2016 National Drosophila Board Meeting Agenda

Wednesday July 13, 2016, 3:00 - 6:00 PM
New York/New Orleans room of the Orlando World Center Marriott

1. Introduction (David Bilder) 3:00-3:05

ADRC
2. Report of the 2015 Meeting Organizing Committee (Sue Celniker) 3:05-3:15
3. Treasurer's Report (Debbie Andrew) 3:15-3:20
4. Report of the GSA Senior Director (Suzy Brown) 3:20-3:30
5. GSA and the Drosophila Board (Lynn Cooley) 3:30-3:35
6. Sandler Lectureship Committee (Daniela Drummond-Barbosa) 3:35-3:40
7. Victoria Finnerty Undergraduate Travel Award (Alexis Nagengast) 3:40-3:45
8. Image Award (Michelle Arbeitman) 3:45-3:50
9. 2017 & 2018 Fly Meetings Update (Amy Kiger) 3:50-3:55
10. ADRC Rejuvenation ad hoc committee (Howard Lipshitz) 3:55-4:05

Community
11. Drosophila Board Election Report (Amy Bejsovec) 4:05-4:10
12. Revisions to Fly Board Charter (Ken Irvine) 4:10-4:15
13. Janelia Drosophila Research Ecosystem Meeting (David Bilder) 4:15-4:20
14. Identifying members of the Fly Community (David Bilder) 4:20-4:25
15. Advocacy & Communications (Andrea Page-McCaw) 4:25-4:35
16. Primarily Undergraduate Institutions (Alexis Nagengast) 4:35-4:40

BREAK 4:40 - 4:55

Resources and Projects
17. White Paper (Ken Irvine) 4:55-5:05
18. FlyBase (Norbert Perrimon) 5:05-5:20
19. MOD support letter (David Bilder) 5:20-5:25
20. Bloomington Stock Center (Kevin Cook) 5:25-5:35
21. VDRC stock centers (Lisa Meadows) 5:35-5:40
22. Species Stock Center (Maxi Richmond) 5:40-5:45
23. Drosophila Gene Disruption Project (Hugo Bellen) 5:45-5:50
24. Harvard Drosophila RNAi Screening Center (Stephanie Mohr) 5:50-5:55
25. Harvard Transgenic RNAi Project (Liz Perkins, Jonathan Zirin) 5:55-6:00
26. Berkeley Drosophila Genome Project (Sue Celniker) 6:00-6:05
27. DIS (Jim Thompson)

Adjourn

Table of Contents for Reports and Discussion Items:

Discussions and Decisions made

1. Introduction: David Bilder

2. Report of the 2015 Meeting Organizing Committee: Susan Celniker, Nancy Bonini, David Bilder and Ross Cagan

The 2016 Organizing Committee was assembled in 2013. Susan Celniker was recruited by Ken Irvine and Amy Bejsovic, current and past Board Presidents, respectively to be the lead organizer under advice from Suzy Brown of the GSA to have an experienced Committee Organizer for this exceptional Genetic Conference that encompasses not only the Drosophila community but communities that study Ciliates, Yeast, Zebrafish, Mouse, Worm and Population, Evolutionary and Quantitative Genetics. Sue subsequently recruited Nancy Bonini and together they recruited David Bilder and Ross Cagan. Both Sue and Nancy were organizers for the 49th Drosophila Annual Research Conference in 2004.

We began organizing the 2016 meeting almost immediately interfacing with the “uber” organizers Jeannie Lee and Philip Hieter and the co-organizers from the other model organism communities. We selected cross-organism keynote speakers and with this exception coordinated the Drosophila meeting as in earlier years selecting individuals for the historical panel, as keynote speakers and as platform session chairs. 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.

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.

2016 fly meeting registrations and registration trends. Pre-registration for the 2016 fly meeting is lower than our traditional meetings, with 997 pre-registrants as of June 1, 2016. A comparison to previous years meetings and to other GSA meetings is shown below.

For historical comparison, earlier fly meeting pre-registrations were: 1517 (2015), 1431 (2014), 1555 (2013), 1537 (2012), 1328 (2011), 1516 (2010), 1383 (2009), 1343 (2008), 1345 (2007), 1241(2006), 1451 (2005) and1470 (2004)

At the 2015 Drosophila Board meeting, concern was voiced that the change in time (July) and location (Orlando) might reduce participation and this appears to be true. In particular, there are many competing conferences during the summer (Gordon conferences for example), that likely also contributed to reduced attendance at the fly conference.

