the VDRC was additionally supported through grants obtained by B. Dickson from the city of Vienna and the Austrian Federal Science Ministry. This core funding is expected to resume from July 2010. The IMP and IMBA additionally support the VDRC by providing all overhead costs, including administrative services and core scientific support, free of charge (partly compensated by reduced fees, see below). The generation of the RNAi lines themselves is not funded through these sources, but through separate grants awarded to K. Keleman and B. Dickson, as well as core funding from the IMP and its sponsor, Boehringer Ingelheim.

	2009	Budget 2010
Operating costs	€1,042,185	€862,692
Income		
User fees	€874,258	€618,957
Core funding	€62,500	€250,000
Total	€936,758	€868,957
Annual balance	€-105,427	€6,265

User statistics and user fees:

The VDRC currently has 1516 registered users. Since its opening in 2007, the VDRC has distributed a total of 442,172 lines to Drosophila researchers. The demand has remained relatively constant over the past year, and is currently split approximately evenly between the GD and KK libraries.

The system of user fees was revised in Feb. 2009, with the objective of significantly reducing the costs of large orders to further facilitate large-scale screening, while maintaining the same overall income. The new fee structure is:

Number of lines per order	Cost per line
1st	€35
2nd-5th	€25
6th-20th	€10

21st-50th	€7,50
51st-100th	€5
>100th	€2,50

IMP and IMBA obtain a 20% discount, partially to defray indirect costs paid to the VDRC by these institutes, and as no packaging costs are incurred.

Due to administrative constraints, the VDRC accepts payment by credit card only. Purchase orders can be arranged for orders in excess of 1000 stocks.

Upon registration, users are required to sign a materials transfer agreement (MTA). The MTA is intended to protect the interests of two groups, without imposing any unnecessary restrictions on academic use: (1) Boehringer Ingelheim sponsors basic research at the IMP, and supported the generation of these libraries both directly and indirectly. While they do not themselves conduct research using the library, they have a legitimate right to reclaim appropriate compensation for any commercial exploitation of these resources. (2) In the interests of the fly community as a whole, the VDRC requests that users obtain stocks directly from them rather than secondary sources. Any secondary distribution reduces the ability of the VDRC to recover costs from user fees, and would necessitate increase costs to other users. The MTA has been considerable softened since the opening of the VDRC, and is generally less restrictive than those of most US academic institutions.

16. DROSOPHILA INFORMATION SERVICE (Jim Thompson)

Volume 92 (2009) of Drosophila Information Service was published on schedule at the end of the calendar year. At 188 pages, it remains about the same size as other recent annual issues. As usual, most contributions are received between mid-November and the end of December in response to the annual "Call for Papers", a decades-old tradition. Volume 92 was made freely available on our web site (www.ou.edu/journals/dis) soon after publication, and a limited number of printed copies were prepared in early January 2010. Most of the printed copies go to subscribing libraries. We are also making very good progress in preparing past volumes for electronic access, and I expect we will have all past volumes available for free access before the end of the summer. Articles will be searchable by key words taken from the titles and authorship. For the past couple of years, I have provided free pdf copies of older articles in response to email requests with very short turn-around time. The number of such requests confirms that older DIS articles continue to be a useful source of information.

Electronic access has, however, raised one new concern, and I welcome advice from the Board. Now that the journal is increasingly available on-line, it is easy to make corrections to previously published reports. In the current issue, for example, we publish a correction in which the author discovered that he had made a couple of mistakes on numbers in a protocol published two years earlier. It is my belief that people will access the original protocol without thinking it necessary to search for any later corrections. For that reason, we plan to replace the original on-line version of that article with a corrected one, but with a notation in the on-line Table of Contents for that volume that references

the later note on the correction. In that way, the information in the article that is accessed by researchers is correct and still the history of the change is preserved. If anyone sees an ethical or precedence problem with this approach, I will appreciate hearing from you.

The only change anticipated for next year is an increase in the cost of printed copies to $15.00 (up from $12.00, where it has been stable for many years). We approximately break even on the cost of providing printed copies, except for the binding which is about half the cost of a copy. The shipping and handling costs will not increase. 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.

17. DGRC-DROSOPHILA GENOMICS RESOURCE CENTER (Justen Andrews, Thom Kaufman, and Peter Cherbas)

A. INTRODUCTION

The Drosophila Genomics Resource Center (DGRC) exists to ensure that the research community has access to high quality Drosophila genomics resources. We are currently in our seventh year of operation and have continued to expand activities. Briefly, we now have 6,219 registered users from 2,752 laboratories; and have distributed a total of 40,158 individual reagents (vectors, clones, and cell lines) in 15,197 individual orders.

B. CELL LINES

The cell line collection consists of 118 lines from diverse tissue sources including some non-melanogaster. We have concentrated on the following activities:

1. Distributing the existing cell lines – we shipped 277 samples during the past year.
2. Characterizing the available lines – see Section E.
3. User support- many of the lines, particularly disc and CNS lines, are difficult to grow, and we have devoted considerable time to thawing particularly troublesome lines in-house for re-shipment and answering user queries.
4. Website expansion- We have made considerable efforts to image cell lines and post them on the web so that users may observe the unique characteristics of an individual cell line. We welcome researchers to donate

C. VECTORS AND CLONES

We currently house over 1,000,000 vectors, cDNAs, and fosmid clones. Our activities in the last year are as follows:

1. Distributed 7,298 vectors and clones.
2. Increased the vector collection to from 267 to 295 common vectors.
3. Continued to annotate and publicly provide information on incoming vectors and some older vectors for which little is known.
4. Acquired and begun distributing the Tagged ORF collection (ca. 1000 clones from BDGP).

D. USER SUPPORT

We consistently make efforts to respond quickly to users enquiries to our email helpline. In the past year we received 1,850 user support requests. These issues were resolved through 6,429 individual email messages and further improvements to our web site and user support. To this end, we have achieved the following in the last year:

1. In an effort to improve the quality of the of our web-based user support, we have made changes to our website including: updated FAQs, updated protocols, standardized interface among our divisions to improve usability and updated the design to make it easier for users to navigate to the relevant information. Further, we have added features that aid in identifying cell lines relevant to modENCODE, and created link outs to the modENCODE site.
2. We have worked with FlyBase to make cell line and clone information searchable through their website. For this effort we have exported DGRC molecular stock and cell line information to FlyBase and built an infrastructure for syncing changes.
3. We are hosting an information booth at the 2010 Annual Drosophila Research Conference.

E. DEVELOPMENTS AND EMERGING TECHNOLOGIES

In the last year, our efforts to facilitate the community's adoption of new genomics technologies have included the following.

1. We have ceased printing and distributing microarrays through the DGRC. This decision was in response to recommendations from grant reviewers. While Drosophila microarrays are commercially available, the available arrays are based on outdated genome annotations. Together with Indiana University Center for Genomics and Bioinformatics (CGB), we have negotiated an agreement with NimbleGen to make available (through NimbleGen, not the DGRC) DGRC-designed 12-plex expression arrays. The DGRC will only be involved in the design and re-annotation of these arrays, not distribution.
2. We have worked with modENCODE to guide the use of 25 cell lines in the fly transcriptome project and 4 of these lines in all of the other fly modENCODE projects. A substantial amount of these data are now posted on the modENCODE public website, to which we have provided links from the DGRC pages for each of the cell lines in question.
3. We are in the process of testing Laser Capture Microdissection (LCM) as a potential service.

F. FUNDING

The DGRC is funded partly by a NIH research resources grant (NCRR and NIGMS) and partly by user fees. After approximately one year of bridge funding in 2008, our grant was through to the end of April 2012. We will submit a competitive renewal in June 2011.

G. ADVISORY BOARD

The Advisory Board currently consists of:

Spyros Artavanis-Tsakonas, Harvard Medical School
Ken Burtis, University of California
Reed George, University of California
Alex E. Lash, Memorial Sloan-Kettering Cancer Center
Brian Oliver, NIDDK, NIH
Susan M. Parkhurst, Fred Hutchinson Cancer Center
J. Tim Westwood, University of Toronto
Kevin P. White, Yale University

We note the need for turn over of board membership, and are in the process of recruiting a number of new members.

18. DROSOPHILA SPECIES STOCK CENTER (Therese Markow)

University of California at San Diego --- Therese Markow

The Drosophila Species Stock Center (DSSC) collection consists of 1492 living stocks, representing 220 species. In 2009, the DSSC acquired 202 new stocks from 35 species. 114 of the new stocks were transgenic strains of 9 species created and provided by Thom Kaufman's lab and made available to the community in September 2009. The rest of 88 new stocks, wild-type, represented 27 species, with the majority being *Drosophila melanogaster* (22%) and *D. miranda* (12%). Also acquired were stocks from Artyom Kopp of the species to be sequenced through modEncode. We also decommissioned 80 p-element insert lines of *D. mauritiana.* As we had maintained approximately 100 of these strains, and only a small number had been ordered in five years, the advisory board felt in impractical to spend our limited funds on their maintenance. Unfortunately, 16 stocks were lost in 2009. At the moment, the DSSC has 22 stocks under taxonomic review/quarantine. These stocks will be included in the collection in 2010. Genomic DNA is available for all 12 sequenced species. Genomic DNA is available for all 12 sequenced species.

The DSSC always has consisted of a permanent collection of both ethanol-stored and living stocks.. As of April 5th 2010, the 1492 cultures in the living collection consist of 1044 wild-type stocks (both multi-female and isofemale lines), 250 mutant allele stocks, and 198 transgenic stocks. The living collection represents a diversity of 220 species. On the other hand, the 493 stocks in the ethanol-stored collection contain 409 wild type, 39 mutant, and 45 transgenic stocks. We periodically offer, on a temporary basis, varying number of recently caught isofemale wild-type cultures. These isofemale collections are subsequently made "permanently available" by storing adults in ethanol or at –80°C.

In 2009, the Drosophila Species Stock Center provided to the *Drosophila* research community with 1,243 stocks in 236 shipments representing 157 species. The genome-sequenced species' cultures presented 19.5% of stocks sold. 30.5% of the orders came from international institutions. The top 20 species requested represent 74% of the total stocks sold by the DSSC. Details of the stock sales in 2009 are presented in the tables below.

The annual Drosophila Species Workshop was held in October 2009 at UCSD, with 16 participants enrolled. This was the largest number we've had, and despite the increase in capacity, we still had a waiting list. The 2010 workshop will be held October 28, 29, 30, 31 at UCSD.

Table 1. Transgenic stocks added and ordered in 2009.

