2015 National Drosophila Board Meeting Agenda

Wednesday March 26, 2015, 3:00 - 6:00 PM
Michigan A/B Room of the Sheraton Chicago Hotel & Towers

1. Introduction (Ken Irvine) 3:00-3:05
2. Report of the 2015 Meeting Organizing Committee (Greg Beitel) 3:05-3:15
3. Treasurer's Report (Debbie Andrew) 3:15-3:25
4. Sandler Lectureship Committee (Erika Bach) 3:25-3:30
5. Victoria Finnerty Undergraduate Travel Award (Alexis Nagengast) 3:30-3:35
6. Primarily Undergraduate Institutions (Alexis Nagengast) 3:35-3:40
7. Image Award (David Bilder) 3:40-3:45
8. Report of the GSA Senior Director (Suzy Brown) 3:45-3:55
9. 2016 & 2017 Fly Meetings Update (David Bilder, Adam Fagen) 3:55-4:00
10. Drosophila Board Election Report (Mike O'Connor) 4:00-4:05
11. Proposed redistribution of Board election cycles (Mike O'Connor) 4:05-4:10
12. Identifying members of the Fly Community (David Bilder) 4:10-4:15
13. Advocacy & Communications (Irvine, Page-McCaw, Bilder, Aiyar) 4:15-4:35

BREAK 4:35 - 4:50

Community Resources and Projects 4:50-5:40
14. FlyBase (Bill Gelbart)
15. Bloomington Stock Center (Kathy Matthews, Kevin Cook)
16. Species Stock Center (Maxi Richmond)
17. Drosophila Gene Disruption Project (Hugo Bellen)
18. Harvard Drosophila RNAi Screening Center (Stephanie Mohr)
19. Harvard Transgenic RNAi Project (Liz Perkins)
20. Vienna Drosophila RNAi/Resource Center (Lisa Meadows)
21. Berkeley Drosophila Genome Project (Sue Celniker, read only)
22. DIS (Jim Thompson)
23. Historical Records (Irvine)
24. White Paper & DCM RFI (Irvine)

Adjourn

(White Paper Discussion ~5:45-6:30)

Table of Contents for Reports & Discussion Items

Action Items

2. Report of the 2015 Organizing Committee

Organizers: Greg Beitel, Ilaria Rebay, Michael Eisen, Marc Freeman

The 2015 Organizing Committee was assembled in 2013. Greg Beitel and Ilaria Rebay were invited by Amy Bejsovec to be the lead organizers. Ilaria and Greg subsequently recruited Michael Eisen and Marc Freeman. At the 2014 San Diego meeting, valuable advice was presented at a luncheon meeting that included the 2014 and 2015 Organizing Committees, and the GSA point person, Suzy Brown. The 2014 Organizers offered to share their materials. We began organizing 2015 meeting soon thereafter. Most of our work was done sharing information by email. Given that all of our interactions occurred remotely, there was no particular advantage to having all of the organizers situated in one geographical region. What is advantageous is to select a group of co-organizers with diverse scientific expertise, as this makes the task of identifying appropriate speakers and session chairs much easier. Overall, meeting organization progressed smoothly. Most decisions were made by consensus, although some tasks were assumed by, or delegated to, individual members. Continual guidance and input from Suzy Brown was invaluable, and the entire GSA staff did an outstanding job. Suzy in particular seems to be online 24/7 and had infinite patience for us and our questions.

Interaction with the GSA Office

Suzy Brown, and by extension the whole GSA office, was terrific to work with. The timeline and reminders that Suzy sent us were very useful. Suzy was very helpful in answering all questions that arose and provided invaluable continuity with her knowledge of the workings of previous meetings.

2015 fly meeting registrations and registration trends

Pre-registration for the 2015 fly meeting is strong, with 1,519 pre-registrants as of February 20, 2015. A comparison to previous years meetings and to other GSA meetings is shown in the table below.

	Fly	Worm	Yeast	Fungal
2011	1328	1672		924
2012	1537		522	
2013	1555	1773		932
2014	1431		465	
2015	1517	TBD		907

For historical comparison, earlier fly meeting pre-registrations were:
1516 (2010), 1383 (2009), 1343 (2008), 1345 (2007), 1241(2006), 1451 (2005), 1470 (2004)

At the 2014 Drosophila Board meeting, concern was voiced that science funding issues might be reducing participation in the Drosophila and other GSA meetings, and that the dip in the 2014 fly meeting registrations might be the beginning of a trend. However, with pre-registrations for the 2015 meeting returning to 2012/13 levels, approximately 12% above 2014 levels, the 2015 meeting is already one of the three largest fly meetings in the last 11 years.

Organizer, speaker and special awards compensation
As per previous years, the meeting organizers, plenary speakers, and key note speaker (Dr. Allan Spradling) were provided free conference registration. Everyone had to cover their lodging and travel costs. There were several inquires about registration and travel funds from some of the speakers and session chairs, but in the end everyone except one session chair agreed to fund their own way. That session chair chose to resign their chairship in protest.

The Larry Sandler Award Winner receives complementary airfare, registration, hotel accommodations, and GSA membership.

Victoria Finnerty Memorial Fund travel grants were awarded to six undergraduate researchers, all of whom are presenting posters.

Jonathan Cohen, Swarthmore College
Alexander Kneubehl, Ohio Northern University
Kiu Ming April Kong, York University
Meera Namireddy, Rice University
Irina Pushel, Michigan State University
Anna Zeidman, Brown University

Conference Sessions:
As in recent years, only the schedule and lists of talks and posters are in the program book. The abstracts are available online.

Keynote Speaker, Wednesday night
The 2015 fly meeting will follow the traditional program on the first night, with introductions, Keynote address, the Sandler lecture and announcements from GSA. The organizers invited Dr. Allan Spradling to present the keynote lecture. At the request of the organizers, the GSA attempted to book US Senator Richard Durbin (Illinois), a long time advocate of NIH funding and of basic research, for a special presentation during the opening night on the topic of science funding and advocacy, but as the senate will be in session during the fly meeting, Senator Durbin will be in Washington and unavailable to make an appearance.

Plenary Speakers:
As in previous years, our criteria for choosing plenary speakers were scientific importance and novelty, breadth of topics, gender balance, foreign and domestic speakers, and a mixture of more junior and senior faculty. In addition, we only selected speakers that we have recently heard and are confident that they will give excellent talks. Any speaker that had given a plenary talk within the last 10 years was excluded from consideration. The plenary speakers will be (in order of the program): Yohanns Bellaiche, Maria Dominguez, Matt Gibson, Ulrike Heberlein, Heinrich Jasper, Jurgen Knoblich, Harmit Malik, Chris Rushlow, Stanislav Y. Shvartsman, Angela Stathopoulos, Yukiko Yamashita, Phillip Zamore.

Categories for the abstracts, platform and poster sessions
The 2014 Organizing Committee had suggested in their report and at the Drosophila Board meeting that instead of the fly meeting organizers making changes every year, the Board should consider making “stable” list of keywords. While the Board did not appear to take up this suggestion or communicate any particular plans regarding keywords to the 2015 organizers, the changes to the keywords made in 2015 were executed with the idea of moving the list further towards a stable controlled vocabulary. Whether future Drosophila Boards will choose to establish a more formalized keyword list is unclear, but it should be noted that even with the current evolving list of keywords and categories, the GSA staff were able to provide

detailed and very usable spreadsheets showing usage of keywords over the years. Thus, even without the Drosophila Board tackling the difficult problem of establishing a stable keyword list, the GSA is already able to provide highly usable data that could be used for writing white papers or tracking where Drosophila research is headed.

The 2014 organizers had reduced number of categories for platform and poster sessions to 17 from the previous year's 18. They also revised and redistributed the relevant keywords. The 2015 organizers Ilaria Rebay and Greg Beitel did not make changes to the categories list, but after carefully deliberation, did refine the keywords list to consolidate keywords that had overlapping ideas (and particularly those that had not been used in several years) and to add appropriate new keywords such as "computational approaches" and "optogenetics" that were highly likely to be important in 2015 and in the future (Categories are listed in Table 1 in Appendix A).

Platform chair (co-chair) selection

The 2015 Organizing Committee followed the approach of the 2014 Organizers and used a co-chair approach in which each session would be equally chaired by an established/"heavy hitter" in the field, and a more junior investigator. The "social engineering" goal of including the "heavy hitter" is to get more of the senior/"heavy hitter" researchers to attend the fly meeting, which they otherwise might not do, and thus make the meeting better for all attendees who would then have a chance to interact with, or at least hear from, the "heavy hitters". The goal for the junior researchers is to give them exposure. This worked well for the 2014 fly meeting and is on track to work well again in 2015.

Co-chairs were chosen for the scientific excellence but also to ensure diversity across many dimensions including gender, geography (different parts of US, different countries) and institution type.

As discussed in more detail below, two sets of co-chairs were recruited for several categories such as Cell Biology, which we knew would have more than one session.

The co-chairs for the 2015 meeting who selected abstracts for platform presentations are listed alphabetically below, and in Appendix Table 1 with affiliation and by session.

> Erika Bach, Utpal Banerjee, Patricia Beldade, Giovanni Bosco, Sarah Bray, Nicolas Buchon, Xin Chen, Joanna Chiu, Tiffany Cook, Bruce A. Edgar, Felice Elefant, John Ewer, Rodrigo Fernandez-Gonzalez, Guanjun Gao, Melissa Harrison, Tony Ip, Lan Jiang, Erin Kelleher, Mitzi Kuroda, Nelson Lau, Cheng-Yu Lee, Tom Lloyd, Susan Lott, Erika Matunis, Marek Mlodzik, Denise Montell, Masayuki Miura, Todd Nystul, Kate O'Connor-Giles, Renee Read, Oren Schuldiner, Ali Shilatifard, Neal Silverman, Nic Tapon, David Walker, Coral Warr, Mariana Wolfner, Zeba Wunderlich, Andrew Zelhof, Sheng Zhang

Abstract deadline

The 2014 Organizers moved the abstract submission deadline to Dec. 9 instead of early November (the traditional deadline) in an attempt to encourage submission of higher quality abstracts and reduce number of abstracts already published by the time of the meeting. However, the downside to this approach was that co-chairs needed to review abstracts during a period overlapping the December holidays, and the organizers only had one week in early January to review the final selections. While all co-chairs and organizers had agreed to this timeline, the 2014 Organizers found this to be "a fairly challenging process". Given that it was not obvious to the 2015 Organizers or to the GSA that there was much gained by using a

December deadline, and there was clear evidence of pain, the 2015 deadline reverted to the traditional November deadline.

Submitted abstracts

A total of 977 abstracts were submitted under 17 categories and associated with keywords. Totals in recent years were 894 (2014), 966 (2013), 1005 (2012), 1066 (2011), 1046 (2010), 1020 (2009), 993 (2008), 897 (2007), 910 (2006), 1043 (2005), 972 (2004), 1016 (2003), 1003 (2002). There were 452 requests for platform talks for the 157 platform talks (not including plenary speakers), which resulted in a 35% success rate, which is in line with the rates in recent years. The number of abstracts varied considerably among sessions (see Appendix 1) from 109 in Drosophila models of human disease to 23 in Immunity and Pathogenesis. As discussed in more detail in the section on platform session organization, the fraction of abstracts in a given category that requested talks also ranged widely, from 78% in "Cell Division and Growth Control" to 39% in "Gametogenesis and Organogenesis" and also in "Regulation of Gene Expression". This disparity creates an interesting problem in deciding how to allocate the number of talks to a particular category (see below).

Platform session organization

Organizing platform sessions has two notable challenges that were commented on by the previous meeting organizers:

1) The number of abstracts for each category is shifting, and in some cases shifting quickly. For example, the Drosophila Models of Human Disease has rapidly grown to the category with the most submitted abstracts. Conversely, there has been a decline of Immunity and Pathogenesis category to 23 posters. This dynamic change makes it difficult to in advance assign the number of platform sessions, and therefore number of co-chairs that will be need for a given category, since co-chairs need to be recruited before the abstract submission deadline. For 2015, the organizers allocated the numbers of talks in rough proportion to the number of abstracts submitted for a category (see point number 2 below), but since session chairs were recruited prior to the abstract deadline, some co-chairs had to evaluate many more abstract than other co-chairs. Conversely, some categories shrank so much there an insufficient number of submitted abstracts to justify a whole session. Thus, several sessions ended up with two categories and four co-chairs. From the view of the 2015 organizers, this is not a problem that explicitly needs a solution, as the meeting must adapt to serve the needs of the researchers. However, it is essential that meeting organizers be aware of the issue in their planning and allow flexibility to accommodate dynamic changes in organizing sessions. For 2015, in the initial allocation of sessions to recruit co-chairs, from the previous years trends plus leaving an unallocated session yielded a reasonable match between co-chair and sessions, and still provided flexibility that made it straightforward to make adjustments allocations once the 2015 abstract pool was available.

2) A thorny issue that presents itself annually is how to allocate talks to abstracts. The 2014 meeting organizer report has a detailed discussion of this issue and suggested a number of possible solutions. The 2014 Organizers also suggested that the Drosophila Board may want to establish some consistent approach for abstract selection. As the Board did not volunteer any guidance to the 2015 committee, we debated the issue amongst ourselves and devised what we felt was an equitable solution. The thorny issue, as noted by the 2014 organizers, is that the chances that an abstract requesting a talk will actually get a talk varies widely across the categories, which seems unfair. It is well known that some of the more "crowded" categories such as Cell Biology historically have a lower success rate. We addressed this issue by allocating more sessions to categories that had increased numbers of abstracts, and decreased

the number of talks for categories with few abstracts. On this basis “Drosophila Models of Human Disease” and “Neural Development” were each allocated an entire extra session, where as “”Immunity and Pathogenesis” and “RNA Biology” end up sharing a combined session.