Organizer, speaker and special awards compensation. Unlike previous years, where the meeting organizers, plenary speakers, and keynote speakers were provided free conference registration, this year the budget covered only the plenary speakers with free conference registration. Each organism was given registration and travel funds for three individuals and we used the budget to cover the conference registration for our plenary speakers. 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 agreed to fund their own way.

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

Victoria Finnerty Memorial Fund travel grants were awarded to 8 undergraduate researchers, all of whom are presenting posters (see names below).

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.

Historical Panel Session, Wednesday night. The 2016 fly meeting will follow the traditional program on the first night, with introductions, announcements from GSA, the Sandler lecture and finally the historical panel discussion “Discovery of the Homeobox”. The organizers invited Drs. Matt Scott, Michael Levine and William McGinnis to participate in the panel with Dr. Cassandra Extavour as the panel moderator.

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 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): Pamela Geyer (University of Iowa), Artyom Kopp (UC, Davis). Pierre Léopold (Institut Valrose Biologie), Ingrid Lohmann (Heidelberg University), Adam Martin (MIT), Duojia (DJ) Pan (Johns Hopkins School of Medicine), Iris Salecker (Francis Crick Institute) and Annette Schenck (Radboud University Medical Center)

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 2016 Organizing Committee followed the approach of the 2015 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 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, senior researchers in the fields. The goal for the junior researchers is to give them exposure. This worked well for the 2015 fly meeting and is on track to work well again in 2016.

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 2016 meeting who selected abstracts for platform presentations are listed in Appendix Table 1 with affiliation and by session.

In addition to the session co-chairs this year we asked the chairs to invite a Postdoctoral trainee for each session.

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. The 2016 abstract deadline was March 23, 2016.

Submitted abstracts. A total of 692 abstracts were submitted under 17 categories and associated with keywords. Totals in recent years were 977 (2015), 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 361 requests for platform talks for the 157 platform talks (not including plenary speakers), which resulted in a 43% success rate, which is slightly higher than the rates in recent years. The number of abstracts varied considerably among sessions (see Appendix 1) from 102 in Drosophila Models of Human Disease to 16 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 76% in “RNA Biology” to 37% in “Neural Development”. 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 11 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 2016 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 2016, 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 2016 abstract pool was available.

2) A thorny issue that presents itself annually is how to allocate talks to abstracts. The 2014 and 2015 meeting organizer reports have a detailed discussion of this issue and suggested a number of possible solutions. The 2014 and 2015 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 2016 committee, we debated the issue amongst ourselves and devised what we felt was an equitable solution. The thorny issue, as noted by the 2015 organizers, is that the chances that an abstract requesting a talk will actually get a talk varies widely (26 to 66%) 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. It may be the case that in 2016 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 2017 organizers can evaluate if this approach was successful or considered disruptive to the flow of the meeting.

The 2016 Organizers will communicate this issue to the 2017 Organizers at the information lunch and provide the 2017 Organizers with the relevant spreadsheets so that they can consider the issue before they tackle the 2017 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. Having the alternate list of abstracts was critical for replacing any conflicted talks, for balancing talks among laboratories to assure representation in the field, and for replacing several talks when speakers withdrew abstracts after notification of platform talk assignment.

Poster Session. There are currently 530 posters. The breakdown of posters by category for the regular abstracts is shown in the Tables.

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. Ross Cagan has agreed to coordinate the 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 and the Postdoctoral trainee 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 1^{st}, 2^{nd}, and 3^{rd} 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 order to increase synergy and interaction between the model organism communities at TAGC, Drosophila meeting representatives proposed that interested communities pool selected workshops slots and preferentially select workshops organized by multiple communities whose topics cut across organism boundaries. Most TAGC communities were interested and in the end many of those selected are cross-community workshops. Surveys will evaluate the success of this innovation.