Species	Number Transgenic strains	Number strains ordered	Times ordered
D. simulans	**13**	**9**	**6 (3-2x)**
D. yakuba	**19**	**8**	**6 (3-2x)**
D. erecta	**14**	**7**	**1**
D. sechellia	**1**	**1**	**2 (1-2x)**
D. pseudoobscura	**15**		
D. willistoni	**13**		
D. mojavensis	**2**		
D. mercatorum	**8**		
D. virilis	**29**	**29**	**8 (4-2X)**
Total orders of transgenic stocks = 62			

Table 2: Shipment totals

	2008	2009
SHIPMENTS		
USA	178	165
INT	54	71
Total	232	236
STOCKS		
USA	981	883
INT	291	360
Total	1272	1243

Table 3: Top 20 stocks ordered 2009.

Rank	Species	Total
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

19. FLYBASE (Bill Gelbart)

FlyBase Report to the North American Drosophila Board
March 29, 2010

We are pleased to present our 2010 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. Unlike previous reports, we will make extensive use of screenshots to exemplify some of the new features.

Respectfully submitted,

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

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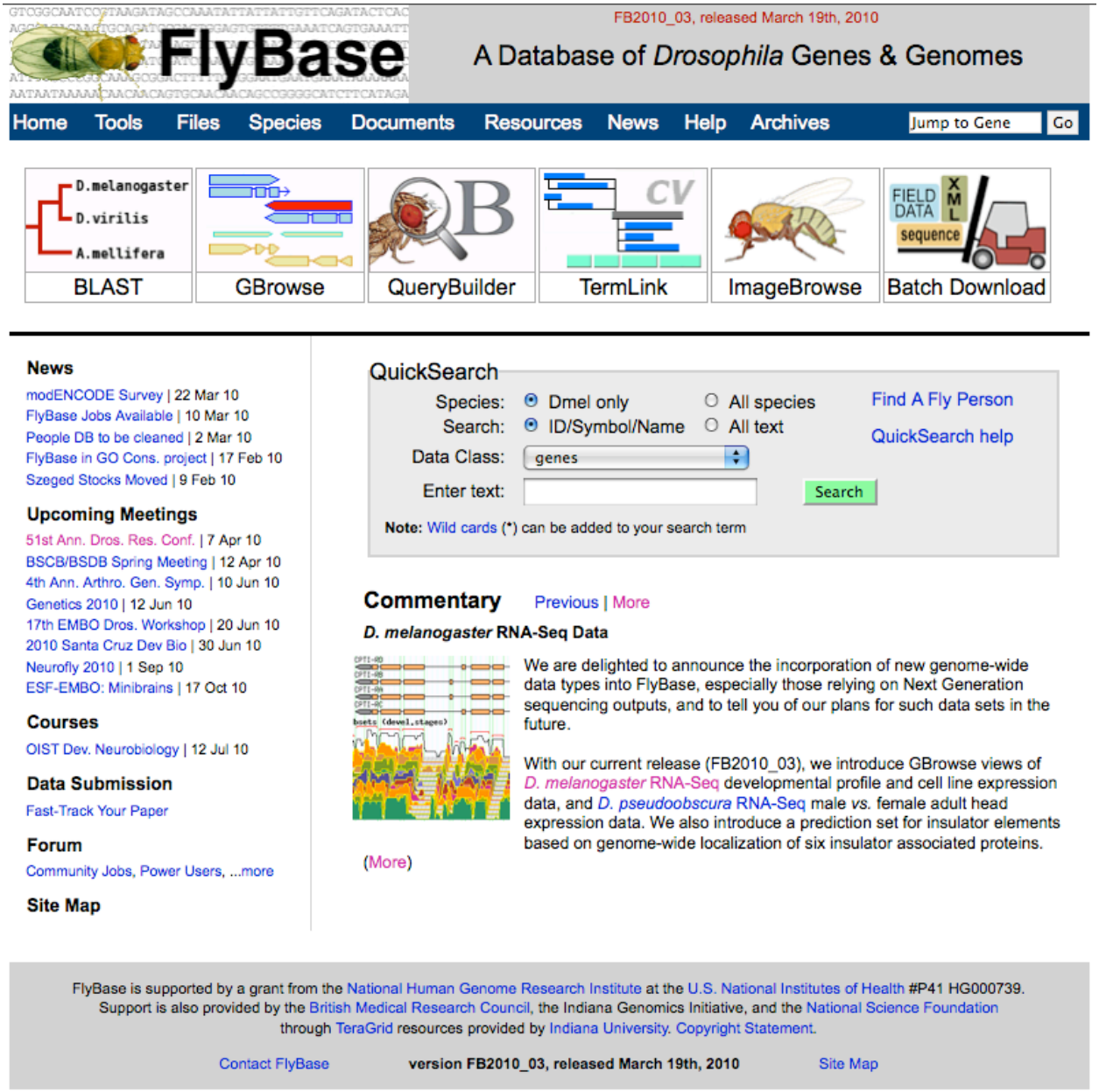
The Current FlyBase Home Page: FB2010_03: March 19th, 2010



FLYBASE REPORT – EXECUTIVE SUMMARY

Progress Report

We are pleased to report that this has been an excellent year for FlyBase. Our plans for the last year on numerous fronts have largely moved forward as anticipated. We are most appreciative of the steady level of funding from our NHGRI grant (we are in the 2nd year of a 5 year renewal which runs through 12/31/2013). Various statistics of FlyBase production are shown in Tables 1-3 (FlyBase report pages 3-5). Some of the highlights from these statistics (with accompanying tabulations) are:

- (Table 1) Continuing to meet our schedule of 10 public releases per calendar year.
- (Tables 2 & 3): Steady progress on literature curation and gene model annotation (exemplified by the data in Tables 2 and 3).
    - ~2,400 new papers in FlyBase with either first-pass or full curation.
    - ~10,500 new fly strains.
    - ~21,000 new mutant alleles.
    - ~16,000 new transposable element (TE) insertions localized to the genome.
    - ~650 *D. melanogaster* major protein-coding gene model changes.
    - ~100 *D. pseudoobscura* protein-coding gene model changes as part of the FlyBase Minority Action Plan (MAP) (see narrative preceding Table 2).

A variety of enhancements to FlyBase

- (FlyBase report pages 6 & 7) Continued 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 Community Data Submission forms (107 submissions in the last year). **We invite the Fly Board to periodically take advantage of the Commentary space on the FlyBase home page to post notices of interest to the Drosophila research community.**
- (FlyBase report page 8) New GBrowse displays for RNA-Seq coverage profile and for Insulator/Boundary Element data.
- (FlyBase report pages 9-11) New GBrowse graphical displays of sequence-localized deletion/duplication and allelic data.
- (FlyBase report page 12) Additional insect genomes in FlyBase BLAST database.
- (FlyBase report pages 13-15) New classes of FlyBase reports for non-genic Sequence Features, Library/Collection metadata and Drosophila Cell Lines.
- (FlyBase report page 16) Batch converters to relate older FlyBase identifier sets to identifiers for current objects and between releases of *D. melanogaster* sequence assembly coordinates.
- (FlyBase report pages 17-19) Enhancements to functionality for Controlled Vocabulary (CV) TermLink, BatchDownload and QueryBuilder interfaces.

Challenges for the Future

- Literature curation:
    - Data capture prioritization necessitated by the increase in the amount, scope and depth of the primary scientific literature (including supplementary data).
    - 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* resequencing 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

- We are delighted to report that 2010 is the 3rd year in which we will produce 10 web site releases per annum (see the table below). The investment in 2005-2007 in totally reengineering our central database, data flow and web site, which left us with very limited time or personnel to devote to public updates during this period has resulted in a robust production pipeline that will remain at 10 releases per year for the foreseeable future. Some benchmarks associated with particular releases are shown in the Notable Events column.

TABLE 1: FLYBASE PRODUCTION REPORT TO FLYBOARD – 2010 MARCH 27			
Neo-FlyBase – Schedule of Future 2010 Releases			
Release Date	*Release ID*	*Dmel annotation version*	*Notable Events*
2010 November 12	FB2010_10	Dmel Release 5.33	To be scheduled: • Dmel Release 6 migration • DGRP & DGPG variation data • Next Dmel GenBank submission • DPiM protein-protein interactions • Additional modENCODE data • RNA-Seq Junction Data
2010 October 08	FB2010_09	Dmel Release 5.32	
2010 September 03	FB2010_08	Dmel Release 5.31	
2010 July 23	FB2010_07	Dmel Release 5.30	
2010 June 25	FB2010_06	Dmel Release 5.29	
2010 May 28	FB2010_05	Dmel Release 5.28	
2010 April 23	FB2010_04	Dmel Release 5.27	
Neo-FlyBase – Actual Releases			
Release Date	*Release ID*	*Dmel annotation version*	*Notable Events*
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
2008 August 08	FB2008_07	Dmel Release 5.10	Dmel 5.10 submitted to GenBank
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
2007 August 02	FB2007_01	Dmel Release 5.2	Dmel 5.2 submitted to GenBank
2006 December 08	FB2006_01	Dmel Release 5.1	NEW: Totally New Web Site Introduced
Paleo-FlyBase – Actual Releases			
Release Date	*Release ID*	*Dmel annotation version*	*Notable Events*
2006 March	--	Dmel Release 4.3	Dmel 4.3 submitted to GenBank
2005 July	--	Dmel Release 4.2	NEW: pseudoobscura genome
2005 April	--	Dmel Release 4.1	Dmel 4.1 submitted to GenBank
2004 November	--	Dmel Release 3.2.2	NEW: Dmel heterochromatin added.
2004 August	--	Dmel Release 3.2.1	
2004 February	--	Dmel Release 3.2.0	
2003 December	--	Dmel Release 3.1	Dmel 3.1 submitted to GenBank
2003 October	--	Dmel Release 3.1	

SELECTED FLYBASE DATA CAPTURE STATISTICS

- Literature curation is proceeding at an improved pace, which should increase further as open positions are filled and our new curators become fully trained.
- *D. melanogaster* gene model annotation is proceeding steadily (see Table 3).
- *D. pseudoobscura* manual gene model annotation has begun at our new U. New Mexico Genome Annotation Center, which is part of our new MAP (Minority Action Plan) which is part of the NHGRI mission to create a much more diverse set of scientists conducting genome research.