A significant confounding factor that makes coming up with a truly “fair” solution to allocating talks difficult, and perhaps impossible, that was not considered in the 2014 organizer report is that the fraction of abstracts requesting talks varies dramatically across categories. For example, only 39% of “Drosophila Models of Human Disease” and “Regulation of Gene Expression” abstracts requested talks, but 78% of “Cell Division and Growth Control” abstracts requested talks. If the organizers were simply to equalize the success rate of talk requests across categories, “Cell Division and Growth Control” would be significantly over-represented in platform sessions, which not be fair to the “Regulation of Gene Expression” attendees who might have come to hear about work in their field. While it could it be the case that researchers working in the “Cell Division and Growth Control” field are doing higher quality work and therefore deserve talks more than the researchers in “Regulation of Gene Expression” field, it might alternatively be the case that researchers in the “Regulation of Gene Expression” field just like the spotlight more. As there is little basis for making such assessments, the 2015 organizer committee chose a blended approach for assigning numbers of talks to categories. Based on the reasoning that proportional representation was a reasonably fair way to allocate talks, achieving a relatively consistent ratio of talks per submitted abstracts (poster plus platform session) was weighted fairly heavily in allocating the number of talks to a category. However, the success rate in requested talks between sessions was also considered, as was the practical point that it is considered undesirably to break up sessions beyond switching categories at a coffee break. The final distribution of talk requests and success rate relative to all abstracts and to abstracts requesting talks is shown in Table 2 of the Appendix. It may be the case that in 2015 we have more aggressively split sessions than previous organizers (i.e. having unrelated categories in one session, but maintaining coherency by changing categories during the coffee break), but doing so allowed better distribution of the talks. The 2016 organizers can evaluate if this approach was successful or considered disruptive to the flow of the meeting.

The 2015 Organizers will communicate this issue to the 2016 Organizers at the information lunch and provide the 2016 Organizers with the relevant spreadsheets so that they can consider the issue before they tackle the 2016 session organization.

Platform session speaker selection

Speakers for the platform sessions were selected by the co-chairs on the basis of scientific excellence, breadth, gender balance, and a mixture of graduate students, postdocs, junior faculty, and senior faculty. The number of speakers for each category was determined by the four organizers (detailed above). Co-chairs presented the organizers with a rank ordered list of abstracts for talks, plus several alternates, from the abstracts listing the category as their primary choice. For categories with more than one session, and therefore four co-chairs, the four co-chairs worked together to select the platform sessions rather than the organizers dividing the abstracts into separate pools for the two sets of co-chairs to consider. The four organizers reviewed the choices of the co-chairs, and only had to make several changes to coordinate between sessions. Two labs each had been awarded three talks, which historically, and also by the present organizers, was viewed as too many to maintain diversity at the meeting. The PIs of the labs were consulted, and one talk from each lab was reassigned to a poster presentation. Having the alternate list of abstracts was important for replacing the conflicted talks, and for replacing several talks when speakers withdrew abstracts after notification of platform talk assignment.

Poster Session.
There are currently 820 posters (780 regular and 40 late). The breakdown of posters by category for the regular abstracts is shown in the Appendix.

Selection of abstracts for media presentation
Given the ongoing pressure on basics research funding, as well as specific and disparaging comments about Drosophila research by some American politicians, the GSA is making a much appreciated effort to publicize the positive contributions of Drosophila research to human health. At the request of the GSA, which was fully supported by the organizers, we asked co-chairs to identify two (or more for the Drosophila models of human disease) abstracts that would highlight the relevance of Drosophila research to human disease. Both talks and posters were equally eligible for consideration.

Poster Awards
Based on the recommendations of the previous organizers and GSA, posters will be judged by the traditional approach of having the session chairs select the best posters in their group. To simplify judging, session chairs have to option to identify a short list of potential poster award winners for each category (postdoc, graduate student, undergrad) based on abstracts and opt to review only those posters instead of the entire group in that category. The selection will be based on science and poster design, not on the poster presentation, given the time constraints of the meeting.
The results will be communicated to the Organizing Committee who will examine the session winners, and pick 1st, 2nd, and 3rd places for each class. Ribbons will be pinned on the wining posters so that attendees can examine the winning posters. The winners will be recognized during the plenary session on Sunday and their posters displayed outside the room. The GSA provides cash prizes, a year of GSA membership and copies of Conversations in Genetics videos to the awardees.

Workshops
In addition to the traditional pre-meeting Ecdysone workshop and (new as of 2014) the Workshop for Undergraduate Researchers that runs concurrently with the main plenary session, there are 12 researcher-initiated workshops. These sessions were selected from 20 workshop applications. In two cases, the organizers merged two proposed workshops into a single workshop. Three proposed workshops were rejected because there was already significant coverage of those topics in platform sessions and one was rejected for being too narrow in focus. Organization of the workshops themselves was left to the workshop organizers.

<u>Workshop Schedule:</u>

Wednesday
Ecdysone Workshop

Friday
Plenary Session and Workshop for Undergraduate Researchers
Communicating Your Drosophila Research to Scientific and Non-scientific Audiences
Feeding Behavior, Nutrition and Metabolism
Integration of Computational Approaches and Big Data to Tackle Systems-Biology Problems in Drosophila and other Model systems
Tools for Functional Genomics Analyses
Harnessing Community Resources for Drosophila Neuroscience

Saturday

Diverse Applications of CRISPR-Cas9 Genome Engineering
Drosophila Research and Pedagogy at Primarily Undergraduate Institutions (PUI)
Everything You Ever Wanted to Know About Sex
Cracking the Cis Regulatory Code: New Computational and Physical Approaches
Homologous Recombination Mechanisms and Metrics
Developmental Mechanics
New Tools and Approaches for Behavioral Phenotyping in Drosophila

Planned assistance to the 2016 Drosophila Conference Organizing Committee
All of the worksheet templates, and the tables listing previous speakers and session chairs will be made available to the 2016 Organizing Committee. In addition, a lunch with the current and next year's organizers is planned for Saturday to discuss and answer any questions that the new organizers may have.

Greg: no dip in attendance, bounce back to 2013 #s, a robust meeting.
Decided not to create established keyword/vocabulary for sessions. Leave at level of meeting organizers.
Ken: Were workshop #s OK? Greg: tension between attendance at all and overall #. Only 4 turned down. Suzy: there is a space issue also.

Appendix

Table 1. 2015 Drosophila Meeting Session Co-Chairs

Category	Co-chairs
Cell biology and Cytoskeleton	Rodrigo Fernandez-Gonzalez, University of Toronto, Ontario Denise Montel, University of California, Santa Barbara
Cell biology & Signal Transduction	Utpal Banerjee, University of California, Los Angeles Andrew Zelhof, Indiana University, Bloomington
Cell cycle and Cell Death	Bruce A. Edgar, DKFZ & Center for Molecular Biology, University of Heidelberg, Germany Masayuki Miura, The University of Tokyo, Japan
Cell Division and Growth Control	Giovanni Bosco, Geisel School of Medicine at Dartmouth, Hanover, NH Nic Tapon, Cancer Research UK London Research Institute, UK
Physiology, Organismal Growth, and Aging	David Walker, University of California, Los Angeles Joanna Chiu, University of California, Davis
Gametogenesis and Organogenesis	Lan Jiang, Oakland University, Rochester, MI Erika Matunis, Johns Hopkins University, Baltimore, MD
Stem cells	Todd Nystul, University of California, San Francisco Tony Ip, University of Massachusetts Medical Center, Worcester
Immunity and Pathogenesis	Neal Silverman, University of Massachusetts, Medical School, Worcester Nicolas Buchon, Cornell University, Ithaca NY and Joanna Chiu, University of California Davis
Neural Development	Cheng-Yu Lee, University of Michigan, Ann Arbor Oren Schuldiner, Weizmann Institute, Rehovot
Neurophysiology and Behavior	Coral Warr, Monash University, Clayton, Australia John Ewer, Universidad de Valparaiso, Chile
Drosophila Models of Human Diseases	Tom Lloyd, Johns Hopkins University School of Medicine, Baltimore, MD Sheng Zhang, University of Texas Health Science Center, Houston Erika Bach, NYU School of Medicine, New York Renee Read, Emory University, Atlanta, GA
Evolution and Quantitative Genetics	Patricia Beldade, Instituto Gulbenkian de Ciência, Portugal Erin Kelleher, University of Houston, TX Mariana Wolfner, Cornell University, Ithaca, NY Susan Lott, University of California, Davis
Pattern Formation	Marek Mlodzik, Mt. Sinai School of Medicine, New York Zeba Wunderlich, University of California, Irvine
Regulation of Gene Expression	Sarah Bray, University of Cambridge, England Melissa Harrison, University of Wisconsin, Madison Ali Shilatifard, Northwestern University, Feinberg School of Medicine, Chicago, IL Tiffany Cook, Cincinnati Children's Hospital Medical Center, OH
Chromatin and Epigenetics	Felice Elefant, Drexel University, Philadelphia, PA Xin Chen, Johns Hopkins University, Baltimore, MD
RNA Biology	Mitzi Kuroda, Harvard Medical School, Boston, MA Nelson Lau, Brandeis University, Waltham, MA
Techniques and Resources	Guanjun Gao, Tsinghua University, Beijing Kate O'Connor-Giles, University of Wisconsin, Madison

Table 2. Platform Session Planning: Abstracts, talk requests, allocated talks & success rate

Session	Abstracts	Posters	Talks req.	% talk req.	Talks allocated	% of all abstracts	% of req. talks
Cell biology and Cytoskeleton	82	67	52	63	15	18	29
Cell biology & Signal Transduction (I & II)	49	42	27	55	7	14	26
Cell cycle and Cell Death	30	23	18	60	7	23	39
Cell Division and Growth Control	54	46	42	78	8	15	19
Physiology, Organismal Growth, and Aging (I & II)	66	54	34	52	12	18	35
Gametogenesis and Organogenesis	51	43	20	39	8	16	40
Stem cells	35	28	17	49	7	20	41
Immunity and Pathogenesis	23	19	12	52	4	17	33
Neural Development	46	38	18	39	8	17	44
Neurophysiology and Behavior (I & II)	77	63	38	49	14	18	37
Drosophila Models of Human Diseases (I and II)	109	95	44	40	14	13	32
Evolution and Quantitative Genetics (I + II)	100	86	44	44	14	14	32
Pattern Formation	27	23	20	74	4	15	20
Regulation of Gene Expression	71	64	28	39	14	10	25
Chromatin and Epigenetics	51	44	22	43	7	14	32
RNA Biology	24	20	11	46	4	17	36
Techniques and Resources	36	28	17	47	8	22	47

3. Treasurer's Report (Debbie Andrew)

MEETING REVENUES AND EXPENSES 2012-2015 (ESTIMATE)

	Chicago 2012	Wash DC 2013	San Diego 2014	Chicago Budget	Chicago Est
REVENUE					
Registration Fees	$293,130	319,904	307,272	320,950	340,000
Sponsorships	0	4,000		4,000	1,000
Hotel Rebates		16,145	0	0	0
Exhibit Fees	34,900	33,000	43,034	45,000	41,530
Miscellaneous (t-shirts, etc.)	5,555	5,452	5,011	5,000	3,500
	$333,585	378,501	355,317	374,950	386,030
EXPENSE					
Salary, Payroll Tax and Benefit	$65,276	74,719	72,735	76,000	76,000
Printing/Mailing/Promotion	9,864	8,763	15,880	13,600	15,000
Education					
Receptions and Catered Events	154,106	152,425	121,311	147,000	160,000
Posters/Exhibits	18,993	22,408	20,821	24,000	22,000
Supplies/Duplicating/Signs	357		3,497	2,600	3,000
Hotel and Travel	7,401	3,369	2,533	7,500	7,500
Audio Visual Services	77,469	59,165	57,461	66,000	70,000
Other Contracted Services	8,760	6,862	5,895	6,300	6,000
Awards	26,000	6,000	6,000	6,000	6,000
Telephone/Internet/Fax	8,919	7,557	3,824	8,000	8,000
Credit Card Fees	12,485	9,507	9,198	9,000	10,000
Insurance, Promotion, etc.	5,856	2,389	7,359	9,200	8,000
Overhead	19,583	22,416	21,821	22,800	22,800
	$415,069	375,580	348,335	398,000	414,300
NET GAIN (LOSS)	($81,484)	$2,921	$6,982	($23,050)	($28,270)

Table 2: Summary of income and attendance since 2010

Meeting Year	Location	Net Income	Fund Balance*	# Meeting Attendees
2010	Washington, DC	27,082	261,359	1,668
2011	San Diego	64,471	325,830	1,541
2012	Chicago	(81,484) (Includes 20,000 to Sandler and 6,000 to Finnerty Finnerty)	244,346	1,537
2013	Washington DC	$2,921	**$247,267**	1,555
2014	San Diego	$6,982	$253,282	1,431

- The GSA Board (Sept. 2003 meeting) established a required *minimum* reserve fund of one-half of the meeting expenses. No cap figure stated.
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- **MEETING ATTENDANCE**