<u>Workshops; * denotes cross-organism involvement:</u>

*Plenary Session and Workshop for Undergraduate Researchers
*Automated Tracking for Quantitative Phenotyping
*Integrating Research and Teaching: Professional Development for Current and Future Faculty Members
*Informatics Resources to Aid the Genetic Dissection of Neural Circuitry
*Everything you Wanted to Know about Sex
*modMetabolome: Model Organism Metabolomics Consortium Workshop
*Feeding Behavior, Nutrition and Metabolism: Emerging Model Organisms
*Functional Genomics for Conserved Gene Function Discovery
*Cell Competition in Flies and Mice
*Developmental Mechanics
*Model Systems in Drug Discovery
*CRISPR/Cas9 - Techniques and applications in Fish, Flies, & Mice
*Utilizing NCBI Databases for Model Organism Research
*Systems Genetics in Complex Populations
*The InterMOD Consortium: A common interface to model organism data
*Spotlight on Undergraduate Research using Genetics Research Models
The Ecdysone Workshop
*Genetic and Genomic Models of Polyploidy
Microbiota

Planned assistance to the 2017 Drosophila Conference Organizing Committee. All of the worksheet templates, and the tables listing previous speakers and session chairs will be made available to the 2017 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.

Overall, the 2016 summer meeting planning, not unexpectedly, did not go as smoothly as a standard meeting, due to changes in plenary sessions, need to integrate sessions and timing with other model organism sessions, altered deadlines, and conflicts with other meetings. However, this pilot meeting achieved generating a template, such that if the decision becomes to do a meeting like this again, or in particular years going forward, the overall planning should hopefully proceed in a smoother manner.

Table 1. 2016 Drosophila Meeting Session Co-Chairs

Category	Co-chairs	
Cell Division & Growth Control	Erika Bach	New York University, NY, NY
	Terry Orr-Weaver	Whitehead Institute, MIT, Cambridge, MA
Neural Development	Ron Davis	The Scripps Research Institute, La Jolla, CA
	Krystyna Keleman	Janelia Research Campus, HHMI, Ashburn, VA
Organogenesis & Gametogenesis	Mark van Doren	Johns Hopkins University, Baltimore, MD
	Erika Matunis	Johns Hopkins Medicine, Baltimore, MD
Cell Cycle & Cell Death	Arash Bashirullah	Univ. of Wisconsin- Madison, Madison, WI
	Sarah Siegrist	University of Virginia, Charlottesville, VA
Evolution & Quantitative Genetics	Marta Wayne	University of Florida, Gainesville, FL
	Anthony Long	Univ. of California, Irvine, Irvine, CA
Pattern Formation	Ana Busturia	Centro de Biología Molecular Severo Ochoa, Madrid, Spain
	Liz Gavis	Princeton University, Princeton, NJ
Cell Biology & Cytoskeleton	Nasser Rusan	National Institutes of Health, Bethesda, MD
	Liz Gavis	Princeton University, Princeton, NJ
Chromatin & Epigenetics	Gary Karpen	Lawrence Berkeley Natl. Laboratory, Berkeley, CA
	Amanda Larracuente	Univ. of Rochester, Rochester, NY
Physiology, Organismal Growth & Aging	Ting Xie	Stowers Institute for Medical Research, Kansas City, MO
	Jason Tennessen	Indiana University Bloomington, Bloomington, IN

Techniques & Resources	Norbert Perrimon	Harvard Medical School, Boston, MA
	Kate O"Connor-Giles	Univ. of Wisconsin- Madison, Madison, WI
RNA Biology	Howard Lipshitz	Univ. of Toronto, Toronto, Canada
	Ben Brown	Lawrence Berkeley Natl. Laboratory, Berkeley, CA
Cell Biology & Signal Transduction	Margot Quinlan	Univ. of California, Los Angeles, Los Angeles, CA
	Lucy O'Brien	Stanford University, Stanford, CA
Drosophila Models of Human Disease	Hugo Bellen	Baylor College of Medicine, Houston, TX
	Hannele Ruohola-Baker	University of Washington, Seattle, WA
Regulation of Gene Expression	Julie Zeitlinger	Stowers Institute for Medical Research, Kansas City, MO
	Michele Markstein	University of Massachusetts, Amherst, MA
Organelles & Trafficking	Helmut Kramer	UT Southwestern Medical Center, Dallas, TX
	Amy Kiger	Univ. of Calif., San Diego, San Diego, CA
Immunity and Pathogenesis	Nathalie Franc	The Scripps Research Institute, La Jolla, CA
	François Leulier	Ecole Normale Superieure de Lyon, Lyon, France
Stem Cells	Tor Erik Rusten	Oslo University Hospital, Oslo, Norway
	Daniela Drummond-Barbosa	Johns Hopkins Bloomberg School of Public Health, Baltimore, MD