TABLE 2: CURRENT FLYBASE STATISTICS COMPARED W/ PREVIOUS YEAR (ALL DATA FROM FLYBASE WEB SITE RELEASE NOTES)

Category	***March 20, 2009***	***March 19, 2010***
General Statistics	**FB2009_03**	**FB2010_03**
Number of References in FlyBase	190,642	194,014
----- Research papers	80,250	82,638
----- Personal Communications	4,489	4,841
Number of Fly Strains	90,173	100,692
Fly Workers Registered with FlyBase	7,518	7,614
***D. melanogaster* Genetic Object Statistics.**	**FB2009_03**	**FB2010_03**
Number of Gene records	31,206	31,129
----- Genes w/ Gene Models	15,172	14,824
----- Genes w/o Gene models	16,034	16,305
Number of Alleles	108,525	129,331
----- Alleles of genes w/ Gene Models	89,406	110,399
----- Alleles of genes w/o Gene Models	19,119	18,932
Number of Chromosomal Aberrations	18,455	18,889
----- Deficiencies	7,823	8,101
----- Deficiencies w/ Mapped Endpoints	1,817	2,044
Number of TE Insertions	104,152	117,466
----- TE Insertions Localized on Genome	43,640	57,245
***D. melanogaster* Annotation Statistics.**	**Dmel Rel_5.16**	**Dmel Rel_5.26**
-- Protein-Coding Genes		
Number of Genes	14,086	13,732
----- Mean Length Genes (bases)	5,537	5,638
Number of Transcripts	21,647	21,921
----- Mean Length Transcripts (bases)	2,394	2,475
Number of Exons	69,206	69,209
----- Mean Exon Size (bases)	481	485
Number of Introns	51,433	51,989
----- Mean Intron Length (bases)	1,406	1,414
-- Non-Protein-Coding Genes		
rRNA Genes	161	160
tRNA Genes	314	314
snRNA Genes	47	47
snoRNA Genes	249	249
miRNA Genes	90	90
Miscellaneous Non-Coding RNA Genes	127	129
Miscellaneous Non-Coding Transcripts	153	157
Pseudogenes	98	101
-- Repeat Features in Genome		
Natural Transposable Elements	5,620	5,620
Annotated Repeat Regions	10,159	10,159
***D. pseudoobscura* Annotation Statistics.**	**Dpse Rel_2.3**	**Dpse Rel_2.9**
Number Protein-Coding Genes	16,071	16,153
Number of Exons	58,063	58,358
Number of Introns	41,476	41,606

FLYBASE *D. MELANOGASTER* GENE MODEL ANNOTATION PROGRESS REPORT

- There has been a steady effort to update gene models, with ***major changes*** to about 650 gene models having taken place during the last calendar year (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. A major contributor to the large number of deleted gene models were partial gene models in heterochromatin that were determined upon re-examination to be weakly supported. (Annotation of heterochromatin, because of the dense distribution of complex repetitive sequences, is particularly challenging.)
- Another ~1,500 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.*
- With important new data sets emerging 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)

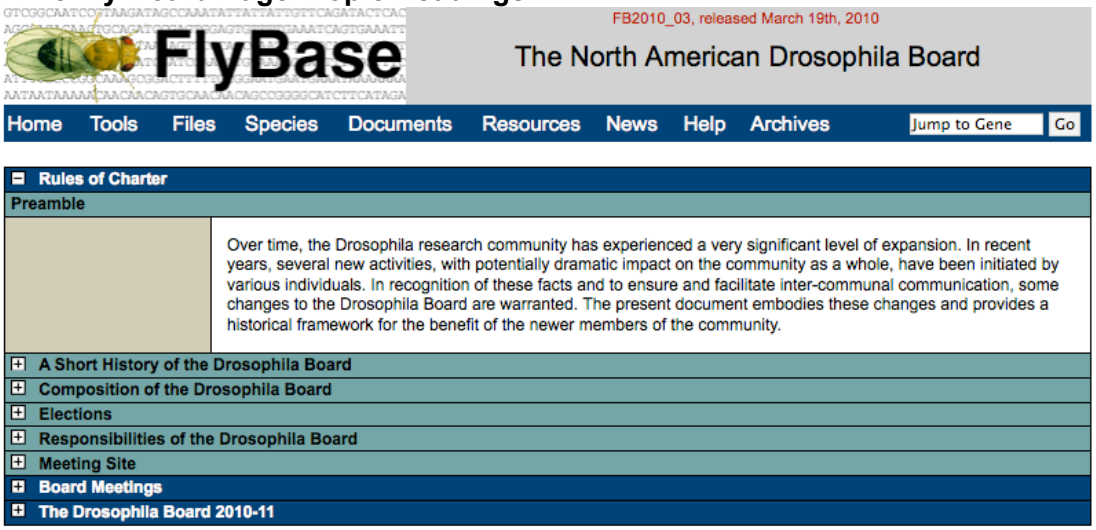
Dmel Release	PROTEIN-CODING GENE MODEL CHANGES FROM PREVIOUS RELEASE					
	NEW	RESTORED	DELETED	MERGED	SPLIT	COMPLEX
Rel_5.17	7	1	4	4->2	0	0
Rel_5.18	6	0	5	14->6	0	0
Rel_5.19	11	0	151	8->4	0	0
Rel_5.20	1	0	1	13->6	0	0
Rel_5.21	8	0	120	4->2	0	0
Rel_5.22	1	0	0	0	6->12	1
Rel_5.23	4	0	24	0	0	0
Rel_5.24	10	0	1	0	0	0
Rel_5.25	7	0	22	46->22	0	0
Rel_5.26	28	9	73	18->8	0	0
TOTALS	**83**	**10**	**401**	**107->50**	**6->12**	**1**

FLYBASE AND FLY BOARD / COMMUNITY ACCESS & INPUT

- FlyBase posts the Fly Board membership, the annual reports and the Board-sponsored white papers under the “News” dropdown menu on the banner.
- FlyBase posts announcements of interest to the community.
- ***FlyBase invites the Fly Board to write one or more Commentaries to reach out to the community and that would appear prominently on the FlyBase home page.***

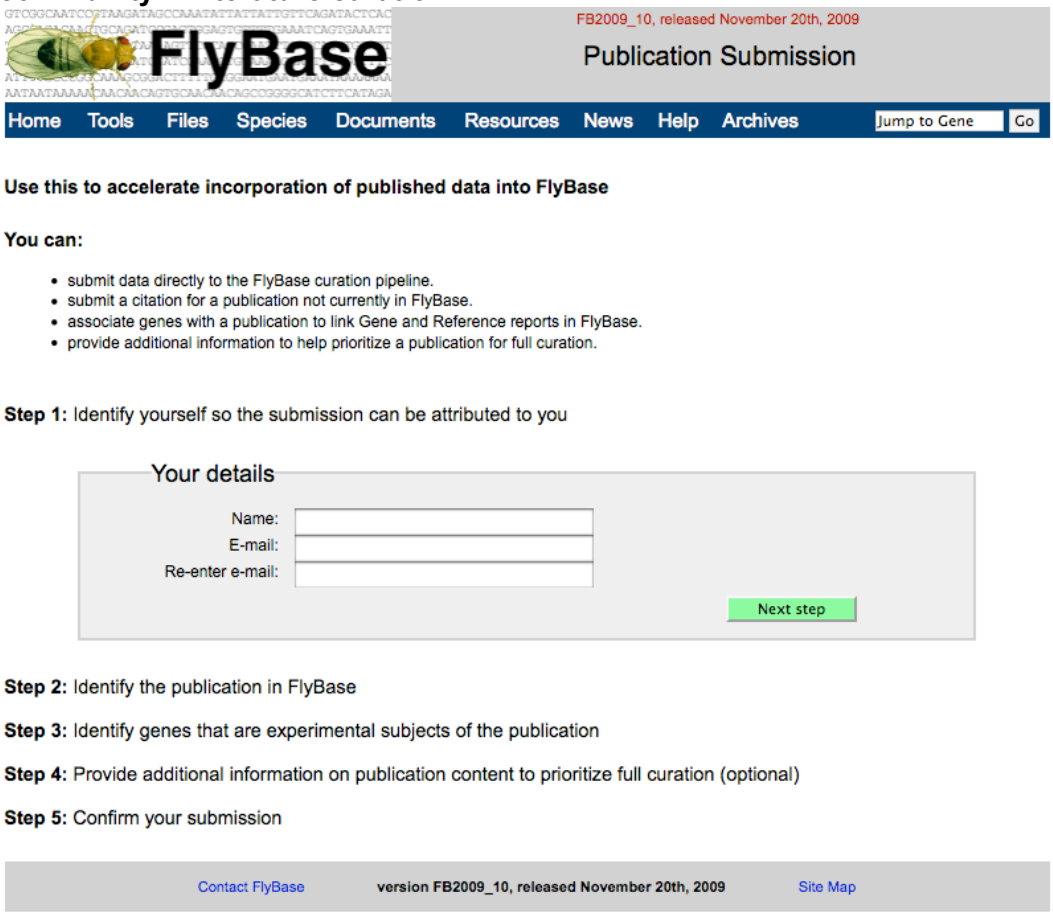
- **Fly Board & Community-Relevant Postings on the FlyBase home page.**

- **The Fly Board Page: Topic Headings**



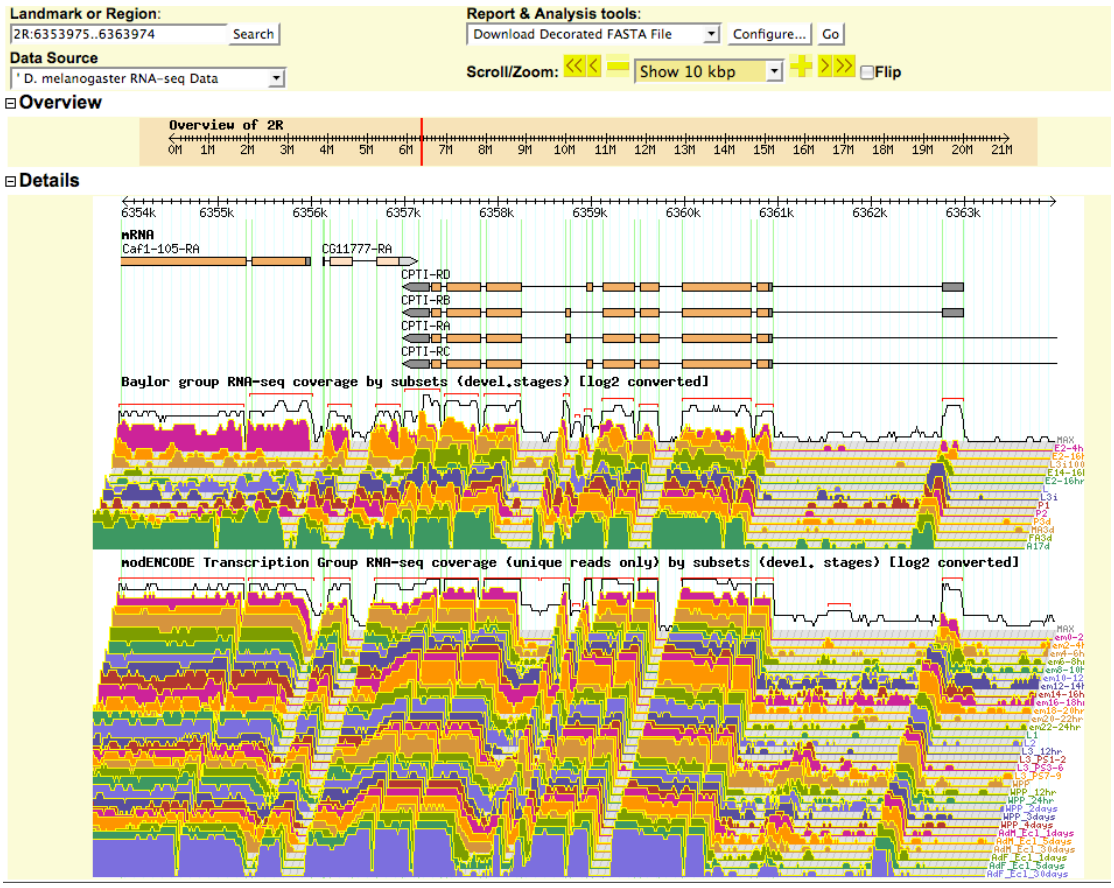
- **FlyBase hosts a Community Forum**

- **FlyBase has a Community Data Submission page to engage the research community in literature curation.**