Pre-registration 2015 (Chicago, IL):	1,496	$313,373
Total registration (estimate) 2015:	*1,530*	*$340,000*
Pre-registration 2014 (San Diego, CA):	1,335	$274,642
Total registration 2014:	1,431	$307,272
Pre-registration 2013 (Washington, DC):	1,403	$268,795
Total registration 2013:	**1,555**	**$319,904**
Pre-registration 2012 (Chicago):	1,367	$234,928
Total registration 2012:	**1,537**	**$293,130**
Pre-registration 2011 (San Diego, CA):	1,328	$243,004
Total registration 2011:	**1,541**	**$307,237**
Pre-registration 2010 (Washington, DC):	1,529	$261,246
Total registration 2010:	**1,668**	**$306,393**
Pre-registration 2009 (Chicago):	1,383	$256,800
Total registration 2009:	**1,506**	**$294,266**
Pre-registration 2008 (San Diego) :	1,343	$214,856
Total registration 2008:	**1,447**	**$281,093**
Pre-registration 2007 (Philadelphia):	1,345	$234,000
Total registration 2007:	**1,507**	**$288,067**
Pre-registration 2006 (Houston):	1,241	$222,165
Total registration 2006:	**1,402**	**$274,350**
Pre-registration 2005 (San Diego):	1,451	$264,440
Total registration 2005:	**1,515**	**$297,750**
Pre-registration 2004 (Wash DC)	1,470	$266,110
Total registration 2004:	**1,617**	**$313,645**
Pre-registration 2003 (Chicago):	1,488	$256,130
Total registration 2003:	**1,603**	**$283,270**
Pre-registration 2002 (San Diego):	1,219	$211,000
Total registration 2002:	**1,552**	**$290,170**
Pre-registration 2001 (Wash DC):	1,372	$240,240
Total registration 2001:	**1,627**	**$297,915**

Table 3: Summary of Sandler fund expenses

Year	Investment Gain/transfers	Travel expenses	Supplies/ Mailing expenses	Net Income	**Balance**
2001				(234)	31,654
2002				(846)	30,808
2003				(2,431)	28,377
2004				432	28,809
2005	1076	1,208	37	(169)	28,640
2006	1963	469	15	1,479	30,119
2007	2187	501	15	1,671	31,790
2008	-859	441	20	(1,320)	30,470
2009	1198	768		430	30,900
2010	947	1,482		(555)	30,345
2011	555	420		135	30,480
2012	23,821*	826		22,995	53,475
2013	6,847	1,171		5,676	59,151
2014	4,865	580	0	4,285	63,436

*includes $20,000 transfer from meeting fund

Ken: Sandler funds are doing well, future boards should think about this. What is the appropriate level of Sandler funds to keep to maintain award, as economy goes up and down? Maybe redirect a bulk of funds to Finnerty endowment? Alternatively, give out a Sandler Undergraduate Travel Fellowship?
Action item: GSA/Adam to estimate endowment balance required to generate $1200 annually to support Sandler lectureship. Board will consider in future what to do with difference, including building Finnerty endowment.
Resolution: since investment returns are unpredictable, Board will evaluate availability of Sandler Funds for other purposes on a year-by-year basis. For this year, use of funds for undergraduate travel (see below) are consistent with the mission of the Fund.

4. Sander Award Committee 2014-15 Report (Erika Bach)

Committee members
Erika Bach, NYU School of Medicine (Chair)
Daniela Drummond-Barbosa, Johns Hopkins School of Public Health
Wes Grueber, Columbia University
Artyom Kopp, University of California, Davis
Louisa Wu, University of Maryland, College Park

Chair 2015-16
Daniela Drummond-Barbosa, Johns Hopkins School of Public Health

Total 2014 Nominees: 22
Total Male Nominees: 10 Total Male advisors: 14 (one applicant had 2 mentors, both male)
Total Female Nominees: 12 Total Female advisors: 9

Winner: Zhao Zhang (currently at Principal Investigator/Staff Associate at the Carnegie Institution for Science). Dr. Zhang's graduate work (with Phil Zamore and Bill Theurkauf at UMasaMed) characterized the mechanisms piRNA biogenesis and transposon silencing in *Drosophila*. His thesis work focused on how germ cells differentiate piRNA precursor from mRNAs for piRNA biogenesis and the heterotypic Ping-Pong mechanism between Aub and Ago3.

Runners up:
Feng Chen, formerly in Mark Krasnow's lab at Stanford.
Zhihuan Li, from Michael Welte's lab at University of Rochester.

2014 Applicants

Nominee	**Gender**	**Mentor**	**Gender**
Barton, Lacy	F	Pam Geyer	F
Bosch, Justin	M	Iswar Hariharan	M
Chakrabarti, Sveta	F	Bruno Lemaitre	M
Chen, Feng	F	Mark Krasnow	M
Chrostek, Ewa	F	Luis Teixeira	M
Depetris Chauvin, Ana	F	Fernanda Ceriani	F
Durham, Mary	F	Jeff Leips	M
Ellis, Stephanie	F	Guy Tanentzapf	M
Herszterg, Sophie	F	Yohanns Bellaiche	M
Khadilkar, Rohan	M	Maneesha Inamdar	F
König, Annekatrin	F	Halyna Shcherbata	F
Li, Zhihuan	M	Michael Welte	M
Ma, Xianjue	M	Lei Xue	?M
Merino, Marisa	F	Eduardo Moreno	M
Moy, Ryan	M	Sara Cherry	F
Oliveira, Marisa	M	Christen Mirth	M
Schulman, Victoria	F	Mary Baylies	F
Spracklen, Andrew	M	Tina Tootle	F
Staller, Max	M	Angela DePace	F
Tran, Vuong	M	Xin Chen	F
Younger, Meg	F	Graeme Davis	M
Zhang, Zhao	M	Phil Zamore and Bill Theurkauf	both M

Erika: recommends committees continue to read reports about potential for gender bias. Also, concern about disparity amongst applicants. Since the eligibility was extended past one year, some get to be considered 2x, others only 1x. Also, selection of winner included work published after initial submission/thesis. Committee for perhaps past several years has not read complete theses; decision based on thesis abstracts, CV, letters of recommendation.

Action item: *Erika to consult with past committee members/chairs and write a report on suggested rules and guidelines (e.g. revise period of eligibility, how many theses to read, notification of non-winners), to be approved by Board in consultation with Scott Hawley. David will contact Scott.*

Resolution: Guidelines for future Sandler Award committees:

Larry Sandler Award Guidelines:
"For the most outstanding Ph.D. dissertation submitted this year in an area of Drosophila research"

1. Call for Nominations: GSA/Suzy Brown puts out a call for nominations in early Fall for a November 15 deadline.
2. Eligibility: For the Award presented in year X, any student completing a Ph.D. in an area of Drosophila research between July of year X-2 and December of year X-1 is eligible and may be nominated by his/her thesis advisor. The completed thesis must be available by Dec. 15. **A student may be nominated only once**.
3. Documents required: Nominations must include curriculum vitae, a thesis abstract of one or two pages, and a letter of nomination from the thesis advisor rolled into a single pdf file and emailed to the Chair.
4. Selection of Chair of the Committee: The Chair of the previous year's committee asks one member of the committee to serve as the next Chair.
5. Selection of the Committee: The Chair selects members of the committee who have demonstrated expertise in a particular area of Drosophila research. It is recommended that the committee have 4 or 5 members including the Chair. It is suggested that the areas of expertise represent neuroscience, stem cells, evolution, immunity and growth control/patterning. Other areas of expertise are also acceptable and a committee member may be an expert in several areas. While no particular rank (assistant, associate, full professor is required), the committee member should have experience in training graduate students. It is also suggested that the committee contain both male and female members.
6. Recommended reading for the committee: To be aware of gender-bias, the Chair should suggest to the committee that Amy Bejsovec's Presidential Report on Gender-bias be read as well as Carnes et al Journal of Women's Health Volume 14, Number 8, 2005 "NIH Director's Pioneer Awards: Could the Selection Process Be Biased against Women?". These documents should be emailed to the committee members and also provided in the dropbox where the Chair uploads the application.
7. Reviewing the applications: Soon after the November 15 deadline, the Chair should upload the applications to a dropbox (or similar type of shared folder). It is suggested that the Chair create a document containing the name and gender of the applicant and the name(s) and gender(s) of the nominators and that this file is shared with the committee at the outset.
8. Selection of 3-4 top candidates whose dissertations will be read by the committee. Soon after the Nov 15 deadline, the Chair should set a date for each committee member to email her/his top 5 candidates to the Chair. A suggested date for this deadline is December 15.

9. Review of the dissertations: The Chair will contact the mentors of the top 3-4 candidates and obtain a pdf file of the dissertation. The dissertations will be distributed amongst the committee members for review over the winter holidays.
10. Selecting a date for a skype conference call to decide the winner and 2 runners-up. In mid-December, the Chair will use a doodle (or similar) poll to pick a date when the committee members can participate in a skype conference call to select the finalists. This should occur in early or mid-January as a decision should be made no later than mid-January.
11. In the event that a student defended a significant period of time before the deadline, for example, 12-15 months, and/or if the student remained in the mentor lab for a short postdoc, and had publications post-defense, the Chair may contact the mentor for clarification of what parts of the paper(s) were produced during graduate training.
12. The Chair emails Suzy Brown and FlyBoard President the names of the Winner and Runners up.
13. Notification:
    a. The Chair emails the Winner and her/his mentor(s) that s/he has won the Sandler Award, including the details of when the lecture will take place.
    b. The Chair emails the Runners-up and their mentor.
    c. The Chair emails the mentors of the applicants who were not selected as finalists. This courtesy is much appreciated by all involved.
    d. Suggested formats for the email content are below.
14. The Chair writes a report on the Sandler committee, the applicants, genders of applicants and nominators, the finalists and sends this to the FlyBoard President. A suggested format is below.
15. The Chair asks one of the Committee members to be the Chair of the following year's committee.
16. The Chair makes every attempt to attend the Fly Meeting and arrive in time to present the Sandler Award on the first evening. If the Chair cannot attend the meeting, s/he asks one of the committee members to present the award. If this is not possible, the FlyBoard President presents the Award.
17. The Chair will be invited to present the report at the FlyBoard meeting, which usually occurs on the afternoon of the first day of the Fly Meeting, typically from 3-6 pm with the Sandler report occurring at ~3:30 pm.
18. Suzy Brown has helped with making PPT slides for the presentation. It is suggested that the first slide have the names of the Runners-up and the committee members. The second slide should contain a photo of the winner with her/his name (provided by Suzy).

5. Victoria Finnerty Undergraduate Travel Award (Alexis Nagengast)

Report to the North American Drosophila Board, March 4, 2015, Chicago
Alexis Nagengast, Chair of Victoria Finnerty Undergraduate Travel Award Committee

This year we received 52 applications for the Victoria Finnerty (VF) Undergraduate Travel Award and funded the top 6 for a total of $4705 (awards ranged from $590-1000). The awardees are:

- Jonathan Cohen (Poster #463C), Swarthmore College, $1000
- Alexander Kneubehl (Poster #835C), Ohio Northern University, $750

- April Kong (Poster #586C), York University, $735
- Meera Namireddy (Poster #467A), Rice University, $830
- Irina Pushel (Poster #799C), Michigan State University, $590
- Anna Zeidman (Poster #874C), Brown University, $800

We respectfully request that you stop by their posters to show your support for undergraduate research.

This year we had $9,000 in the fund with $6,000 from the Drosophila board and $3,000 from Mike Finnerty. Last year, the Drosophila board specifically mentioned that the committee should not spend all of the money, so that we can build up the fund instead of spending it out every year. Our intent was to spend no more than $6,000 and we spent $4705, leaving a reserve of $4295.

We have been talking to Beth Ruedi at the GSA about ways to fund raise. Several of us remembered a conversation we had at the 2014 board meeting that suggested that a line be added to the Drosophila registration form asking people if they would be willing to donate money to the VF Award. We thought that the line on the form should specifically state that it is an undergraduate travel award and suggest the amount $5, $10 and other. The thought was that if we ask a small enough amount, all 2000 registrants may donate.

This year's selection committee was Helen Salz (chair), me (PUI Drosophila board representative), Janis O'Donnell (who knew Victoria Finnerty), Matt Wawersik and Jim Erickson. I will be taking over for Helen Salz as the chair of the selection committee and we will need two new members to replace outgoing members Helen Salz and Janis O'Donnell.

ACTION ITEMS

1. We propose to name ONE of the undergraduate travel awards given each year the Victoria Finnerty Award. Others, supported by the board, could be Drosophila board undergraduate travel awards.

2. We propose that we establish a mechanism for people to donate money for an undergraduate travel award on the Drosophila registration form. This can be given "in honor of" or "in memory of" someone and we think it will be better for fundraising if people can give to honor someone they know. We envision that at some point in the future we could have an endowment, with several "named" awards for undergraduates to attend the fly meeting.

3. We request that the Drosophila board supports undergraduate travel awards again next year with a budget allocation of $6000.

Action item: *GSA/Adam will implement a way to bill donations to the Finnerty fund (and T-shirts etc.) separately from registration fees before next meeting –this is important for appropriate grant reimbursement. This previous action item did not get done last year; it should be done this year in time for meeting registration.*

Action item: *GSA/Adam will determine a $ amount that, through a one-time donation, would be sufficient to sustainably endow additional (named) travel awards. When this number is known, it will be communicated to the fly community via Fly News.*

Resolution: $30,000 endowment is estimated to generate $1000 return, but a $20,000 endowment with a $750 return may be sufficient for most years/cases. If shortfall is not large, the Board can supplement these Awards as they currently do to Finnerty fund.