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

Session_Topic	Abstracts	Poster	Talks req	% Talks req	Talks allocated	Talks allocated % of all abstracts	Talks allocated % of req talks
01. Cell Biology & Cytoskeleton	41	33	30	73.17%	8	19.51%	26.67%
02. Cell Biology & Signal Transduction	34	25	19	55.88%	9	26.47%	47.37%
03. Cell Cycle & Cell Death	27	19	13	48.15%	8	29.63%	61.54%
04. Cell Division and Growth Control	45	35	26	57.78%	10	22.22%	38.46%
05. Physiology, Organismal Growth & Aging	68	58	29	42.65%	10	14.71%	34.48%
06. Gametogenesis & Organogenesis	45	37	18	40.00%	8	17.78%	44.44%
07. Stem Cells	36	25	20	55.56%	11	30.56%	55.00%
08. Immunity and Pathogenesis	16	11	11	68.75%	5	31.25%	45.45%
09. Neural Development	24	18	9	37.50%	6	25.00%	66.67%
10. Neurophysiology & Behavior	57	47	24	42.11%	10	17.54%	41.67%
11. Drosophila Models of Human Diseases	102	82	46	45.10%	20	19.61%	43.48%
12. Evolution & Quantitative Genetics	58	44	33	56.90%	14	24.14%	42.42%
13. Pattern Formation	17	13	8	47.06%	4	23.53%	50.00%
14. Regulation of Gene Expression	44	28	30	68.18%	16	36.36%	53.33%
15. Chromatin & Epigenetics	33	26	15	45.45%	7	21.21%	46.67%
16. RNA Biology	17	9	13	76.47%	8	47.06%	61.54%
17. Techniques Resources	28	20	17	60.71%	8	28.57%	47.06%

Table 3. Platform Session Postdoctoral Trainees

Session	Trainee	Institution
Cell Division & Growth Control	Dr. Kari Barlan	University of Chicago, Chicago, Ill
Neural Development	Yang Wu	HHMI Janelia Research Campus, Ashburn, VA
Organogenesis & Gametogenesis	Pradeep Bhaskar	Johns Hopkins University, Baltimore, MD
Cell Cycle & Cell Death	Conor Sipe	University of Virginia, Charlottesville, VA
Evolution & Quantitative Genetics I	Sharon Greenblum	Stanford University, Stanford, CA
Pattern Formation	Mo Weng	Princeton, Princeton, NJ
Cell Biology & Cytoskeleton	Todd Schoborg	National Heart, Lung, and Blood Institute, NIH, Bethesda, MD
Chromatin & Epigenetics	Aniek Janssen	LBNL, Berkeley, CA
Physiology, Organismal Growth & Aging	Matt Sieber	Carnegie Institute for Science, Baltimore, MD
Techniques & Resources	Benjamin Housden	Harvard Medical Schol, Boston, MA
RNA Biology	John Laver	University of Toronto, Toronto, ON
Cell Biology & Signal Transduction	Parthive Patel	Zentrum für Molekulare Biologie der Universität Heidelberg, Heidelberg, DE
Drosophila Models of Human Disease I	Rebecca Kreipke	University of Washington, Seattle , WA
Regulation of Gene Expression I	Robin Fropf	Stowers Institute for Medical Research, Kansas City, , MO
Organelles & Trafficking	Kari Lenhart	University of Pennsylvania School of Medicine, Philadelphia, PA
Drosophila Models of Human Disease II	Hsiao-Tuan Chao	Texas Children's Hospital, Clinical Care Center, Houston, TX
Gene Expression & Chromatin II	David Doupé	Harvard Medical School, Boston, MA
Immunity and Pathogenesis	Dali Ma	Institute de Génomique Fonctionnelle de Lyon, Lyon,
Neurophysiology and Behavior	Jacob Berry	Scripps Research Institute,Jupiter, FL
Stem Cells	Ming-Chia Lee	Carnegie Institution for Science, Baltimore, MD

DISCUSSION: Sue suggested that feedback from the TAGC meeting is important: was it viewed as successful? Do we want to repeat it in coming years? How often?
In discussion, Suzy pointed out that feedback from the Fly Board is especially important. It was generally agreed that the TAGC meeting encouraged positive cross-community interactions. Lynn Cooley suggested that a "Genetics" meeting, without separate MOD groupings, is worth considering in the future.