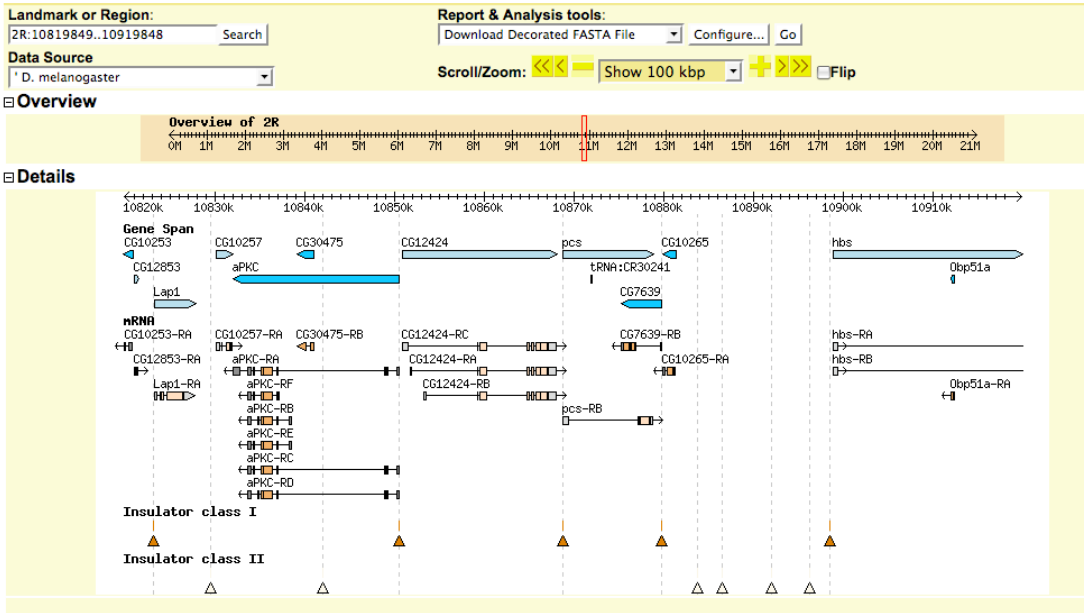


NEW GENOME-WIDE DATA SETS:

- **RNA-Seq Data (Developmental Profiles) (Daines & Chen, Baylor College of Medicine; Celniker, Graveley, modENCODE; Sturgill & Oliver, NIDDK-NIH):**

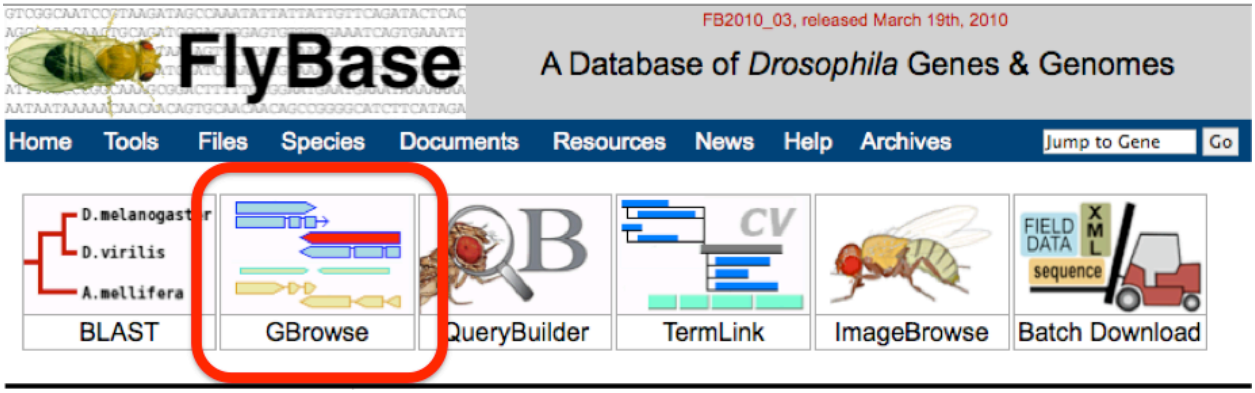


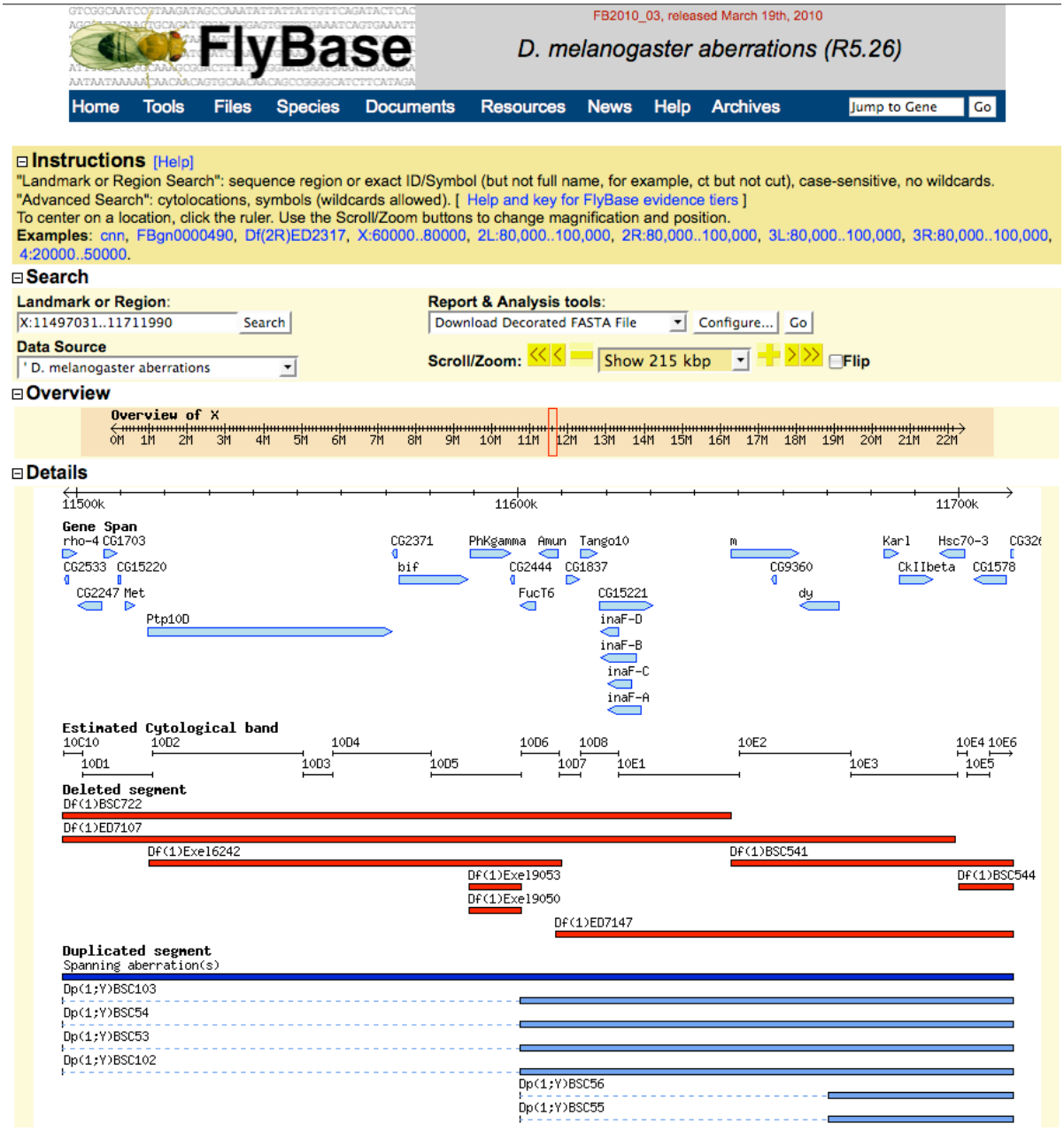
- **Insulator Predictions (Nègre et al., 2010, PLoS Genetics 15: e1000814): modENCODE.**