Action item: The Board voted to transfer $6000 from the general funds to the Finnerty fund for next year, with the hopes that part will go towards endowing the fund.
Resolution: Approved 3/13.

Action item: The Board also approved in principle the use of Sandler Funds to sponsor a Sandler undergraduate travel award, contingent on consultation with Scott Hawley (David will contact).
Resolution: As long as Sandler funds permit, the Finnerty committee will select one undergrad applicant to receive the 'Larry Sandler Undergraduate Travel Award'. Applicants whose work focuses on genetics would be particularly appropriate.

6. Primarily Undergraduate Institutions (Alexis Nagengast)

Report to the North American Drosophila Board, March 4, 2015, Chicago

The Primarily Undergraduate Institutions (PUI) representative continues to work with Beth Ruedi, GSA Director of Education and Professional Development, to implement initiatives at the Drosophila conference to help make the Fly Meeting a productive and positive experience for undergraduate students and their professors/Pis. Activities at this year's meeting include:

- New: Undergraduate Student Mixer at breakfast on Thursday morning before Plenary Session I
- Education Special Interest Group Mixer for faculty interested in pedagogy on Wednesday night
- "Genetics Conference Experience" program for invited students from local institutions and their professors during Plenary Session I on Thursday morning
- Undergraduate Plenary for undergraduate researchers attending the meeting on Friday afternoon. This year's speakers will be Nadia Singh from North Carolina State University and Brian Calvi from the Indiana University Bloomington and Wendi Neckameyer. Additionally there will be a graduate student panel discussing the process of applying to graduate school and the life of a graduate student.
- Drosophila Research and Pedagogy at Primarily Undergraduate Institutions Workshop on Saturday evening. There will be four 15 minute talks from undergraduate researchers followed by break out sessions on pursuing a career at a PUI, pedagogical methods that include *Drosophila* and discussions of professional issues that affect PUI faculty.
- Reduced registration fees for undergraduates

This was the third year that the PUI representative served on the selection committee for the Victoria Finnerty Undergraduate Travel Award for the Drosophila Conference.

There are a few concerns from PUI faculty about being able to attend both Fly Meetings in Orlando (July 2016) and San Diego (March 2017). Our institutional travel funds typically cover one meeting per academic year which runs from July 1, 2016 to June 30, 2017. Both meetings fall in the same academic year and many PUI faculty will have to choose between the two.

7. IMAGE AWARD COMMITTEE (David Bilder)

This year's competition had 51 total submissions, including 11 videos.

The winners this year were :

Salil Bidaye, for his video displaying 'moonwalking' flies generated through identification of neurons for backward walking.

Gerit Linneweber, for his image revealing tracheal remodeling on the intestine in response to nutrition

The runner-ups were:

Oguz Kanca, for his video using 'Raeppli' multicolor clonal labeling to visualize wing eversion *in vivo*.

Pauline Speder, for her video showing how calcium oscillations relay nutritional information across the blood-brain barrier.

Michelle Arbeitman will make the Award presentation at the meeting.

8. REPORT OF THE GSA SENIOR DIRECTOR (Suzy Brown, CMP)

56th ANNUAL DROSOPHILA RESEARCH CONFERENCE

As you can see from the information in the treasurer's report, I am anticipating a loss of approximately $28,000. While attendee revenue is slightly over budget, exhibit fees and sponsorship is slightly down. The reserves are still strong and can handle the loss but **we will need to continue to increase registration costs to keep up with rising costs and years of unchanged registration fees**. Currently the highest early registration fee is only $21 more than the cost of a double sleeping room for one night so these slight increases should not cause much, if any, impact on registrations.

Registration:

The total registration number for 2015 as of February 16 is 1,507. This number is up 12% from last year.

Hotel Rates and Pick-up:

While attendance is up from last year, our sleeping room pickup is down. My best guess is that people may be staying elsewhere or not going through the meeting booking system. I have asked the hotel to check our registrant list to their guest list. Our pickup is important not only because cost-saving concessions are tied to it but there is the possibility that we would have to pay an attrition fee if we dip below 80% of our contracted block. Normally we are at 95% or more of our contracted block. This year we are just under 80% at this point. Something that all planners continue to have challenges with is the constantly changing pricing available on the Internet. While we are protected to some degree by adding a contractual clause that makes sure the hotel counts anyone in the hotel that did not go through the meeting website but are attending our meeting, we currently have no control over those who decide to stay elsewhere. Many groups have begun to charge a higher amount to those who do not stay at the contracted hotel.

FUTURE CONFERENCES

Dates and rates have been confirmed through 2020. Detailed below is the schedule for the next five years:

2016 – 57th Annual Drosophila Research Conference: July 13-17, Orlando Marriott World Center. $135

2017 – 58th Annual Drosophila Research Conference: March 29-April 2, The Town and Country Resort and Hotel, San Diego, CA. $166/$176/$186.

2018 – 59th Annual Drosophila Research Conference: April 11-15, Philadelphia Marriott. $219

2019 – 60th Annual Drosophila Research Conference: March 27-31, Sheraton Dallas. $199.

2020 – 61st Annual Drosophila Research Conference: March 25-29, The Town and Country Resort and Hotel, San Diego, CA. $174/$184/$194.

Registrations – 2015

	Number	Amount
Faculty/Lab Tech Members	446	$123,616
Faculty/Lab Tech NonMembers	78	$37,272
Postdoc Members	163	$39,833
Postdoc Nonmembers	65	$26,194
Grad Student Members	408	$50,088
Grad Student Nonmembers	104	$25,724
Undergrad Members	140	$6,045
Undergrad Nonmembers	25	$2,971
Complimentary	78*	0
Early/Regular	**1,507**	**$318,917****

***Exhibitors, plenary speakers, organizers, Larry Sandler Award Winner**

****Additional $7,174 revenue from t-shirt and luncheons**

Registrants by Country

United States	1178	South Korea	7
Canada	67	India	6
United Kingdom	38	Turkey	5
France	27	Belgium	4
Germany	26	Brazil	4
China	23	Chile	3
Japan	23	Denmark	3
Switzerland	14	Italy	3
Taiwan	12	Singapore	3
Israel	10	Czech Republic	2
Austria	9	Portugal	2
Mexico	9	Colombia	1
Spain	9	Norway	1
Australia	8	Puerto Rico	1
Sweden	8	Romania	1

Total number of countries: 303 for 1,507 registrants
Suzy: trainee registration prices are particularly low, and 65% of attendees are trainees. We may need to couple registration fees to occupancy of sponsored hotel ('discount' for staying at this hotel). Consider raising prices in future years. While registration prices in 2016 will be higher, overall cost to attend will be lower due to significantly lower hotel cost. She doesn't anticipate much of an increase for 2017 but will adjust fees according to actual, anticipated expenses.

9. 2016 & 2017 Fly Meetings Update (David Bilder, Adam Fagen, Suzy Brown)

2016 Meeting Organizers (within Allied Genetics Conference)
Sue Celniker, David Bilder, Nancy Bonini, and Ross Cagan
-Change in venue (Orlando, Florida),
-Change in dates (July 13-17)
-Change in format (multi-organism meeting).
-Shared keynotes:
Drosophila keynote speaker will be Amita Sehgal

2017 Meeting Organizers
Leanne Jones, Amy Kiger, Claude Desplan, and Doris Bachtrog

Suzy: mostly the same meeting in Orlando except for joint plenaries, also sessions on similar topics will be scheduled so that they are not overlapping. There will be some recording and on-site viewing, with further web distribution at the discretion of presenters.
Allan, Debbie, David: encourage other crosstalk between model organism communities. Rare opportunity, take advantage of it to bring together fragmented community as a single group with shared interests. Joint workshops may be one easy way.
Action item: Allan, David share ideas for promoting crosstalk with other communities with Suzy.

10. Drosophila Board Election Report (Mike O'Connor)

The Election committee consisted of Mike O'Connor (Chair), Claude Desplan (continuity from 2014), Anthea Letsou, and Kristi Wharton. Positions open included President Elect and regional representatives for the Midwest and Canada. The committee assembled a list of candidates including suggestions solicited from the outgoing representatives and previous nomination lists and then selected two candidates along with a backup candidate for each position. In choosing candidates, we considered previous involvement in the fly community, our sense of their level of responsibility, career level (preference for mid or early), institutional and gender balance. The chair contacted the candidates and all accepted the nomination. The chair asked the candidates to submit a short biographical paragraph to be included on the ballot. FlyBase set up a SurveyMonkey website to facilitate voting and vote counting and sent an email (appended below) and a reminder email to Drosophila researchers to encourage voting. A total of 557 votes

were cast for President, with slightly fewer votes for the regional representatives.

Year	Votes	Regions up for election
2015	557	Midwest, Canada
2014	530	Northwest, Southeast, Heartland, Great-Lakes
2013	594	Mid-Atlantic, California, Oceania, Asia, Europe
2012	466	Midwest, Heartland, Canada
2011	361	Northeast, southeast, New England, Great Lakes
2010	355	California, Mid-Atlantic, and Primarily Undergraduate Institutions

The elected individuals were:

President elect:	Laura Johnston
Midwest	Bing Zhang
Canada	Esther Verheyen

We want to bring attention to several issues relevant to future elections. As was done in 2014 elections were held early– voting opened on October 14, one reminder was sent on November 6 and closed on December 5. This time frame is longer and earlier than years prior to 2014 and appears to be working well since voter participation has been strong in the past couple of elections. We recommend keeping this time frame in the future. Second, we felt that the biographical paragraphs, which were instituted two years ago, are a valuable addition to the process and should be continued.

Email sent announcing opening of Voting

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

http://flybase.org/static_pages/news/board_whitepapers.html

This year we are electing the President-elect, who will serve as President starting with the fly meeting in 2016. We are also electing representatives for the Midwest and Canadian regions, who will all serve 3-year terms starting with the fly meeting in March 2015.

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:

https://www.surveymonkey.com/s/2015FlyBoardElection

Please remember **you may vote for candidates in ALL categories** even though you do not reside in the region represented by the candidates.

Balloting will end **December 5th, 2014**.

Thank you,
Drosophila Board Election Committee
Michael O'Connor
Claude Desplan
Kristi Wharton
Anthea Letsou

11. Proposed redistribution of Board election cycles (O'Connor/Bejsovec)

There is a lot of variation in the board member turnover rate from year to year. Some years, such as in 2015, only two representatives (+ President) were up for election, while in 2016 there will be 9 openings – Treasurer, California, New England, Mid-Atlantic, Undergrad Institution rep, and all International reps.

Current elected Board Positions (aside from President)

Term ends 2015
Canada - Laura Nilson
Midwest - Seth Blair

Term ends 2016
Treasurer - Deborah Andrew
California - Angela Stathopoulos
New England – Giovanni Bosco
Mid-Atlantic – Jessica Treisman
Primarily Undergraduate Institution – Alexis Nagengast
Australia/Oceania – Gary Hime
Asia – Shigeo Hayashi
Europe - Daniel St. Johnston
Latin America - Mariana Melani

Term ends 2017
Great Lakes Scott Barolo
Mountain Sarah Certel
Southeast Andrea Page-McCaw
Heartland Michael Galko

Term ends 2018
Midwest representative: Bing Zhang
Canadian representative: Esther Verheyen

The elections committee felt that this much turnover in one year might disrupt board continuity. One idea is to ask a few of the present reps to serve one additional year so that future turnover is more even.

Action Item:
1. Request board approval to extend the term of some currently serving board members
2. Identify board members willing to serve for 1-2 extra years

A possible solution:
Shifting 4 members from 2016 to 2017, and 3 members from 2017 to 2018, would result in an even distribution of 5/5/5.
- Identify 3-4 board members whose terms expire in 2016 who would be willing to serve an extra year.
- Identify 2-3 board members whose term expires in 2017 who would be willing to serve an extra year.

Board approves extension of representative terms. Volunteers will contact Ken.
Term currently ends 2016, shift to 2017
Gio Bosco
Debbie Andrew
Gary Hime
Alexis Nagengast

Term currently ends 2017, shift to 2018
Michael Galko
Scott Barolo
Andrea Page-McCaw

12. Identifying members of the Fly Community (Bilder)

I wanted to briefly raise the point of identifying our community. The Board is here to serve the community, but we have an imperfect sense of who that is. The major way we disseminate important information is via email lists; knowing the number of fly researchers is also relevant for outreach and advocacy efforts. It is worth thinking how we could improve the currency of these.

At the moment, our main email list for communications comes from self-registration as a Fly Person at Flybase. But there's no prompt or real reason to do this. I suspect that a lot people who have joined the field recently, especially as junior researchers, have not done so, and may not even know about it.

I'd like to hear suggestions about ways to encourage more registration.

-Announcement at the opening session of fly meeting?
-add 'Register as a Fly Person' slide to the between-sessions rotation?
-do the above at the European fly meeting also?
-add a prompt during the process of Fly Meeting Registration? (option to automatically add info to Flybase)
-send an email to PI mailing list (from Fly People and/or Bloomington list) encouraging lab members to register?

Relevant info (from Thom, Kathy, Suzy)

Flybase list: **3011** (1366 US, 1645 overseas)
GSA fly meeting mailing list: **9195** (deduped past registrants + current Flybase)
BDSC: **2999** accounts (81% ordered stock since 1/1/2012)
'PI or lab head' in Flybase: **1760**
FlyBase Community Advisory Group: **550 (**recent call to designate 1 member/lab)

[as an aside, voting in recent elections has been ~400-600. By comparison per Adam, GSA election voting and other GSA communities has 20-40% participation.)