ACTION ITEM: Follow up on the GSA's hiring of a firm to analyze the TGAC meeting, using feedback from the Fly Board, meeting attendees and non-attendees.

3. Treasurer's Report: Debbie Andrew

Table 1: Summary of expenses: 2012-2016

	Chicago 2012 Actual	Washington DC 2013 Actual	San Diego 2014 Actual	Chicago 2015 Actual
REVENUE				
Registration Fees	$293,130	$319,904	$307,377	$344,451
Sponsorships	0	4,000		1,000
Hotel Rebates		16,145	0	0
Exhibit Fees	34,900	33,000	43,034	41,530
Miscellaneous (t-shirts, etc.)	5,555	5,452	5,011	3,719
TOTAL REVENUE	**$333,585**	**$378,501**	**$355,422**	**$390,700**
EXPENSES				
Salary, Payroll Tax and Benefit	$65,276	74,719	72,735	81,655
Printing/Mailing/Promotion	9,864	8,763	15,880	12,388
Education				
Receptions and Catered Events	154,106	152,425	121,311	164,867
Posters/Exhibits	18,993	22,408	20,821	30,766
Supplies/Duplicating/Signs	357		3,497	2,336
Hotel and Travel	7,401	3,369	5,912	4,329
Audio Visual Services	77,469	59,165	57,461	59,202
Awards (Sandler 2012, Finnerty			6,000	
2012-2015)	26,000	6,000		6,000
Other Contracted Services	8,760	6,862	5,895	3,435
Telephone/Internet/Fax	8,919	7,557	2,196	9,600
Credit Card Fees	12,485	9,507	9,198	10,319
Miscellaneous (t-shirts, etc.)	5,856	2,389	5,718	2,764
Overhead	19,583	22,416	21,821	24,496
TOTAL EXPENSE	**$389,069**	**$369,580**	**$348,445**	**$412,157**
NET GAIN (LOSS)	**$(81,484)**	**$2,921**	**$6,977**	**$(21,457)**

B. MEETING ATTENDANCE

	Attendees	Registration Fees

Pre-registration 2015 (Chicago, IL):	1,496	$313,373
Total registration 2015:	**1,569****	**$344,451**
Pre-registration 2014 (San Diego, CA):	1,335	$274,642
Total registration 2014:	**1,431**	**307,377**
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**

C.ACCOUNT BALANCES

C.1. Drosophila Main Fund

Table 2: Summary of income and attendance since 1993

Meeting Year	Location	Net Income	Fund Balance*	# Meeting Attendees
1993	San Diego	$17,105	$ 25,146	1,165
1994	Chicago	2,800	27,946	1,222
1995	Atlanta	8,417	36,363	1,103
1996	San Diego	15,035	51,398	1,423
1997	Chicago	31,663	83,061	1,382
1998	Wash DC	21,522	104,583	1,378
1999	Seattle	(6,053)	98,530	1,366
2000	Pittsburgh	(56,060)	42,470	1,183
2001	Wash DC	71,656	114,126	1,627
2002	San Diego	60,661	174,787	1,552
2003	Chicago	(22,993)	151,794	1,603
2004	Wash DC	23,026	174,820	1,617
2005	San Diego	89,943	264,763	1,515
2006	Houston	6,196	270,959	1,402
2007	Philadelphia	16,663	287,622	1,507
2008	San Diego	(5,410)	282,212	1,447

2009	Chicago	(47,935)	234,277	1.506
2010	Washington, DC	27,082	261,359	1,668
2011	San Diego	64,471	325,830	1,541
2012	Chicago	(81,484) (Meeting expenses include 20,000 to Sandler Fund and 6,000 to Finnerty Fund)	244,346	1,537
2013	Washington DC	$2,921 (Meeting expenses include 6,000 to Finnerty Fund)	$247,267	1,555
2014	San Diego	$6,982 (Meeting expenses include 6,000 to Finnerty Fund)	$254,249	1,431
2015	Chicago	(21,457) (Meeting expenses include 6,000 to Finnerty Fund)	**$232,792**	1,569**

***** The GSA Board (Sept. 2003 meeting) established a required *minimum* reserve fund of one-half of the meeting expenses. No cap figure stated
**First year exhibitor bodies (29) are included in the total.