GRAPHICAL VIEWS OF MOLECULARLY-DEFINED MUTATIONS & ABERRATIONS

- **Genome-wide GBrowse views of molecularly-defined deletions/duplications**





- **Graphics in Aberrations Reports**

FB2010_03, released March 19th, 2010

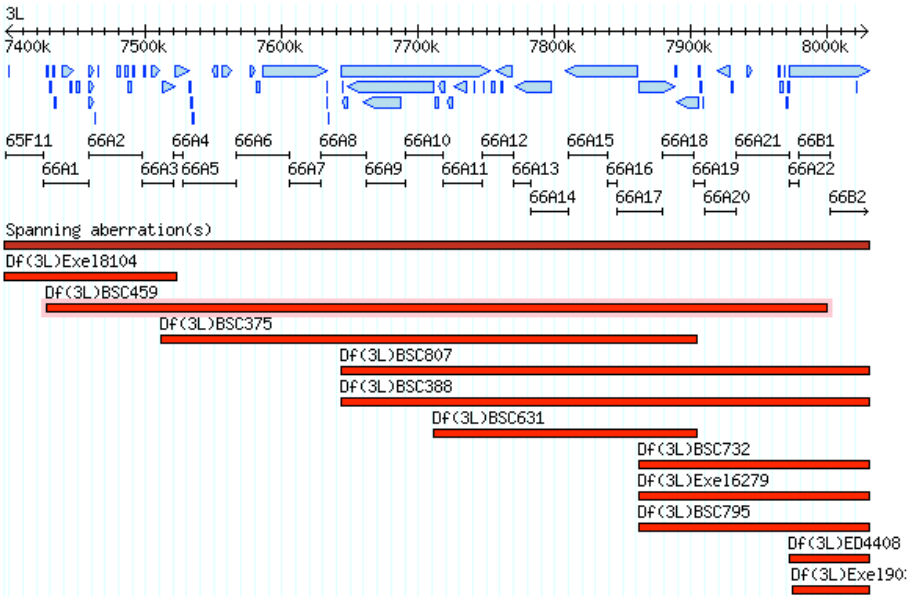
FlyBase

Aberration Dmel\Df(3L)BSC459

Home Tools Files Species Documents Resources News Help Archives Jump to Gene Go

Profile Manager Help Open All Close All

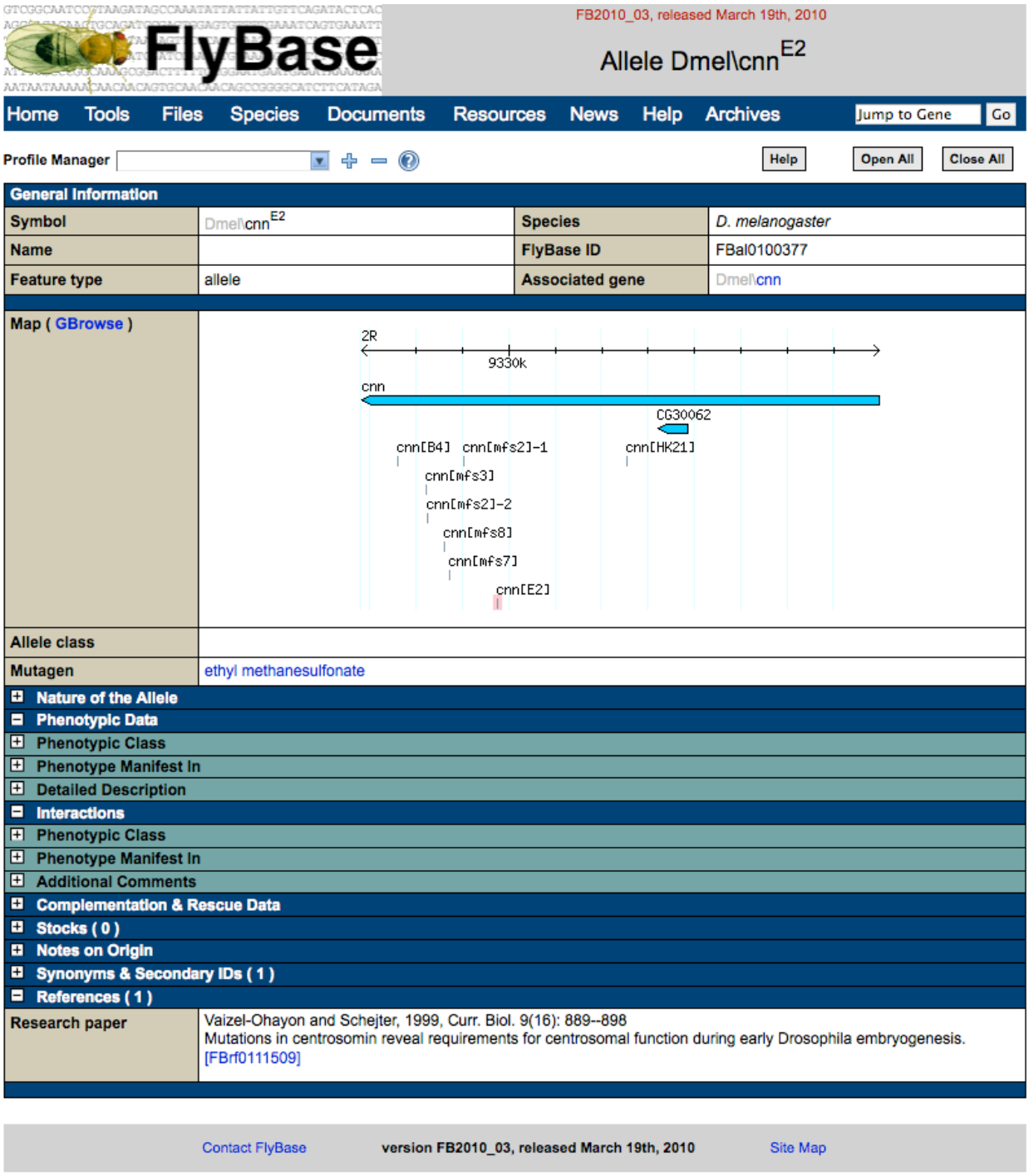
General Information			
Symbol	Dmel\Df(3L)BSC459	Species	*D. melanogaster*
Name		FlyBase ID	FBab0045281
Feature type	chromosomal_deletion		

Computed Breakpoints include	[66A1-66A1];[66B1-66B1];
Deleted segment	66A1--66B1
Map (GBrowse)	

Sequence coordinates	3L:7,427,327..7,427,491 (Df(3L)BSC459:bk1)	(*Bloomington Drosophila Stock Center, 2008.8.7*)
	3L:7,999,689..7,999,689 (Df(3L)BSC459:bk2)	(*Bloomington Drosophila Stock Center, 2008.8.7*)

- Nature of the Aberration
- Gene Deletion & Duplication Data
- Phenotypic Data
- Position Effect Variegation Data
- Stocks (1)
- Notes on Origin
- Balancer / Genotype Variants of the Aberration
- Separable Components
- Other Comments
- Synonyms & Secondary IDs (1)
- References (4)

- **Graphics in Allele Reports**



NEW CLASSES OF FLYBASE REPORTS:

- **Sequence Feature Reports (Non-Genic Features)**
  - Will include natural genome features such as exon-exon junctions, cis-regulatory elements, protein-binding sites, chromatin marks, origins of replication, insulators and artificial features such as dsRNAi amplicons and microarray features.

FlyBase

FB2010_03, released March 19th, 2010

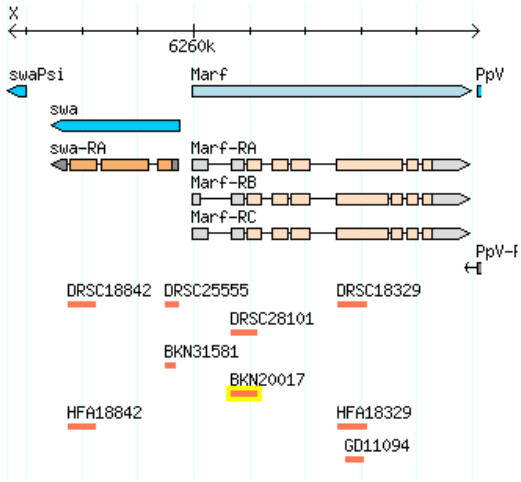
Sequence Feature BKN20017

Home | Tools | Files | Species | Documents | Resources | News | Help | Archives | Jump to Gene | Go

Profile Manager | Help | Open All | Close All

General Information			
Symbol	BKN20017	Species	*D. melanogaster*
Feature type	RNAi_reagent	FlyBase ID	FBsf0000040961
Collection	BKNAmplicon	Associated gene(s)	Marf
Genomic Location			
Chromosome (arm)	X	Sequence location	X:6,260,684..6,261,114 [+]

Map (GBrowse)



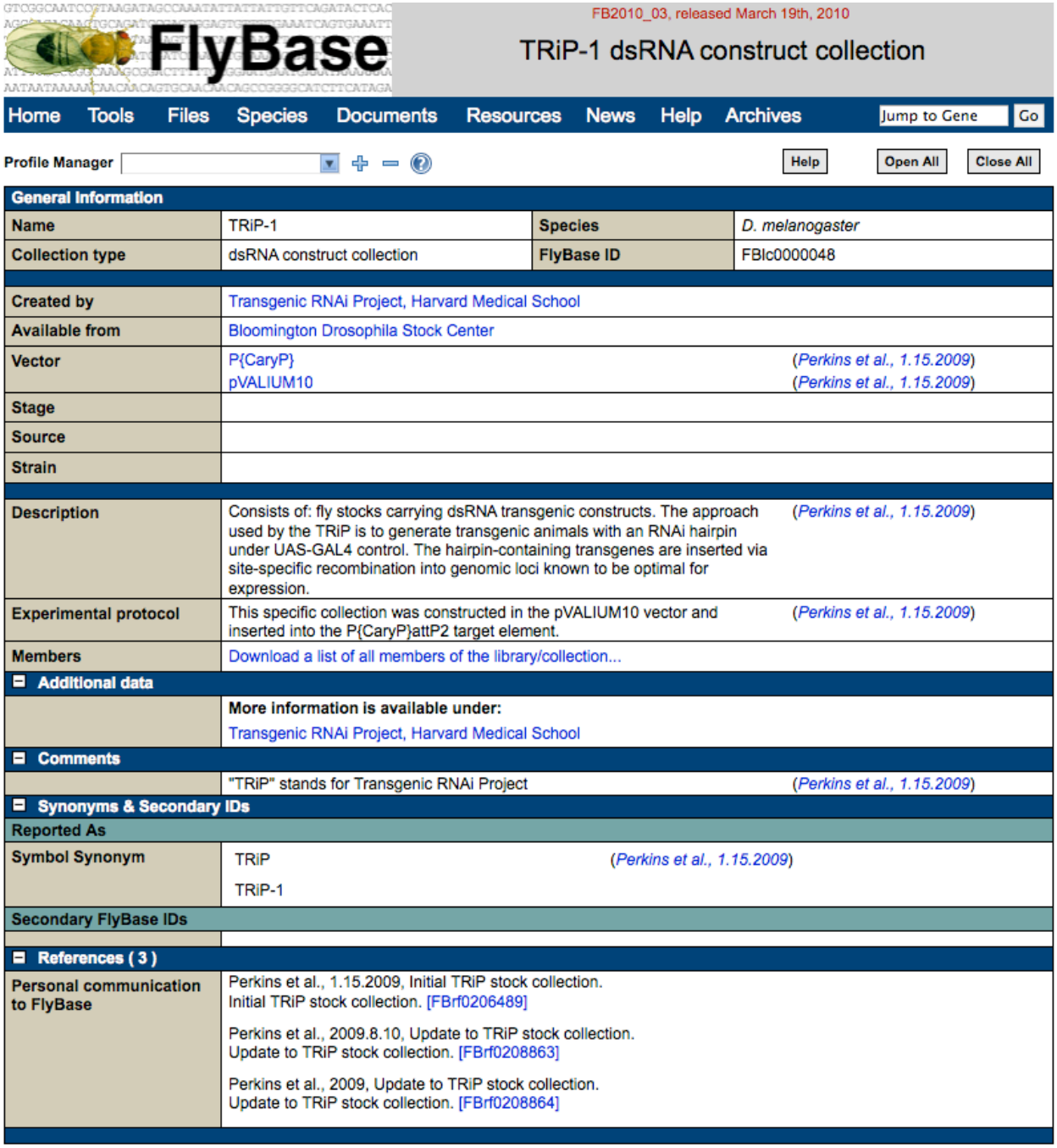
Sequence Data

Length	431
Comments	
Sequence	TGAGCAAATACCCCCAAAAGCAATATAACACACAATAAACAGAGATAGTT AAGTTTTGAGTTTCGGGTTGGCGGCGAAGTTGCAGAAGTTGGAAGTCTGA ACAACCAAATCCCCTGGGCTGCATACCTTTTGTTTTGTATCGCAATTCTC TTCTTCTACCAAAAAACCATCTGCTAAACCGAATCAACCATAAACCGGAT CCCGAAATGGCGGCCTACTTGAACCGCACCATCTCGATGGTGACCGGGCA AACGGGCCCCGCCGACGACGACCGTCACGCCTCCTCCACGGACACGGTGG ACAAATCCGGACCCGGTTCCCCGCTATCCCGGTTCAACTCATCGCTGCAA CAATCCGGCTCCACAATGGCCGCCAATCTGCTACCGGAATCGCGGCTCTA TCAATCCAACGACAAATCACCGCTCCAGATC