Suggestions: add species center email list, DIS list. De-dup with Suzy's list. Either invite everyone to register, or just PIs/Account holders to ask their lab to register. Explain why it's important, what it will be used for, what impact it will have.
Action item: David will look into methods to encourage FlyPerson registration updates during coming year.

13. Advocacy & Communications (Irvine, Page-McCaw, Bilder, Aiyar)

The necessity of communicating the important and ongoing contributions of *Drosophila* research – to the general public, politicians, funding agencies, and fellow scientists – has been an ongoing concern. Members of an ad hoc Communications Committee (Irvine, Page-McCaw, Bilder, Galko, Nilson) discussed ways to respond to criticism of Drosophila research by a US Senator, and discussed strategies to communicate the value of *Drosophila* research more broadly. We are also fortunate to have some individual members of the fly community forcefully defending Drosophila research (Thanks to Hugo Bellen for his article in Genetics & contacting NIH program officers) Nonetheless, it has been difficult for the fly community as a whole to transition from concern to action.

Proposed Action Items:

1. Establish a standing Drosophila Board Communications Committee

Rationale: The transient, ad hoc nature of previous committees has resulted in poor transfer of knowledge regarding what has been discussed and tried in the past, and made it difficult to progress from talking to action. It is hoped that having a more formal structure, and a more permanent structure, will enable the committee to be more productive.

Draft Motion to establish Fly Board Communications Committee

"Recognizing the growing importance of educating both governmental officials and the general public about the utility of Drosophila research and the importance of continued support for it, the Fly Board has established a Communications Committee. This standing committee consists of a Chair, who serves as an *ex officio* member of the Board, and 3-6 members, each serving a two or three year term. The Chair selects the members, oversees the committee activities, and files a report with the Board annually. Chairs serve a one year term as chair and nominate their successors, with approval of the Fly Board.

The goals of the Committee include:
- to advocate for Drosophila research in the press and in public, and to facilitate such advocacy for Drosophila researchers
- to disseminate advocacy information through media, including social media
- to manage a website educating non-specialists about the values of Drosophila research

- to assist the fly board in promoting rapid and authoritative community responses to arising events such as political commentary"

Membership of Drosophila Board Communications Committee
In order to accelerate the process of establishing said committee, the board Presidents (Irvine, Bilder) have identified members of the community willing to serve on the initial Communications Committee: Andrea Page-McCaw (Chair), Michael Galko, Gio Bosco, Stephanie Mohr, Gary Hime.

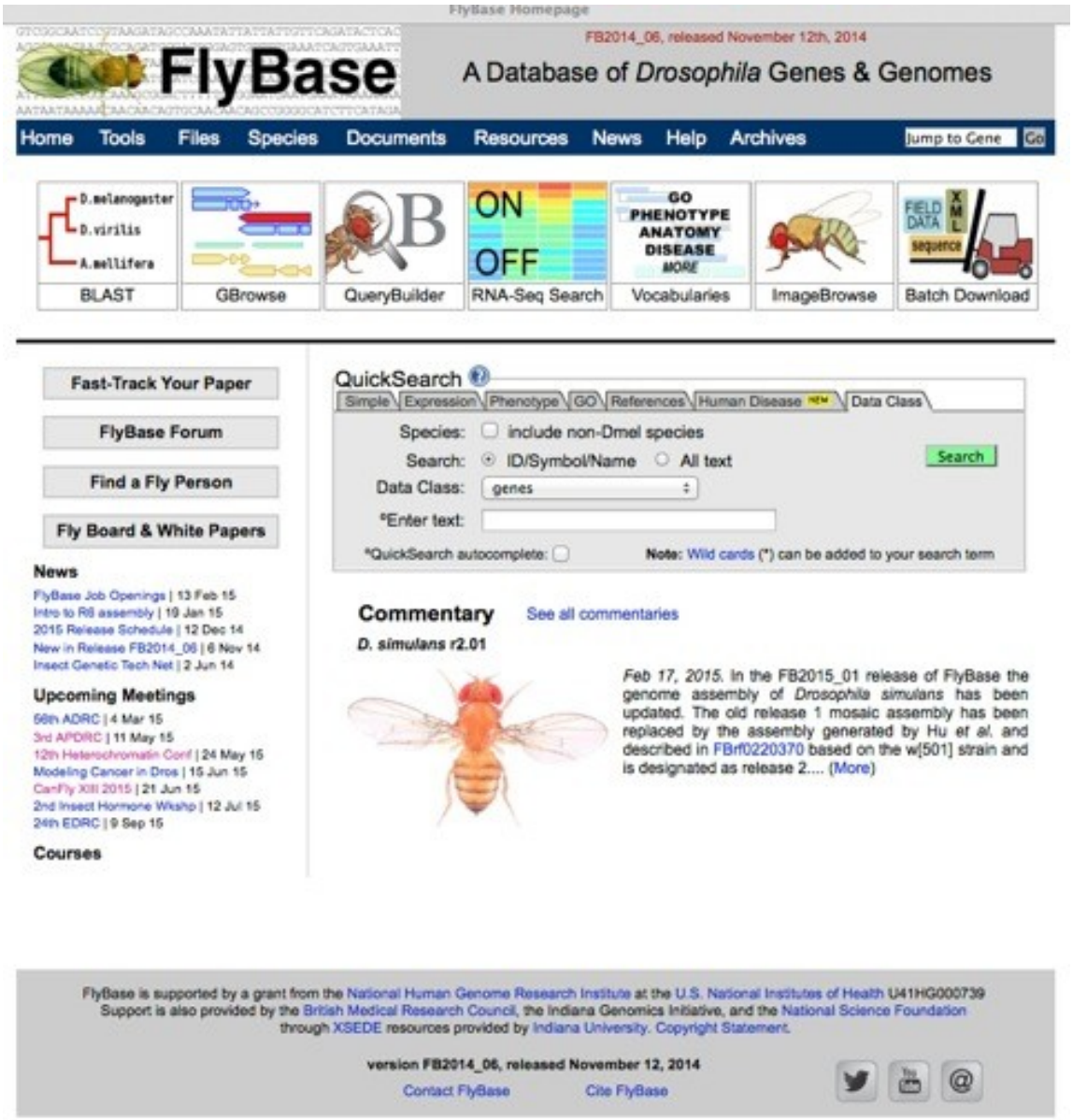
2. Drosophila advocacy web site
One idea that was discussed is to have a web site that would be controlled by the Drosophila board whose purpose would be advocacy for Drosophila research and whose target audience would be the general public/politicians/journalists. While there have been mixed opinions as to the effectiveness of a web site versus other forms of out reach, the board presidents agreed that this could be an effective supplement to various forms of outreach. It is envisioned that maintaining such a web site could eventually be part of the Communications Committee responsibilities, but for the first year at least it will be a separate task. David Bilder has agreed to take charge of overseeing this project. The GSA is interested in working together with us on this, they will host the web site, and Raeka Aiyar,(GSA Communications and Engagement Manager) will work together with David & other members of the fly community to put it together.

- Additional Point for general Discussion:
In response to a letter written by Hugo Bellen to some NIH Program Officers (co-signed by Irvine, Gelbart, and Kaufman) regarding the relative lack of funding of Drosophila grants at many NIH Institutes, Bob Finkelstein at NINDS asked " This leads to the question of what is causing the decline in funded fly grants? Do you think review is biased against such grants? That PI's are reluctant to submit them? I'm interested to know your interpretation of what's going on."

Overall approval for this item. Discussion from floor: expand website to other model organisms, also to issues that don't have to do with human health. Will people/press understand the website on their own? Have contacts. Allan: stable of knowledgeable people from our community who are ready to respond. Mike: website is chronic response, team is acute response. Ken, Debbie, Gary: reach out to Sean Carroll for video production with ideas to come out of communications committee. Angela: zebrafish heart commercials as a precedent for fly research. Greg: partner with ACS or someone who has supported fly biomedical research.

Hugo: his Perspective stimulated an active response from NIH Directors. They've asked him to join a meeting on model organisms and their funding.
Some discussion of importance of fly researchers reading fly grants.

14. FlyBase (Bill Gelbart)



MARCH 2015
FLYBASE REPORT TO THE DROSOPHILA BOARD

First, we want to express our gratitude to NHGRI for its long and deep support of FlyBase (continuously since August 1992), even in the current difficult funding climate. We continue to be committed to make FlyBase as cost-effective and valuable a resource as possible for the benefit of the Drosophila and broader biomedical research communities.

FlyBase will continue to play its role as the core genetic and genomic informatics repository for the major biomedical model, *Drosophila melanogaster*, and other species of the family Drosophilidae. We will continue to integrate information harvested from the literature along with high throughput data from large-scale data production centers and the major sequence data

archives. In this report, we will highlight a few of our accomplishments and initiatives since last year's report.

SOME HIGHLIGHTS: APRIL 2014 TO THE PRESENT

- **Migration to the Release_6 BDGP Assembly for *D. melanogaster.*** As of the FB2014_04 public release (July 21, 2014), the reference genome sequence for FlyBase was shifted to the BDGP Release_6 assembly. The reference gene model annotations and other data aligned to the genome were migrated to Release_6. The modENCODE RNA-Seq data were *de novo* mapped to the Release_6 assembly, which means that the newly assembled parts of the genome have aligned RNA-Seq data. However, many other datasets were simply lifted over onto Release_6 and the newly assembled parts of the genome are not represented in those datasets. We hope over time that most important datasets will be *de novo* aligned to Release_6.
- **Literature Curation.** About 2,500 research papers entered the FlyBase bibliography during 2014. All of these were triaged or fully curated, depending upon the kinds of information they contained. More than half (53%) of papers were triaged by authors using the "Fast Track Your Paper" tool. 1,131 papers were fully curated for genetic data and Gene Ontology (GO) terms. Tissue and temporal gene expression data were curated for 458 genes from 171 references leading to 1,269 new expression statements. 2,106 macromolecular interactions were curated from 201 papers for 979 distinct genes (868 proteins and 127 RNA).
- ***D. melanogaster* Gene Model Annotation:** Over 4,000 gene models were reviewed (2,953) or created (1,126) during 2014 (*D.* melanogaster annotation Release_5.55 to Release_6.03. This time period overlapped the end of our whole-genome sweep to review all gene models in light of new high throughput data, such as RNA-Seq coverage data, RNA-Seq junction data, and transcription start site data. Over 85% of new gene model annotations were for long non-coding RNA genes. Curators developed guidelines for annotation of new genes (not straightforward in regions of diffuse or low-level RNA-Seq signal), including criteria for annotation of coding vs. non-coding genes. Published predictions of new lncRNAs and genes encoding small polypeptides were also assessed, using all available data and applying the same guidelines and criteria. Availability of the new Release 6 genome sequence assembly allowed significant improvement of annotations in heterochromatic regions, especially on the Y chromosome.
- **Non-*melanogaster* Genomes and Gene Models.** The current gene models for the sequenced genomes of the 11 non-melanogaster species analyzed as part of the NHGRI-funded "12 *Drosophila* Genomes Project" date back to 2006 and are quite stale. For comparative analysis, including their ability to inform features on the *D. melanogaster* genome, it would be valuable to improve these annotations. FlyBase and NCBI have collaborated to upgrade these annotations, taking advantage of current *D. melanogaster* annotations and the availability of species-specific RNA-Seq data for the other species to improve the predictions of the NCBI GNOMON annotation pipeline. In addition, for one of the species, *Drosophila* simulans, which was kfnown to have severe assembly quality issues, a new assembly has been contributed to GenBank by Hu *et al.*, 2013. In FlyBase public release FB2015_01 (23 Feb 2015), the upgraded *D. simulans* assembly replaces the previous one, and new annotation sets are provided for *D. simulans*, *D. yakuba*, *D. erecta*, *D. ananassae* and *D. pseudoobscura*. In the following public release FB2015_02, the upgraded annotation sets for *D. willistoni*, *D. virilis* and *D. mojavensis* will be made available. The other three species will not be upgraded because of either low quality assemblies (*D. sechellia* and *D. persimilis*) or absence of RNA-Seq data (*D. grimshawi*).
- **Human Disease Model Curation:** This is now part of regular genetic literature curation at FB-Cambridge and has been visible on the website since the FB2014_02 release. As

of the FB2014_06 release, there are 2,778 disease annotations from 566 references, involving 1,753 alleles from 824 genes. Models of 146 different human diseases have been annotated (approximately two-thirds of which are of neurological diseases). As a separate effort, a new FlyBase report format that provides an integrated view of research in flies related to human health is being developed. These reports are designed especially to facilitate access by non-fly researchers, providing summaries, tables, and links. Our initial emphasis is on specific diseases (or disease sub-types) that are defined in OMIM with single causative genes. Major sections of the report: 1) Overview of Drosophila model; 2) Ortholog information; 3) Description of the disease in humans (symptoms, genetics, molecular information) and synonyms used; 4) Table of disease sub-types (if applicable; for example, there are 17 molecularly defined sub-types for Parkinson disease in OMIM); 5) Summary of experimental data in Drosophila; 6) Table of appropriate allele-level curation, including links to allele reports; 7) Genetic reagents; 8) References. To date, we have completed development of a prototype report format and initial data capture. The Harvard developers have completed development of the required database structures and data processing software. We have received feedback from a group of interested PI's that were asked to comment on mock-ups (using the prototype report format and data curated from literature). Based on this feedback, final changes to the report format are being implemented and we expect these reports to become public in mid-late 2015.