C. 2. Sandler Lecture Fund
Table 3: Summary of Sandler Fund

Year	Investment Gain/transfers	Travel expenses	Supplies/ Mailing expenses	Net Income	Balance
1993				1417	25,964
1994				(451)	25,513
1995				1,595	27,108
1996				1,142	28,250
1997				1,119	29,369
1998				1,385	30,754
1999				877	31,631
2000				257	31,888
2001				(234)	31,654
2002				(846)	30,808
2003				(2,431)	28,377
2004				432	28,809
2005	1076	1,208	37	(169)	28,640
2006	1963	469	15	1,479	30,119
2007	2187	501	15	1,671	31,790
2008	-859	441	20	(1,320)	30,470
2009	1198	768		430	30,900
2010	947	1,482		(555)	30,345
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		4,285	63,436
2015	369	428		(59)	63,377

**Includes $20,000 transfer from meeting fund*

DISCUSSION: Discussion of funds dispersal and transparency. Most funds come from meeting registration, and as such arise from the participating members of the Fly community.

The appropriateness of funds dispersal by the FlyBoard and how transparent this should be was discussed. It was agreed that transparency is an important consideration. One suggestion was to include a clear statement of funds dispersal on the ADRC registration form.

4. Report of the GSA Senior Director: Suzy Brown, CMP

57th ANNUAL DROSOPHILA RESEARCH CONFERENCE/TAGC

Since the ADRC is part of TAGC "experiment" this year, there is no financial risk but here are some preliminary observations. Currently no future joint conferences are planned until we get feedback and analysis from the current meeting.

- Overall a tremendous amount of excitement for the meeting
- Main hotel block is already full (as of 5/24/16).
- Overflow block (at the much lower rate with a shuttle too) is picking up slowly which seems to indicate that the sleeping room price is not as much of a factor as we initially thought. Dros typically pays more for a sleeping room and less for registration.
- Abstract submissions are down approximately 30% compared with 2015. Some of that may be explained by the new PEQG meeting.
- Attendance is down approximately 24% compared with 2015at the same time. Some of that may be explained by the new PEQG meeting.

FUTURE CONFERENCES

It has increasingly become a sellers' market in the hotel meeting industry. It is getting more and more difficult to get the kind of concessions we have gotten in the past. One of the key factors is the amount of space we need for posters. Hotels look at the ratio of sleeping rooms to meeting space needed and our ratio is heavy on space and lighter on sleeping rooms. So while we use all meeting space in most properties, we do not fill up the sleeping rooms which means that the hotel is not able to attract another group that needs meeting space and has to hope that they get transient business to fill up the sleeping rooms. Transient business is generally very short term-business. Since we need a great deal of space, we should book five years out. Since Spring is a peak meeting time for societies/associations it can be harder to find space that will also be able to provide the type of sleeping room rate we need to maximize attendance. So we tend to be at a cross-roads. If the option exists to rotate posters up and down, that could open up some new opportunities for us. Dates and rates have been confirmed through 2020 but we need to start thinking about 2021. With formation of the ad hoc ADRC rejuvenation committee, the timing is perfect to consider some changes. Detailed below is the schedule for the next four years:

2017 – 58th Annual Drosophila Research Conference: March 29-April 2, The Town and Country Resort and Hotel, San Diego, CA. $166/$176/$186.
Note – this hotel is under new ownership and has received a substantial infusion of funds, which are being used to update all sleeping rooms, the grounds and other areas. So our attendees will have a significantly updated hotel. Although the hotel's rates will start to go up, we anticipated this and are locked in on rates for 2017 and 2020. The one gray area may be that the resort will now be charging a resort fee and it is not something guests can "opt out of." I have been working with the hotel on that issue for 2017 and 2020 without a resolution at this point. I feel pretty confident that we will be able to have the resort fee waived for 2017. There is less certainty for 2020.