Associated Information
Experimental Data
Collection Information
Comments
Stocks Listed in FlyBase (0)
External Crossreferences & Linkouts
Synonyms & Secondary IDs (1)
References (1)

Contact FlyBase | version FB2010_03, released March 19th, 2010 | Site Map

- **Library/Collection Metadata Reports**
  - FlyBase is incorporating an ever increasing range of large-scale datasets which represent thousands or even millions of data points harvested from the same source of material under a set of standard experimental conditions and analyzed in the same way.
  - Providing a central report page to describe these shared properties as well as the relevant primary literature is an important way to organize these large data sets.



FB2010_03, released March 19th, 2010

FlyBase

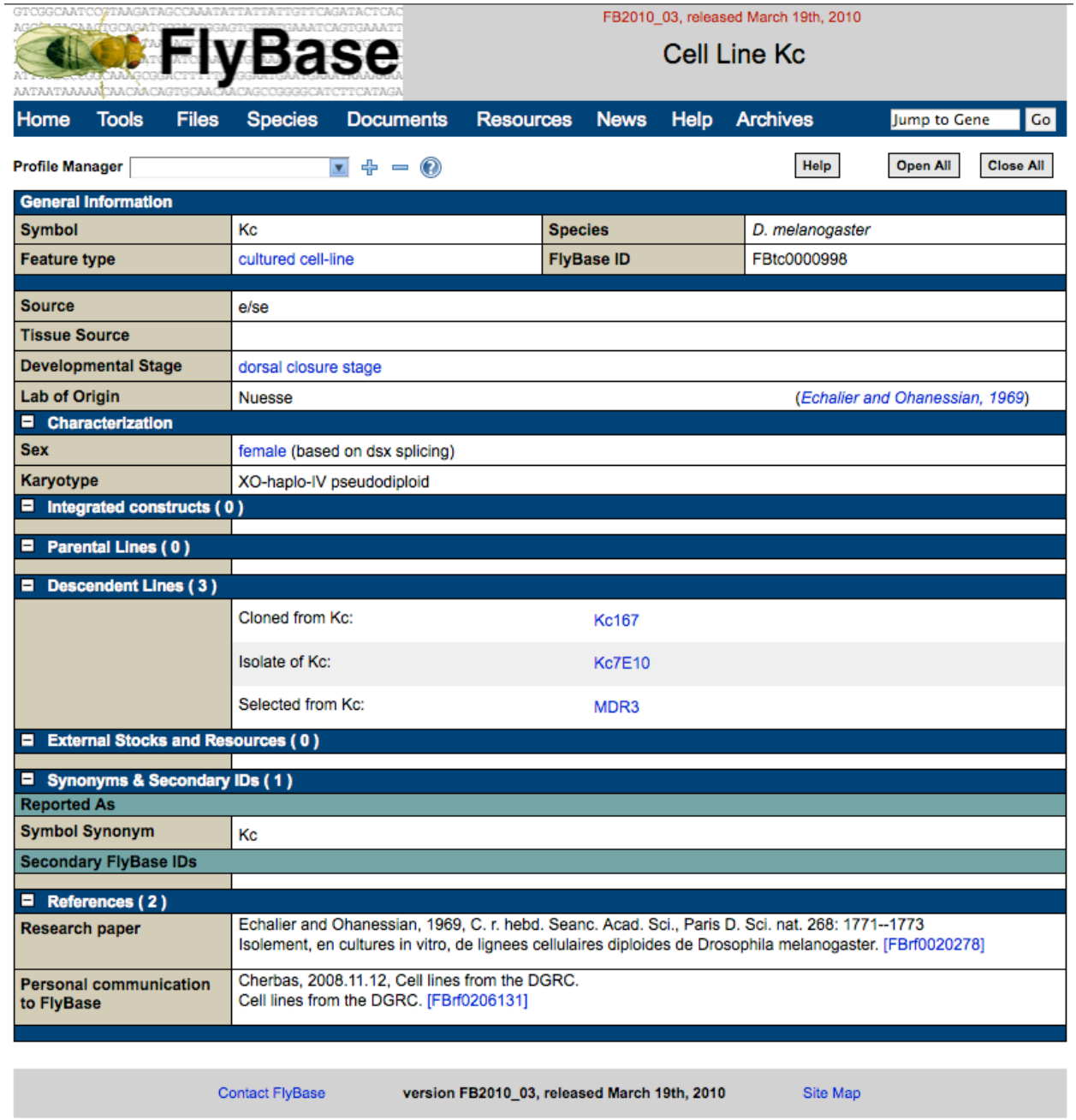
TRiP-1 dsRNA construct collection

Home | Tools | Files | Species | Documents | Resources | News | Help | Archives | Jump to Gene | Go

Profile Manager | Help | Open All | Close All

General Information			
Name	TRiP-1	Species	*D. melanogaster*
Collection type	dsRNA construct collection	FlyBase ID	FBlc0000048
Created by	Transgenic RNAi Project, Harvard Medical School		
Available from	Bloomington Drosophila Stock Center		
Vector	P{CaryP} (*Perkins et al., 1.15.2009*) pVALIUM10 (*Perkins et al., 1.15.2009*)		
Stage			
Source			
Strain			
Description	Consists of: fly stocks carrying dsRNA transgenic constructs. The approach used by the TRiP is to generate transgenic animals with an RNAi hairpin under UAS-GAL4 control. The hairpin-containing transgenes are inserted via site-specific recombination into genomic loci known to be optimal for expression. (*Perkins et al., 1.15.2009*)		
Experimental protocol	This specific collection was constructed in the pVALIUM10 vector and inserted into the P{CaryP}attP2 target element. (*Perkins et al., 1.15.2009*)		
Members	Download a list of all members of the library/collection...		
Additional data			
	More information is available under: Transgenic RNAi Project, Harvard Medical School		
Comments			
	"TRiP" stands for Transgenic RNAi Project (*Perkins et al., 1.15.2009*)		
Synonyms & Secondary IDs			
Reported As			
Symbol Synonym	TRiP (*Perkins et al., 1.15.2009*) TRiP-1		
Secondary FlyBase IDs			
References (3)			
Personal communication to FlyBase	Perkins et al., 1.15.2009, Initial TRiP stock collection. Initial TRiP stock collection. [FBrf0206489] Perkins et al., 2009.8.10, Update to TRiP stock collection. Update to TRiP stock collection. [FBrf0208863] Perkins et al., 2009, Update to TRiP stock collection. Update to TRiP stock collection. [FBrf0208864]		

- **Cell Line Report**
  - Special thanks to Lucy Cherbas and her colleagues for providing these data.
  - With extensive use of cell lines for high throughput RNAi library and chemical library screens, as well as for genome-wide assessment of genome features (modENCODE), the availability of fundamental data on cell lines is extremely valuable to the community.



FB2010_03, released March 19th, 2010

FlyBase

Cell Line Kc

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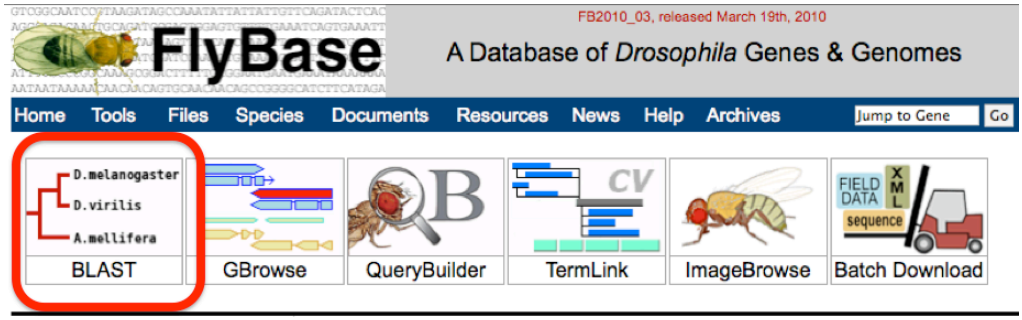
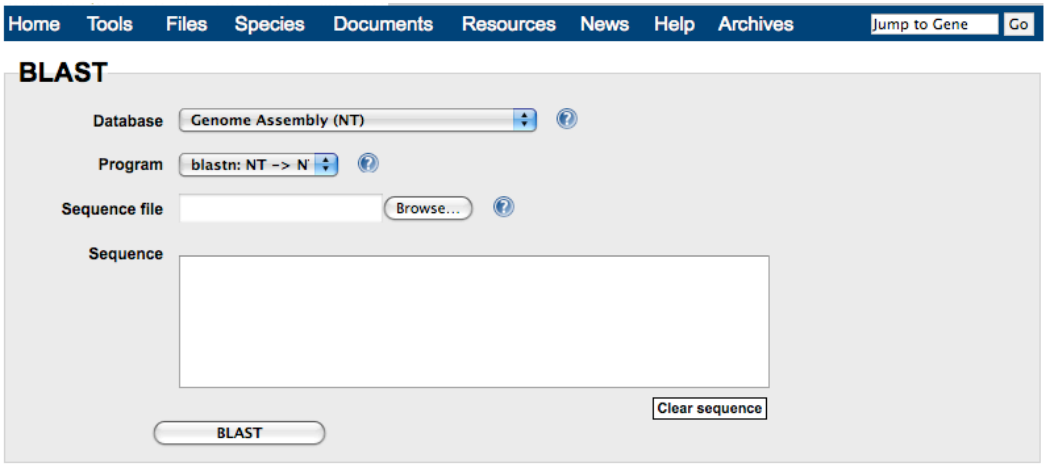
General Information			
Symbol	Kc	Species	*D. melanogaster*
Feature type	cultured cell-line	FlyBase ID	FBtc0000998
Source	e/se		
Tissue Source			
Developmental Stage	dorsal closure stage		
Lab of Origin	Nuesse (*Echalier and Ohanessian, 1969*)		
Characterization			
Sex	female (based on dsx splicing)		
Karyotype	XO-haplo-IV pseudodiploid		
Integrated constructs (0)			
Parental Lines (0)			
Descendent Lines (3)			
	Cloned from Kc:	Kc167	
	Isolate of Kc:	Kc7E10	
	Selected from Kc:	MDR3	
External Stocks and Resources (0)			
Synonyms & Secondary IDs (1)			
Reported As			
Symbol Synonym	Kc		
Secondary FlyBase IDs			
References (2)			
Research paper	Echalier and Ohanessian, 1969, C. r. hebd. Seanc. Acad. Sci., Paris D. Sci. nat. 268: 1771--1773 Isolement, en cultures in vitro, de lignees cellulaires diploides de Drosophila melanogaster. [FBrf0020278]		
Personal communication to FlyBase	Cherbas, 2008.11.12, Cell lines from the DGRC. Cell lines from the DGRC. [FBrf0206131]		