- **Curation and Display of Drosophila 'Gene Groups'**. FlyBase wants to improve its representations of how genes and their products relate functionally or evolutionarily to one another. As part of this, we are developing "Gene Group Reports." Related sets of genes or gene products, such as gene families, subunits of protein complexes or other functional groupings, are frequently described in the literature. We have been systematically compiling such 'gene groups' for the past 2 years, and plan to display these data as 'Gene Group Reports' in FlyBase in the coming months. These Reports will tabulate the membership of each group, clearly attributed to source references, together with buttons to export the member genes to FlyBase tools to facilitate further analyses. Gene Group Reports will also include a brief description of the group, links to parent/child groups within FlyBase, and links to orthologous groups available at external sites such as HGNC, WormBase and TAIR. Through doing this work and adopting a 'group' approach to curation, we have also been able to improve the consistency and accuracy of Gene Ontology annotations and nomenclature of related genes.
- **Community Feedback & Input:** The FlyBase Community Advisory Group (FCAG) was launched in September 2014 with the aim of gaining greater feedback from the community about changes in FlyBase. The group consists of representatives from any lab worldwide that uses FlyBase as part of its research, and in just 6 months we already have over 550 members from more than 40 countries. To date FCAG has helped us by responding to two surveys, on the usefulness of our automated gene summaries and the layout of our new gene group pages.

Respectfully submitted to the Drosophila Board,

Bill Gelbart, Harvard University
Thom Kaufman, Indiana University
Nick Brown, University of Cambridge (UK)
Maggie Werner-Washburne, University of New Mexico
Rich Cripps, University of New Mexico

Thom: NHGRI doesn't want to be sole support for model organism database. Looking for new funding model: other countries? Tithe other NIH institutes? Subscription? Flybase leadership attending meetings. 2.5 years left on Flybase grant.

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

Stock Holdings as of 2/11/2015

- 53,791 stocks with 56,544 unique genetic components
- 10,531 annotated *D. melanogaster* genes are associated with alleles or constructs in the collection

2014 Use Statistics

- 236,340 subcultures shipped in 13,739 shipments
- 6 orders per stock on average, range 0–153; 76% of stocks ordered at least once, 23% ordered 6 or more times, 13 stocks ordered >100 times, *nos-Cas9.P* (#54591) was the most popular
- 2,959 registered user groups, 1,876 of which ordered stocks
- 6,114 registered users, 3,106 of whom ordered stocks

Growth

4,899 stocks were accessioned in 2014:

- 755 Janelia Farm *lexA* drivers
- 1,208 Gene Disruption Project *Mi{MIC}* insertions
- 1,735 Transgenic RNAi Project stocks
- 157 gustatory receptor *GAL4* and odorant receptor (*A. gambiae*) *UAS* lines from John Carlson
- 100 X chromosome EMS lethals from Bellen *et al*.
- 89 *mir* knockout lines from Steve Cohen
- 66 multi-tagged protein lines from Kevin White
- 789 stocks from other donors

Staff now consists of 41 stockkeepers (21 full-time equivalents) and 6 managers/scientists.

Grant Funding We are in year 1 of a 5 year grant from NIH, $440,921 direct costs. Increased income from user fees is paying for growth of the collection.

Cost recovery Fees for 2015 were reduced by eliminating service charges for all account types.

New Stocks We expect to add 5,030 to 6,040 new stocks in 2015:

- 2,000-2,500 Transgenic RNAi Project lines
- 2,500 Gene Disruption Project insertions
- 30-40 X chromosome lethal mutations from Hugo Bellen
- 500–1,000 stocks in all categories from the community at large

Pruning We plan to discard several hundred older P insertions in 2015.

Scientific Advisory Board

- Hugo Bellen, Baylor College of Medicine (chair)
- Nancy Bonini, University of Pennsylvania
- Lynn Cooley, Yale University
- Susan Parkhurst, Fred Hutchinson Cancer Research Center
- Norbert Perrimon, Harvard Medical School

- Benjamin White, NIH, National Institute of Mental Health

Kevin: happy with current funding, 5 year grant.

16. Species Stock Center (Maxi Richmond & Therese Markow)

2015 Drosophila Species Stock Center Report, UC San Diego

- Stocks held: 1540
- Species represented: 228
- Registered Users: 1,525 (an increase from 1,423 in 2013)
- Shipped in 2014: 1,149 subcultures (covers 97% of species represented in collection) in 232 shipments (about the same as 1,137 subcultures in 253 shipments in 2013)
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- • **Funding:**

a• o We are currently at the end of our last year of a 4-year NSF grant. Our total operating budget for 2014 was $145,468, and NSF funding covered 79% of direct operating costs. A new 3-year NSF award will start April 2015 with continued decreases in the percentage of direct operating costs that will be covered (59% by Year 3).

b• o Revenue from user charges in 2014 (excluding postage and courier charges) was $45,612 (an increase from $33,877 in 2013, although short of the $60,000 goal we would like to reach). Revenue increased from 2013, even though the number of stocks shipped was comparable, due to Special Service hours and increased orders for genomic DNA.

• **Growth:**

o 52 new stocks from 19 species were accessioned in 2014 § Five stocks, including one new species to the DSSC, from our own collecting efforts in the United States and Mexico

§ Eight new stocks, including five new species to the DSSC, were donated by Dr. Ary Hoffman & Dr. Michele Schiffer (University of Melbourne)

§ Four new stocks, including two new to the DSSC, were donated by Jean David (Le Centre National de la Recherche Scientifique, Paris, France)

§ 19 new *D. simulans* lines (9 from Madagascar, 10 from Nairobi, Kenya) and 16 new *D. yakuba* lines (8 from Nguti, Cameroon, 8 from Nairobi Kenya) were donated by Dr. Kevin Thornton (UC Irvine). These lines were part of a genome resequencing project and have publicly available genome data.

• **Costs:**

o Stock center daily operations and stock maintenance accounts for 92% of costs § Average annual maintenance cost per stock: ~$98

a• o DSSC annual expenses do not exceed annual income but this reflects our understaffing.

b• o Stockkeeping staff consists of 9 undergraduate part-time employees providing 1.25 full time equivalent (FTE). Management staff is 1.25 employees providing 2 FTE and needs to be expanded.

c• • **Cost recovery:**

d• o Price per stock: $35

e• o 20 ug genomic DNA: $127

f• o Special services/requests: $135/hour

• **New stocks:** We expect to add ~15 new stocks from 15 species this year
o Approximately 15 additional stocks are being sent by the Hoffman lab (University of Melbourne)

• **Pruning:** We continuously evaluate usage of stocks and remove any that are not commonly ordered.
a• o Ten stocks were pruned from the collection due to contamination
b• o There were 23 additional stocks lost in 2014 due to reproductive failure and/or bacterial contamination.

• **Drosophila Species Workshop**
a• o The workshop mechanism, which familiarizes researchers with the attributes of a range of species, has been a major driver in the community's ability to take advantage of the variation in the genus and thus in the demand for stocks.
b• o The 2014 workshop was held with the 2014 Drosophila conference in San Diego on March 25th and 26th, 2014
c• o Number of participants and instructors in 2014 was 21
d• o The 2015 workshop will be held in Guanajuato, Mexico in October 2015
e•
f• • **Scientific Advisory Board**
g• o Patrick O'Grady (University of California, Berkeley)
h• o Kathy Matthews (Indiana University)
i• o Sean Carroll (University of Wisconsin, Madison)
j• o Steve Schaeffer (Penn State)

Maxi: How to find maintenance of resources? Talking with other stock centers.

17. Drosophila Gene Disruption Project (Hugo Bellen)

Current Gene Disruption Project Progress Report (ending in April 2015)
(Bellen, Spradling, and Hoskins Laboratories)

Throughout its existence the GDP has strived to provide publically available strains that facilitate access to the Drosophila genome and all its regulatory and coding elements. As of December 31, 2014, the GDP has generated/selected > 15,000 transposon insertion strains associated with about two thirds of known protein coding genes for public distribution by the Bloomington Drosophila Stock Center (Bellen et al., 2011; Nagarkar-Jaiswal et al., 2015). During the current grant period, the project shifted to tagging every region of the genome, and as many genes as possible, with MiMIC, a *Minos* based transposable element (TE) that allows the use of recombination-based tools to manipulate the genome locally *in vivo* (Figure 1; Venken et al., 2011). The GDP selected > 7,400 MiMIC insertion strains associated with > 5,000 different genes for distribution by the BDSC (Venken et al., 2011; Nagarkar-Jaiswal et al., 2015). We have exceeded the grant targets and have now shifted to using CRISPR rather than transposition to deliver the phiC31-based cassette that allows recombinational manipulation (see next report). During the more than twenty years mutants were generated using transposition, we characterized transposon specificity as a side benefit (Bellen et al., 2011; Spradling et al., 2011).

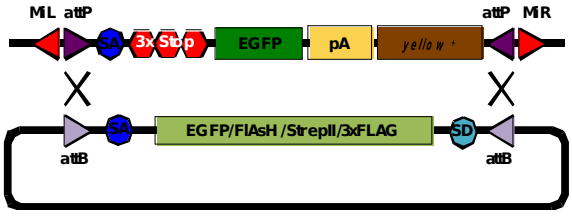

FIG 1. Key features of the MiMIC TE. *Minos* ends (MiL/MiR) for random genomic integration and *attP* sites flank a mutagenic gene trap, EGFP and *yellow+* markers. DNA of any design between *attB* sites (in this case a "reporter" exon) can be swapped by RMCE, replacing *yellow+*. Splice acceptor (SA). Splice donor (SD).

One of the major attractions of the MiMIC system is its potential to generate functional GFP fusions of all Drosophila protein coding genes. So far, about 2,800 out of the GDP MiMIC insertions are present in coding introns, allowing us to generate fusion proteins that contain an artificial exon encoding EGFP-FlAsH-StrepII-3xFLAG (Figure 1). The tagged proteins often retain their activity. Almost all allow the determination of precise protein distribution using light and electron microscopy as well as purification strategies using nanobodies against GFP such as immunoprecipitation (IP) of proteins, chromatin IP for DNA-associated proteins, and IP-mass spectroscopy.

As part of the last grant, we began to convert MiMIC tagged genes into GFP fusion genes and to test the efficacy of this technology. So far a library of about 500 GFP-tagged genes has been generated. We showed that 75% of internally tagged proteins are functional, and that more than 90% can be imaged in unfixed tissues. Moreover, the tagged mRNAs can be knocked down by RNAi against GFP (iGFPi) (Neumüller et al., 2012) and the tagged proteins can be efficiently knocked down by deGradFP technology (Caussinus et al., 2012). The phenotypes associated with RNA and protein knockdown typically correspond to severe loss of function or null mutant phenotypes. Finally, we demonstrated reversible, spatial, and temporal knockdown of tagged proteins in larvae and adult flies. This new strategy and collection of strains allows

unprecedented in vivo manipulations in flies for many genes. The manuscript summarizing these data is in press at eLife (Nagarkar-Jaiswal et al., 2015) and our website (http://flypush.imgen.bcm.tmc.edu/pscreen/) documents the expression patterns and other available information.

Two other teams, Ben White (NIH) (Diao et al., 2015) and Herman Dierick and Koen Venken (BCM) (Gnerer et al., 2015) have developed a very useful variant to insert an artificial exon that encodes T2A-GAL4 in MiMICs inserted in coding introns. This creates a null allele and leads to the production of a GAL4 fusion protein in the endogenous expression pattern, permitting numerous elegant manipulations. We are generating some T2A-GAL4 lines as well. The versatility of the MiMIC genetic strategy have many other applications in the near term that will help maintain the position of Drosophila as the model metazoan with the most powerful genetic resources.

Future Gene Disruption Project (starting in May 2015)
(Bellen, Perrimon, and Spradling Laboratories)

Funding support for the new GDP consortium has been approved (but 25% less than requested) and we thank all of you (there were many) who generously provided letters of support (they make a difference). Given the success of the MiMIC strategy, we now intend to expand the GDP collection by inserting a small MiMIC-like swappable insertion cassette into 4,000 new genes that currently have no MiMIC insertion using CRISPR (Lee et al., in preparation). We named this new strategy CRIMIC. We have prioritized 3,000 of the target genes based on their potential roles in human disease using data from our X-chromosome screen (Yamamoto et al., 2014). The remaining 1,000 will be selected based on input from the community. The CRIMICs will be introduced in the 5'-most intron of sufficient size (more than 100 nt) that can be used to trap all or most of the predicted splice isoforms. The CRIMIC technology is compatible with all the intronic tagging constructs designed for use with MiMIC.

We are also generating protein trap alleles (GFP-MiMIC or GFP-CRIMIC tags) for an additional 1,500 genes using the previously generated MiMICs or lines bearing the new CRIMICs. We have developed a system whereby the conversion into protein traps can be carried out through genetic crosses instead of injections (Nagarkar-Jaiswal et al., in preparation). This saves precious time and labor and will permit tagging of thousands of genes in the next two years. The large-scale generation of protein tags by the GDP represents a major resource for the research community and provides a very versatile tool set (Nagarkar-Jaiswal et al., 2015).

Given the usefulness and versatility of the endogenously functional tagged proteins/genes several teams have approached the GDP to speed up the process. Patrik Verstreken (VIB, Belgium) has volunteered to tag more than 500 genes that carry MiMICs. He also committed to deposit the stocks in the BDSC in a timely manner. Finally, Ulrich Tepass (Toronto, Canada) is submitting a proposal similar in size and scope to the GDP based on CRIMIC to tag several thousand genes in collaboration with

the GDP. We therefore anticipate that more than 50% of the protein coding genes will be tagged in the next 5 years.