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 (as of 6/1) - 2016

	Number
Faculty/Lab Tech Members	307
Faculty/Lab Tech NonMembers	71
Postdoc Members	129
Postdoc Nonmembers	40
Grad Student Members	270
Grad Student Nonmembers	57
Undergrad Members	83
Undergrad Nonmembers	8
Complimentary	32*
Early/Regular	**997**

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

Registrants by Country

United States	771	Sweden	4
Canada	41	Hong Kong	3
United Kingdom	26	Italy	3
Japan	24	Singapore	3
China	18	Netherlands	2
South Korea	17	Austria	1
Taiwan	16	Brazil	1
France	14	Greece	1
Germany	12	Jordan	1
Australia	10	Lebanon	1
Mexico	6	Nigeria	1
Israel	5	Norway	1
Switzerland	5	Portugal	1
India	4	Romania	1
Spain	4		

Total number of countries: 29 for 997 registrants.

5. GSA and the Drosophila Board: Lynn Cooley

The GSA is in the process of hiring a new Executive Director and reviewing priorities for the Society. Lynn is interested in feedback from the Drosophila Board on what is most useful for the GSA to do for the fly community.

DISCUSSION: President Bilder invited Lynn Cooley of the GSA to the FlyBoard meeting, to encourage FlyBoard and Fly community interactions with the GSA. His intention is to foster year-long interactions with the GSA.

ACTION ITEM: President Bilder recommended having a FlyBoard member sit on the GSA Board, an idea that generated the enthusiasm of the FlyBoard.

6. Sandler Lectureship Committee: Daniela Drummond-Barbosa

Committee members:
Daniela Drummond-Barbosa, Johns Hopkins University (Chair)
Sara Cherry, University of Pennsylvania
Bob Duronio, University of North Carolina at Chapel Hill
Daven Presgraves, University of Rochester
Kristin Scott, University of California, Berkeley

Chair 2016-17:
Bob Duronio, University of North Carolina at Chapel Hill

Total 2015 Nominees: 15
Total Male Nominees: 8 Total Male advisors: 13 (incl. 2 mentors for one of the nominees)
Total Female Nominees: 7 Total Female advisors: 3

Winner:
Alejandra Figueroa-Clarevega. Dr. Figueroa-Clarevega obtained her Ph.D. from the University of California, Berkeley, in May 2015. During her graduate work in Dr. David Bilder's lab, she established a new system to investigate tumor-host interactions in *Drosophila*, characterized of a number of cachexia-like phenotypes in adult hosts carrying transplanted larval tumors, and identified the insulin signaling inhibitor ImpL2 as a key tumor-derived mediator of the cachectic response. This work resulted in a first-author publication in *Dev. Cell* (2015).

Runners up:
Valentino Gantz, University of California, San Diego (Ph.D. mentor: Ethan Bier)
Justin Bosch, University of California, Berkeley (Ph.D. mentor: Iswar Hariharan)

2015 Nominees

Nominee	Gender	Thesis advisor(s)	Gender
Olga Antosyuk	F	Vladimir L. Vershinin	M
Luna Ballesteros-Arias	F	Ginés Morata	M
Justin Bosch	M	Iswar Hariharan	M
Riddhita Chakraborty	F	Kent Golic	M
Jieyan (Vera) Chen	F	Timothy Megraw	M
Yim Ling Cheng	F	Deborah Andrew	F
Scott Curran	M	Buzz Baum	M
Jon Iker Etchegaray Langley	M	Kimberly McCall	F
Alejandra Figueroa-Clarevega	F	David Bilder	M
Valentino Gantz	M	Ethan Bier	M
Michelle Henstridge	F	Coral Warr	F

Alexandre B. Leitão	M	Élio Sucena	M
Mads Fristrup Schou	M	Volker Loeschcke Torsten Nygaard Kristensen	M M
Nima Sharifai	M	Akira Chiba	M
Gilles Storelli	M	François Leulier	M

7. Victoria Finnerty Undergraduate Travel Award: Alexis Nagengast

This year we received 20 applications for the Victoria Finnerty (VF) Undergraduate Travel Award and funded the top 8 for a total of $4394 ($3795 from GSA and $599 from the Sandler Fund). We decided to award a maximum of $599 because recipients do not have to pay taxes on amounts less than $600. Lower award amounts matched what was requested by the applicant.