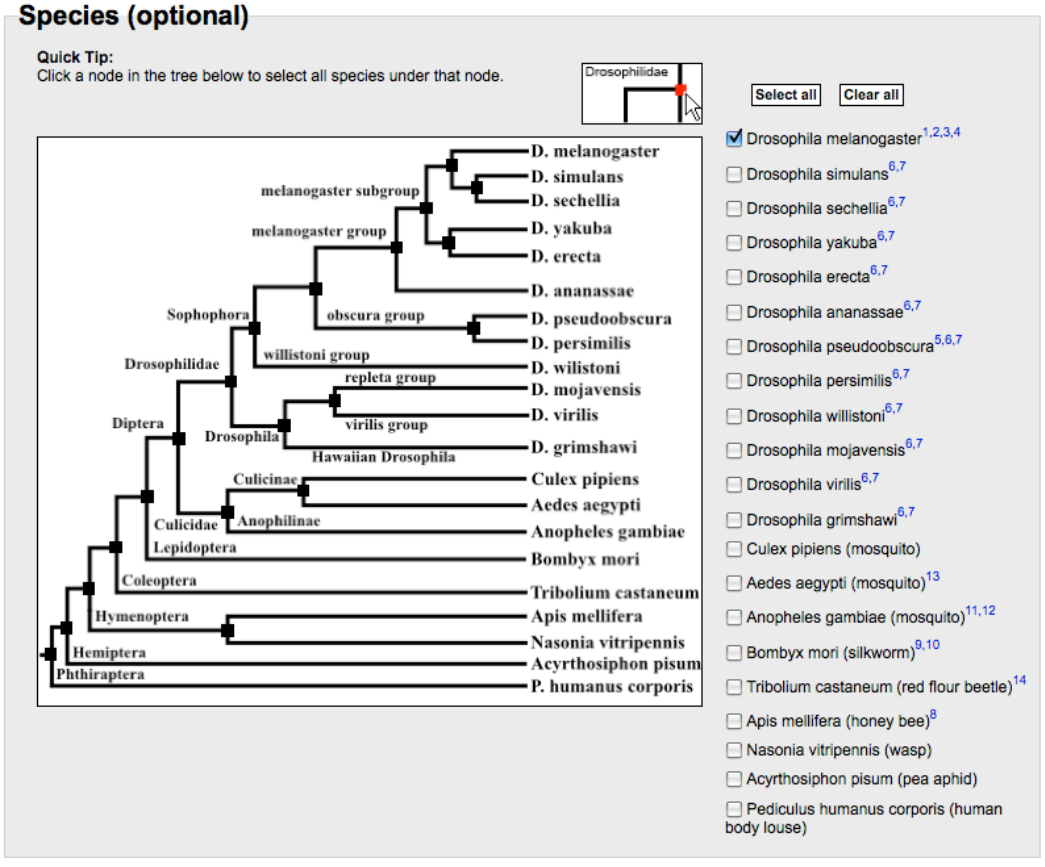
Contact FlyBase version FB2010_03, released March 19th, 2010 Site Map

OTHER NEW OR ENHANCED FEATURES

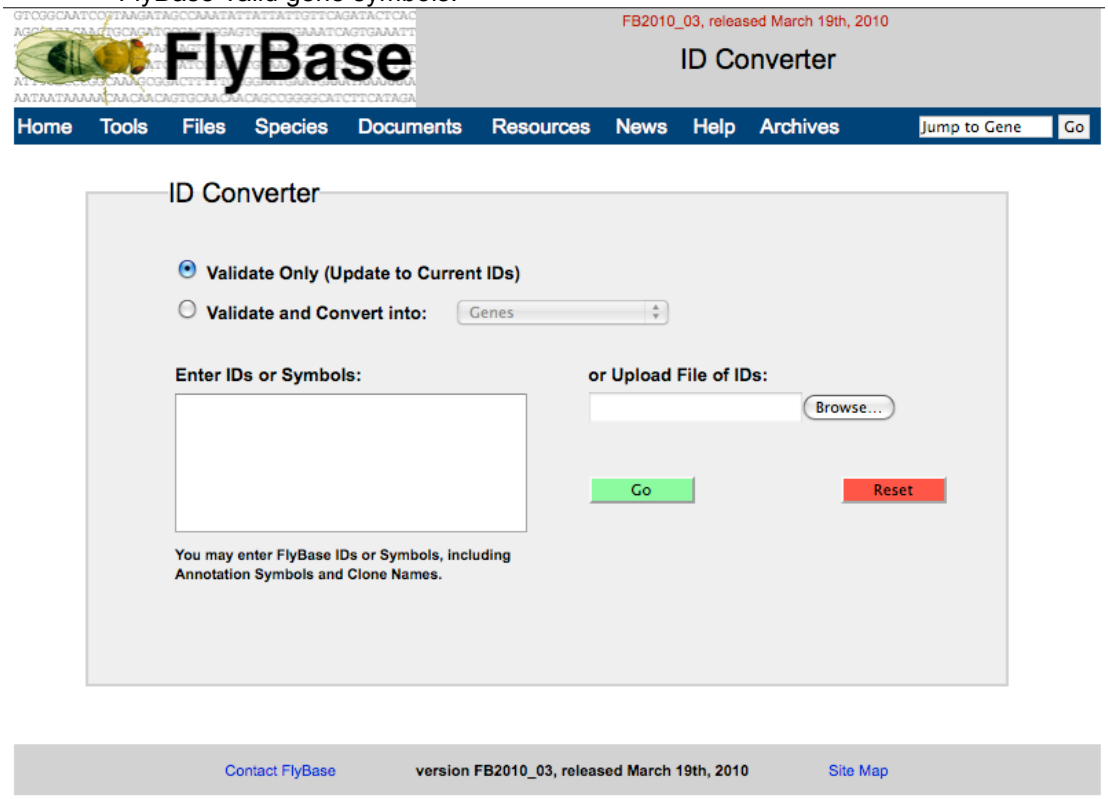
- **Additional insect genomes in FlyBase BLAST database**
  - Currently, 12 Drosophila species and 9 non-Drosophilid insect genomes.



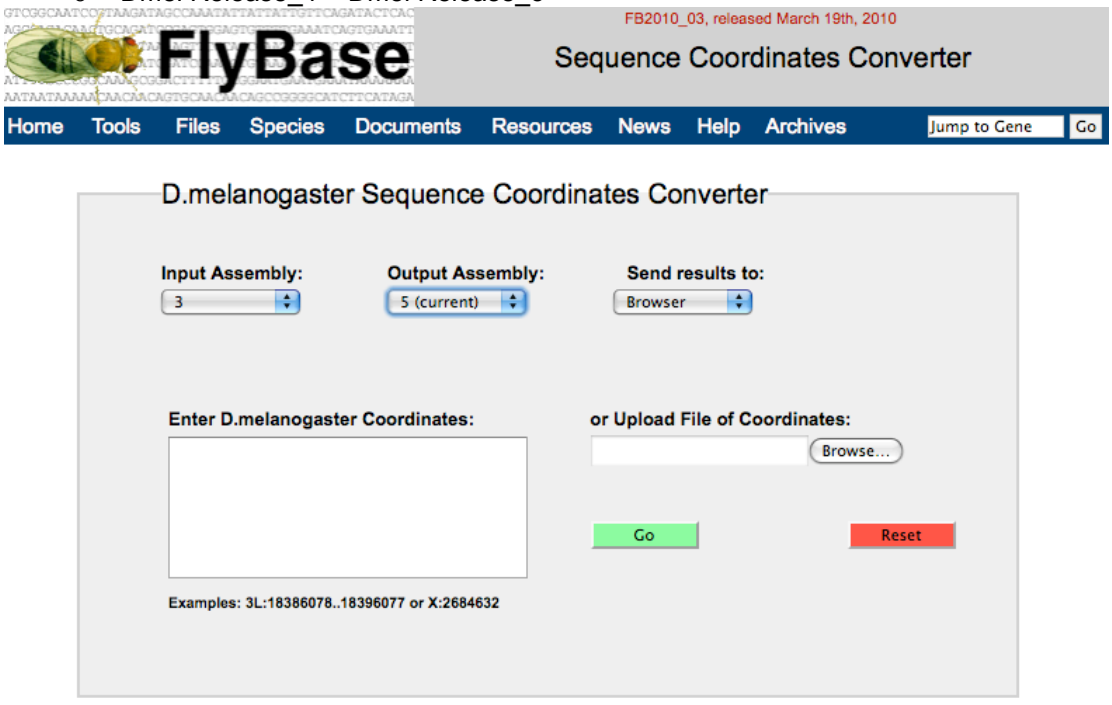




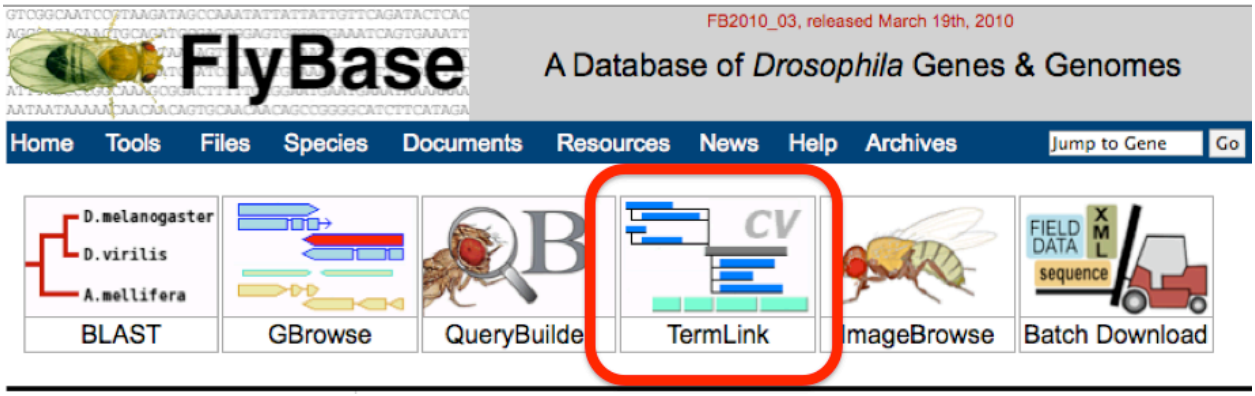
- **ID Converter**
  - Permits forward migration of previous FlyBase identifiers to their current equivalent.
  - Permits identifiers to be converted to other FlyBase objects, e.g., FBgn identifiers into FlyBase-valid gene symbols.