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18. Harvard Drosophila RNAi Screening Center (Stephanie Mohr)

***Drosophila* RNAi Screening Center (DRSC) www.flyrnai.org**
Stephanie Mohr, DRSC Director/Co-Investigator, and Norbert Perrimon, PI

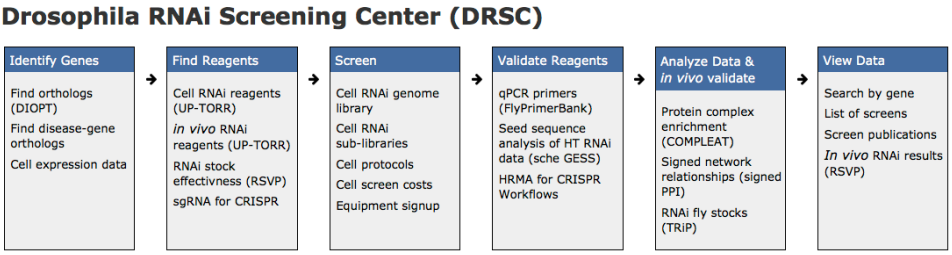
Overview. The DRSC, founded in 2003, is in the last year of our current NIH grant (NIGMS R01 GM067761) and we just submitted an application for renewal. In the last grant period, we provided reagents and services to >50 labs from institutions at >20 US states and overseas. Among the ~30 studies using DSRC libraries that were published in the last four years—in journals such as *Science, Molecular Cell,* and *Nature Cell Biology*—topics included signal transduction, hormone receptor regulation, ion transport, lipid storage, oxidative stress, stress granule biogenesis, piRNA biogenesis, cell or nucleolar morphology, homolog pairing, and dosage compensation. Based on recent screens and inquiries, we expect future projects to similarly interrogate diverse topics using innovative assays. Our proposed grant aims are to continue to support functional genomics screens and continue to serve as a tech transfer center for the community. ***We sincerely appreciate the letters of support we received from the Drosophila board, our scientific advisory committee, and individual labs from across the country for our grant renewal application to NIH***.

CRISPR-Cas at the DRSC. CRISPR-Cas engineering presents an exciting technology that for cell-based studies, serves as an important supplement to RNAi. We have ventured into CRISPR-Cas engineering in at least the following two ways, in close collaboration with the Perrimon lab: ***(1) CRISPR online tools.*** We pre-computed short guide RNAs (sgRNAs) for the fly entire genome. We display these, along with supporting information (e.g. predicted off-targets, convenient restriction sites, efficiency score) at our Find CRISPRs tool http://www.flyrnai.org/crispr2/. We used J-Browse to allow users to view sgRNAs in the context of gene annotations, so the most appropriate sgRNAs for a given application (e.g. knockout) can be selected. The efficiency prediction score, which is based on experimental data and was tested using data from the literature, can be obtained for any sgRNA design using Efficiency Predictor http://www.flyrnai.org/evaluateCrispr/ ***(2) CRISPR knockout and knock-in cell lines.*** A postdoc in the Perrimon lab established techniques for clonal isolation of CRISPR knockout and knock-in cell lines. The DRSC staff are learning, scaling up and refining the protocols. We used GSA Fly News e-mailing and other routes to gage community interest in CRISPR knockout cells (e.g. for assay development, sensitized screens or follow-up studies). We are now collaborating with a half dozen labs to make CRISPR engineered cell lines useful for their projects.

Growing suite of libraries at the DRSC. Altogether we have a genome-wide cell-screening RNAi library, several different focused RNAi 'sub-libraries' with deep coverage (2 or 3 unique dsRNAs per gene), miRNA over-expression and sponge collections, and an open reading frame (ORF) over-expression library. Our sub-libraries now include: kinases and phosphatases; transcription factors, co-factors, and other DNA-binding proteins; transmembrane domain-containing proteins (with NYU RNAi Core); ubiquitin-related proteins (with NYU); GPCRs (with M. Beller, Dusseldorf); RNA binding proteins (with B. Ye, U of Michigan); membrane-bound organelle-localized proteins; and autophagy-related proteins. We ship all libraries for off-site screens. We are also continuing our popular custom small library service (e.g. one or a few 96-well plates of dsRNAs) and small or large-scale 'cherry-picks' of our collection of templates for in vitro transcription at your lab.

Next RNAi cell screening sub-libraries? We are considering production of the following sub-libraries and welcome feedback on community interest: cytoskeletal-related proteins, mitochondrial-localized proteins, *Drosophila* orthologs of known drug targets. Please

contact S. Mohr at harvard_mohr@hms.harvard.edu if you are interested in a proposed library or would like to add a suggestion to the list.



Growing suite of online resources at the DRSC. Our suite of online software grew in past years to include tools related to high-throughput screen data view and analysis (e.g. SignedPPI, COMPLEAT, Online GESS), RNAi reagent identification (UP-TORR), and qPCR analysis (FlyPrimerBank), as well as our ortholog and disease-gene ortholog prediction search tools DIOPT and DIOPT-DIST. We have just undertaken a minor 'face lift' to our website with the goals of improved navigation among our tools and pages, and better compatibility with hand-held devices. See www.flyrnai.org for links to tools, protocols, reagent libraries, and other resources. We also recently updated the look of our DRSC website to facilitate easier navigation of online tools (***see above***) and improved compatibility with handheld devices, as well as launched a website http://flybi.hms.harvard.edu/ for the *Drosophila* binary interaction map project, an NHGRI-funded collaboration among the DRSC/Perrimon, BDSC/Celniker and CCSB/Vidal groups aimed at production of a high-quality large-scale binary interaction map for *Drosophila*.

DRSC online tools are designed to help your research. If you aren't using UP-TORR www.flyrnai.org/up-torr to identify cell-based RNAi reagents and/or *in vivo* RNAi fly stocks, we suggest you check it out! UP-TORR queries not just DRSC and TriP collections but also DKFZ, VDRC and NIG-Japan collections, and is based on up-to-date gene annotations for the most current interpretation of target genes, isoform specificity, off-targets, etc. If you aren't using DIOPT www.flyrnai.org/diopt to search for orthologs, we suggest take a look! We updated the tool to include results from ten different ortholog search algorithms and support for eight different model systems (fission and budding yeast, worm, fly, frog, fish, mice, human). Likewise if you're doing qPCR, check out FlyPrimerBank www.flyrnai.org/flyprimerbank for primer designs.

We are presenting a ***workshop on our online tools*** on Friday afternoon. Folks are welcome to bring lists of their favorite genes or large data sets. We will have test data available, too. We hope to see you there.

Recent and relevant publications:

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Hu Y, Sopko R, Foos M, Kelley C, Flockhart I, Ammeux N, Wang X, Perkins L, Perrimon N, Mohr SE (2013) **FlyPrimerBank: an online database for *Drosophila melanogaster* gene expression analysis and knockdown evaluation of RNAi reagents.** G3 (Bethesda). 3(9):1607-16. PMID: 23893746

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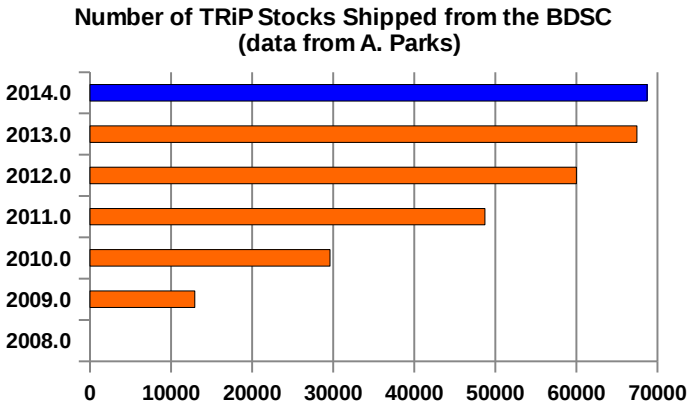
Stephanie: Future of RNAi screening in wake of CRISPR. Intgetrating these advances, including making CRISPR KO cells and new assays.

19. Transgenic RNAi Project (TriP) at Harvard Medical School (Liz Perkins)

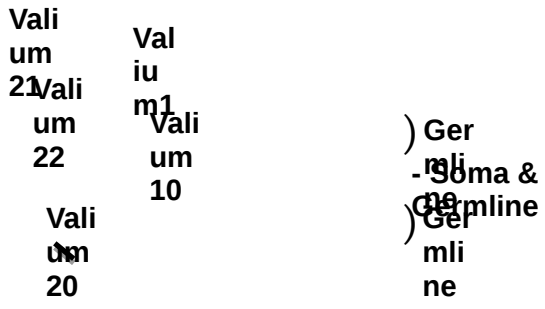
Prepared by Liz Perkins (February 12, 2015)

The Transgenic RNAi Project (the TriP: supported by NIGMS, R01-GM08494; N. Perrimon, PI) is near the end of the third year of its second round of funding (ends June 2016). The goal of the TriP is to generate transgenic RNAi lines and make them immediately and openly available to the community through the BDSC. The TriP facility was established at Harvard Medical School in September 2008 and to date there are approximately **~9,918** stocks completed, ~**4,759** in production and **~107** nominated. These completed stocks, in production and nominated represent **~9,860** unique FBgns which we calculate covers **71%** of the genes in the fly genome (**82%** of highly conserved genes). All completed stocks are annotated on the TriP website (http://www.flyrnai.org/TriP-HOME.html) and on FlyBase, and transferred as soon as possible to the BDSC for distribution to the community. In addition, select stocks are available from the NIG in Japan.

In 2014 the BDSC sent **68,730** subcultures of TriP stocks (985 of these were Toolbox and 883 were UAS-LUC-mir stocks, see below) to **1,271** different user groups at **640** different organizations, in **39** countries (A. Parks, personal communication). As of Feb. 12, 2015 there were **9,970** TriP stocks in distribution at the BDSC and the TriP expects to send 2,000 – 2,500 new RNAi stocks to Bloomington in 2015.



The **first-generation TriP RNAi stocks** contain long dsRNA hairpins (refs #1,2).
VALIUM1: 662 stocks, all available at BDSC
VALIUM10: 1,776 stocks, all available at BDSC.
The **second-generation TriP RNAi stocks** contain short hairpins (shRNAs) (ref #3)**.**
VALIUM20: 5,887 stocks.
VALIUM22 (and the highly related vector **VALIUM21**): 1,593 V22 stocks, 95 V21 stocks.



Through the BDSC, the TriP also provides the community with the "TriP Toolbox", which includes injection stocks for labs wishing to generate their own RNAi lines and commonly used GAL4 lines with UAS-Dcr2 (only for long line for long dsRNAs not shRNAs) to enhance message knockdown. In addition, all of the TriP vectors, including *vermillion* and *white* versions of vectors for over-expression, are available to the community through the plasmid repository of the DF/HCC DNA Resource Core at HMS (http://plasmid.med.harvard.edu/PLASMID/). In addition, in 2012 the TriP, in collaboration with Eric Lai (Sloan-Kettering Institute) and David Van Vactor (HMS), provided the BDSC with 102 microRNA transgenes (the UAS-LUC-mir collection) for conditional expression of fly micro RNAs (see ref #4).

As the TriP continues to expand its collection RNAi stocks, nominations from the fly community continue to be received weekly. In line with the DRSC, the TriP has established a **Gene Groups Project** where we are nearing completion of comprehensive sets of RNAi lines in specific gene categories; e.g., protein kinases, protein phosophatases, transcription factors and transcriptional regulators, secreted proteins, membrane receptors, to name a few. Additionally, with support from ORIP/NCRR R24 RR032668 to N. Perrimon, the recently established **Human Disease TriP Project** (the Hu-Dis TriP) has generated TriP RNAi stocks for **2,142** Drosophila orthologs of human disease-associated genes (http://www.flyrnai.org/HuDis). These include **90%** coverage for **670** high-confidence Drosophila orthologs of high-confidence disease-associated human genes. To generate these stocks we will continue to generate lines at HMS, and in addition, we are coordinating the production of lines by two outside groups, the National Institute of Genetics (NIG) in Japan (coordinated by Drs. Shu Kondo and Ryu Ueda) and the THFC at Tsinghua University in China (coordinated by Dr. Jianquan Ni). Importantly, these outside labs are utilizing established TriP nomenclature and send the lines they generate to the TriP at HMS, where they are checked for quality and then sent to the BDSC. Finally, recent discussions with the VDRC (Vienna) have resulted in a collaboration where the TriP is providing reagents and designing the hairpins for approximately 1,000 RNAi stocks that the VDRC wants to generate to cover gaps in their KK RNAi stock collection.

The TriP has participated with its parent, the DRSC, in the generation of several online tools for stock search and information access (UP-TORR, FlyPrimerBank, see DRSC report and refs #7,8). Particularly relevant to the TriP is the RNAi Stock Validation and Phenotype Project (http://www.flyrnai.org/RSVP.html), a web resource that allows users to search and view information about knockdown efficiency (qPCR data) and phenotypes (text and when available, images) for specific RNAi fly stock/Gal4 driver combinations (supported by the TriP's NIH grant as well as a grant from the NCRR/ORIP). The production pipeline for RSVP qPCR validation and phenotyping was pioneered by Richelle Sopko (a Perrimon PD). Richelle found (based on a tests of more than 300 TriP lines) that on average, 60-80% of TriP stocks display knock down efficiencies of >50% (ref #11). Since it is clear that ~20-30% of the lines we generate are suboptimal, the curation of the lines for the RSVP allows us to decide which lines need to be discarded and which ones need to be remade. In the past year, we expanded RSVP to include results curated by FlyBase for other major stock collections, such as phenotypes associated with VDRC fly stocks. Currently on the RSVP there are 5,935 data entries for 4,832 TriP lines representing 2,576 fly genes. In addition, the RSVP contains 27,657 data entries extracted from FlyBase for 12,823 RNAi lines representing 10,726 genes.