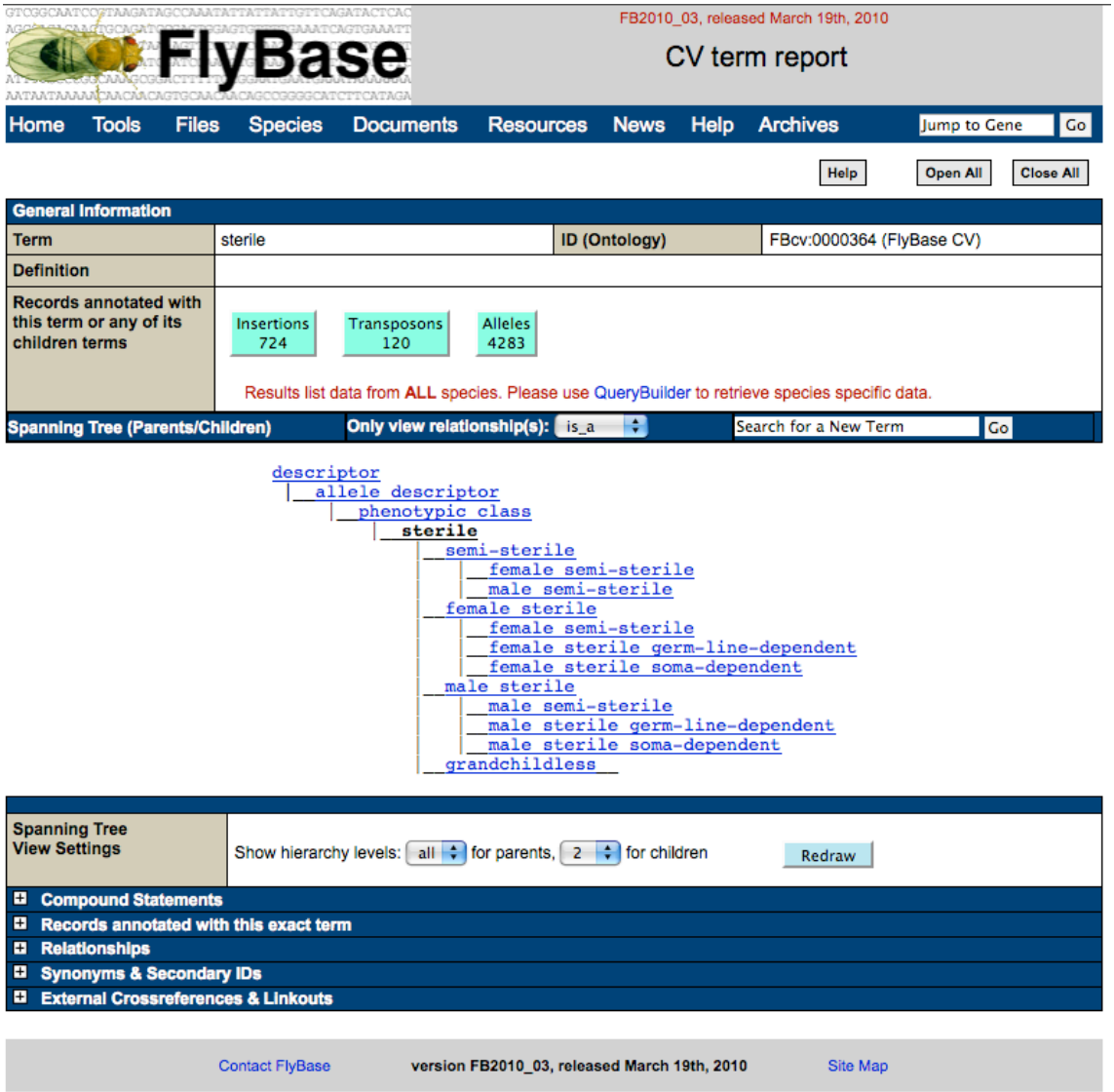


- **Sequence Coordinate Converter (for *D. melanogaster* genome assembly releases)**
  - (Actually from previous year but not well publicized)
  - Dmel Release_3 > Dmel Release_4
  - Dmel Release_3 > Dmel Release_5
  - Dmel Release_4 > Dmel Release_5

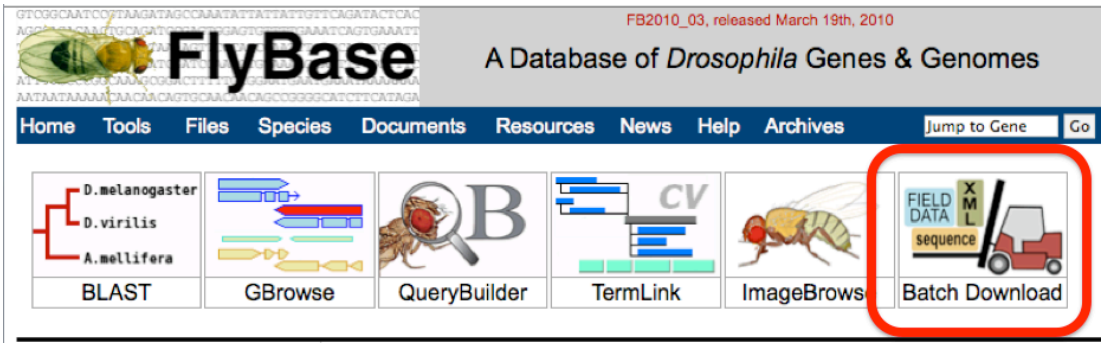


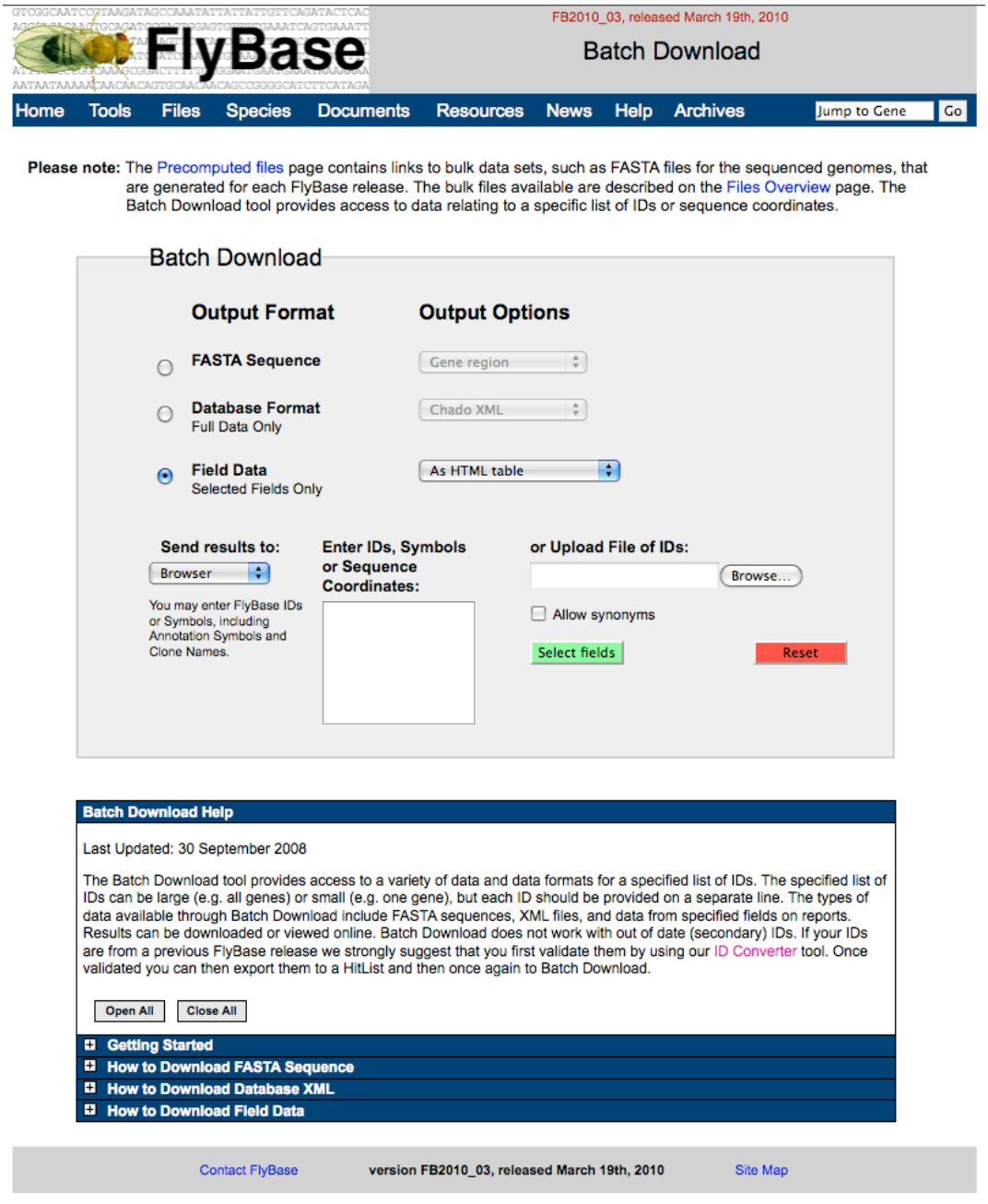
- **Controlled Vocabulary Term Report Enhancements**
  - Compound statements such as “female sterile | dominant” provide more focused record retrieval.
  - Terms can be filtered by relationships.





- **Batch Download Enhancements**
  - FASTA sequence options for “sequence features” and “clones” are available.
  - A Batch Download icon is now on home page.





- **QueryBuilder Enhancements**
  - The “Build a query” field selection pages mirror corresponding report pages for easier selection of relevant fields.
  - Templates support quick customization.
  - Save/import options allow query reuse.