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20. Vienna Drosophila Resource Center), Vienna, Austria (Lisa Meadows)

The VDRC (**www.vdrc.at)** is a non-profit research infrastructure. Its mandate is to maintain and distribute transgenic RNAi lines and other resources to the Drosophila researchers, both locally and world-wide, and to further develop and expand VDRC resources according to the emerging new technologies and community needs.

Key changes during 2014

1. Faster delivery:

In response to consistent customer feedback, we duplicated all RNAi lines enabling us to significantly reduce guaranteed turnaround time for orders of 100 lines or less, from six weeks to less than two (average 6 working days).

2. New fee structure:

Due to a reduction in core funding from the Austrian Federal Ministry for Science and Research and the City of Vienna, 67% of the total costs must now be recovered from user fees. Our prices for small orders were increased to ensure that we continue to reach this target, thus securing the longer term availability of our collection for the community.

3. New name:
We changed our name to Vienna Drosophila Resource Center (formerly Vienna Drosophila RNAi Center) to reflect that we are not restricted to RNAi lines but also offer GAL4 lines, DNA constructs and other resources.

Usage Statistics

- Registered users worldwide: **2,289**
- Stocks delivered externally in 2014: **96,431** in **1,800** separate orders
- Total stocks delivered to Drosophila community since 2007: **>1,030,500**

Resources

Total stocks currently available to the community: **35,045**

- 26,585 RNAi lines (16,763 in GD and 9,822 in KK collection).
- 16 toolkit stocks used for the construction of both RNAi collections.

Collectively, the GD and KK libraries target a total 12,671 Drosophila protein-coding genes (91%). For over 8000 genes, more than one independent RNAi line is available through the VDRC.

- 8,444 enhancer-GAL4 lines (VTs, Vienna Tiles). Expression patterns annotated in adult brain and embryo. Searchable databases available.
- A small number of plasmids and stocks made available to the community from Private Stock Collections.
- 13,848 DNA constructs used for the generation of the GD collection.

Services

VDRC is open to donations of highly used stocks for integration into its community stock center collection, complementary to other stock centers.
In addition, we offer a Private Stock Keeping Service to maintain and distribute personal fly stock/plasmid collections for a reasonable fee.

Future

We are in the process of creating some new RNAi lines with the ultimate aim of having 2 independent lines per gene.
We are also keen to discuss involvement at an early stage to help develop new resources and our team has significant experience in high throughput construct generation, Drosophila injection and transgenic production.

21. Berkeley Drosophila Genome Project (Susan Celniker, Ann Hammonds, Ken Wan, Erwin Frise and Roger Hoskins)

A. Introduction

The BDGP was established in 1992 to sequence the *Drosophila melanogaster* genome. Now in our twenty-third year, we continue to expand activities with the goals of improving the functional annotation of the genome and expanding community resources. Since the sequencing and finishing of the euchromatic portion of the genome, we have continued to improve and extend the assembly and quality of the heterochromatic portion. We have also moved into functional genomics. We have worked with GenBank and FlyBase to release the next version of the genome sequence, Release 6. We continue to characterize the transcriptome using next generation RNA sequencing and to validate gene and transcript models by analysis of full-length cDNAs. We are mapping the modENCODE transcriptome data to Release 6. We continue to use the cDNAs to generate resources for proteomics studies and as templates for probes to determine spatiotemporal gene expression patterns in the embryo.

B. Reference Genome sequence

We completed the Release 6 genome sequence, worked with GenBank and FlyBase to release the sequence to the public, and recently published a paper describing this improved reference. Release 6 incorporates extensive cytogenetic mapping in heterochromatin, clone-based finishing and BAC fingerprint verification, ordering of scaffolds by alignment to cDNA sequences, incorporation of map and sequence data from others, and validation by whole genome optical restriction mapping. Representation of the *Y* chromosome and other heterochromatic regions is particularly improved. This new 143.9 Mb reference sequence effectively exhausts clone-based technologies for mapping and sequencing. We are now working to compare a recent PacBio long-read whole genome shotgun assembly (MHAP) to Release 6 with the goal of producing an integrated consensus assembly that will become Release 7.

C. cDNA Clone Resources

Two new clone resources are on the horizon, an untagged ORF collection for expression in tissue culture and a Gateway expression-ready collection to be used to generate a Y2H map (Mohr, Perrrimon, Vidal, Celniker).

The following are our summary statistics of clones submitted to GenBank - DNA sequence for 258,845 cDNA clones, of which 22,137 were fully sequenced and 19,807 fully support a FlyBase Release 6.02 protein model. The Gold Collection of cDNAs whose amino acid translation matches a FlyBase model with 100% identity, now contains 13,361 clones. From the Gold Collection, we have produced 10,330 expression-ready donor clones lacking the native stop codon (for making C-terminal fusion constructs) and 10,412 expression-ready donor clones containing the native stop codon (for making N-terminal fusion constructs). Using the donor clones, we have generated sets of expression clones in different vectors with a variety of tags (Table 1).

Table 1. Summary of Expression Clones.

Collection	Vector	Promoter	N-term Tag	C-term Tag	ORF Stop Codon?	System	Past year (2/2014 -	Total

							2/2015)	
XO	pDNR-Dual	T7	--	6XHN	No	*E. coli*	96	10330
XS	pDNR-Dual	T7	--	--	Yes	*E. coli*	288	10412
MXO	pMK33-CTAP-BD	Metallothionein	--	TAP	No	Cell culture	0	1961
FMO	pMK33-CFH-BD	Metallothionein	--	Flag-HA	No	Cell culture	190	10051
UFO	pUAST-CFLAGHA-BD-PHI	UAS	--	Flag-HA	No	Gal4-UAS	0	7110
URO	pUAST-C-mCherry-BDatt	UAS	--	mCherry	No	Gal4-UAS	0	257
UGO	pUAST-C-eGFP-BDatt	UAS	--	eGFP	No	Gal4-UAS	0	248
URS	pUAST-N-mCherry-BDatt	UAS	mCherry	--	Yes	Gal4-UAS	0	250
UGS	pUAST-N-eGFP-BDatt	UAS	eGFP	--	Yes	Gal4-UAS	0	242
MSN	pMK33-BD	Metallothionein	-	-	Yes	Cell culture	0	96
GEO	Gateway Entry	-	-	-	No	Y2H*	9823	11953
MSNP	pMK33-N-NoTag-BD-Puro	Metallothionein	-	-	Yes	Cell culture	0	83
MNEP	pMK33-N-EGFP-Puro-BD	Metallothionein	eGFP	-	Yes	Cell culture	0	94
RMO	pMK33-C-mCHERRY-BD	Metallothionein	-	mCherry	No	Cell culture	0	12
GMO	pMK33-C-EGFP-BD	Metallothionein	-	eGFP	No	Cell culture	0	10
CCO	pCopia-C-Clover-BD	Copia	-	Clover	No	Cell culture	346	346
CRO	pCopia-C-Clover-BD	Copia	-	mRuby2	No	Cell culture	345	345
GCO	pCopia-C-EGFP-BD	Copia	-	eGFP	No	Cell culture	23	23

*Not colony purified

Table 2. Summary of clones available at the DGRC:

Collection	Past year (2014Feb-2015Feb)	Cumulative
AU (Gold)	480	11,847

XO	672 ready to ship	9,685
XS	672 ready to ship	9,600
MXO	0	1961
FMO	672	10,051
UFO	0	7,110

D. Embryonic Gene Expression

We continue to collect embryonic spatiotemporal gene expression data from high throughput *in situ* hybridizations using the Gold Collection clones as templates for RNA probes. Annotations assigned by stage to each gene are now included in the FlyBase gene reports. In addition to the wild type gene patterns, we are collecting expression patterns for CRM-driven reporter constructs from the Rubin/Janelia collection and have started to incorporate these experiments into the public database (http://insitu.fruitfly.org) with links to the FlyBase sequence feature reports for these constructs. This year we added to our homepage a separate browse tab for the CRM experiments to improve accessibility. We continue to add new search and discovery tools based on computational image and annotation analysis. In the past year we have added an interactive viewer based on the annotated patterns of 708 site-specific transcription factor genes, using self-organizing maps to show relationships among transcription factor expression patterns in the context of organ system development (http://insitu.fruitfly.org/som). We are active participants in the development of both image analysis and microscope automation tools within the open source image analysis platform FIJI (fiji.lbl.gov). To date annotated experiments for 7916 genes, documented with over 122,000 images, have been deposited into the public database.

E. Other Resources

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

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

F. Technology

cDNA and expression clone sequencing continues to rely heavily on the ABI3730xl capillary sequencer. Characterization of the transcriptome as part of the modENCODE project has primarily been on the Illumina GAII and HiSeq platforms. We note that sequencing technology continues to evolve rapidly, and access to the latest instruments is essential to our mission. LBNL's Life Sciences Division owns a MiSeq, which is located in our lab, providing us with an R&D platform.

G. Funding

The BDGP is funded almost exclusively by NIH grants (NHGRI and NIGMS). The P41 (SEC) project to generate ORF resources has ended. An R01 (SEC) funds the spatiotemporal gene expression studies in no-cost extension through August, 2015. Image analysis research for the spatiotemporal expression studies is funded through an NIH BISTI grant to Erwin Frise. The competitive renewal will be submitted March 5, 2015. The modENCODE project funded by an NHGRI U01 (SEC) ended in 2014. We are also funded under subcontracts from Harvard University (Perrimon, PI, Celniker, co-PI) to construct ORF clones for Y2H studies and the University of Washington (R. Waterston, PI, Celniker and White, co-PIs) to participate in a

consortium performing ChIP-seq analysis of transcription factors in embryonic development. We have one project under private funding from Biogen Idec, Inc.

22. DIS Report (Jim Thompson)

Volume 97 (2014) of Drosophila Information Service was published on our web site (www.ou.edu/journals/dis) and in print on schedule in early January 2015. The final articles for this volume were accepted near the end of December 2014. Using a calendar year seems to benefit contributors, since it allows the somewhat flexible time after the demands of the fall academic semester to finalize a submission. Volume 97 contains 198 pages of research reports, technique notes, teaching notes, and other material. We continue to explore options of moving completely to an on-line version or using an alternative publication outlet that provided on-demand printing, since printed copies are now primarily ordered by libraries.

As noted in previous reports and in DIS, Marshall Wheeler's remaining copies of the *University of Texas Publications in Genetics* are now being distributed by us free except for a small shipping/handling charge. Several new requests were fulfilled this year. We also continue to improve links to earlier issues for free on-line access. This includes uploading some material from the earliest issues that we initially chose not to include. We have learned that material like original mutation descriptions and old stock lists can be important to those tracing historical sources.

First published in 1934, DIS remains an active source for research, teaching, and technique articles relevant to our field. Although I do not know the origin of the traditional "Call for Papers", I know from personal experience that it dates from well before 1960. So, for over 50 years, it has been a useful notice of an opportunity to share information with the larger international *Drosophila* community. We already have several accepted submissions for the 2015 Dros. Inf. Serv. Volume 98. These will be uploaded to our website as "2015 in press" soon. Submissions are accepted at any time, with the firm deadline of 31 December for each calendar year volume. Manuscripts and orders for a printed copy can be sent to James N. Thompson, jr., Department of Biology, University of Oklahoma, Norman, OK 73019; jthompson@ou.edu.

23. Historical Records (Irvine)

Last year Amy Bejsovec included historical records from previous fly meetings, including Meeting Organizers, Historical/Keynote Speakers, Larry Sandler Lectures, Plenary Speakers, and Session Topics/Chairs as an appendix to the agenda. These are valuable resources for future meeting organizers, but to keep the agenda shorter I elected not to include them here. These records are kept in a Dropbox folder maintained by the Board Presidents, and are available upon request.

24. White Paper & DCM RFI (Irvine)

A White Paper has historically been prepared by the board every 2-3 years. The White Paper outlines broad goals and priorities of Drosophila community, largely in terms of resources, tools, and reagents. It is especially valuable for resource grants, as a way to demonstrate support of the community for the goals of the grant. The last White Paper was published in 2012. Last year we discussed briefly whether or not a new White Paper should be prepared, and what should be in it, but no consensus was reached. I think that we should make plans to prepare a new White Paper over the next year, so that it could be approved by the board at or before the next board meeting. It is important to have input both from creators and users of Drosophila resources. An initial planning meeting will be held immediately after the board meeting.
Ken Irvine, Kevin Cook, Mike O'Connor, Stephanie Mohr, Hugo Bellen have already agreed to attend. Others are welcome.

As mentioned in emails to board members, the Division of Comparative Medicine at NIH has published a request for Information for Strategic planning.
http://dpcpsi.nih.gov/orip/StrategicRFI
The board President(s) will submit a response on behalf of the National Drosophila Board. The deadline for response is now March 16th. We have received some good suggestions and will be submitting a response after the meeting.

24: Ken collected some suggestions (Antibodies, U6 guide RNAs, UAS library of human orthologs of fly genes.) Ken will meet with others to brainstorm ideas after Board meeting.
Action item: *Ken will head revision of White paper, to be approved by Board.*