We also selected one recipient to receive the Larry Sandler Undergraduate Travel Award designation based on the applicant's focus on genetics in her/his work. Beth Reudi, GSA Director of Education and Professional Development, requested a change in future naming of this award so recipients still receive the Victoria Finnerty Travel Award with a Sandler distinction to recognize the uniqueness of her/his work. This awardee would receive an extra ribbon on her/his poster to mark the Sandler distinction and this designation would not require a new award mechanism separate from the Victoria Finnerty Travel Award.

The awardees are:

- **Taylor Hinnant** (Poster #D1229A), East Carolina University, $599, Larry Sandler Undergraduate Travel Award
- **Andrew Blake** (Poster #D1266B), Delaware State University, $599
- **Diana Luong** (Poster #D1257B), Loyola University Chicago, $599
- **Katherine Nichols** (Poster #D1245B), Muhlenberg College, $450
- **Abigail O'Conner,** (Poster #D1359B), University of Arizona, $599
- **Samantha St Clair** (Poster #D1128B), Indiana University, $350
- **Nilang Shah** (Poster #D1326B), Emory University, $599
- **Jarrod Shilts** (Poster #D1250A), Vanderbilt University, $599

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

This year's selection committee was Alexis Nagengast (chair and PUI Drosophila board representative), Jim Erickson, Matt Wawersik and new members Sarah Certel and Justin DiAngelo.

ACTION ITEM: President Bilder asked Alexis Nagengast to look into a mechanism for endowing more travel awards.

8. Image Award: Michelle Arbeitman

This year's competition 58 total submissions, including 11 videos.

The winners this year were:
Raghav Chhetri, for his video using a new light sheet microscopy technique to monitor Ca++ dynamics in neurons throughout a living Drosophila larva.

Tanya Wolff, for her image showcasing the ability of multicolor clonal labeling to map the architecture of the Drosophila brain.

The runner-ups were:

Jonathan Enriquez, for his image visualizing subsets of motoneuron targeting in the adult leg.

Justin Bosch, for his image that uses a new genetic mosaic technique to label cell contacts at the interface of two clonal boundaries.

Michelle Arbeitman will make the Award presentation at the meeting.

9. 2017 & 2018 Fly Meetings Update

2017 organizers are Leanne Jones, Doris Bachtrog, Claude Desplan, and Amy Kiger.
Confirmed speakers are:

Keynote speaker
Sean Carroll (U Wisconsin)

Platform speakers
Erika Bach (NYU)
Buzz Baum (UCL London)
Julius Brennecke (IMBA Austria)
Marcos Gonzales-Gaitan (Geneva)
Robin Hiesinger (Berlin)
Bruno Lemaitre (Lausanne)
Irene Miguel-Aliaga (London)
Marta Zlatic (Janelia Farm)
Virginie Orgogozo (IJM France)
Francois Payre (Toulouse)
Nitin Phadis (Utah)
Julia Zeitlinger (Stowers)

DISCUSSION: The 2018 organizers (TBD) will use feedback received from the TAGC meeting in their planning.

10. ADRC Rejuvenation ad hoc committee: Denise Montell, Howard Lipshitz, Leanne Jones

President Bilder tasked us with developing ideas for rejuvenating the Annual Drosophila Research Conference.

Our philosophy:
The conference works pretty well as it is, but every repeating activity requires ongoing innovation to stay fresh and to get people excited about it anew each year. In addition, our community grows and evolves with time, and the meeting needs to grow and evolve to meet changing needs.

Our goals:
1. Do no harm
2. Identify opportunities for improvement
3. Add value to the experience for students, postdocs and PIs

Our approach and results:
We met twice via teleconference. After the first meeting, Denise collected data from Suzy Brown and GSA regarding PI attendance (attachment 1), Howard conducted a survey of Crete Meeting

attendees (attachment 2), and Leanne elicited suggestions and comments (attachment 3) from a focus group composed of ~20 investigators. We also considered suggestions from David Bilder. Based on all of this, we arrived at the following consensus.

1. In order to do no harm, we should probably not make too many sweeping changes at once. We think that continuing the rotation between west coast, east coast and middle of the country is wise. Keeping the meeting in the spring is also probably wise. Even though some people said the normal time conflicts with their teaching, other people will undoubtedly have conflicts at other times.

2. A) One big opportunity for improvement is found in the survey results, which indicate that cost is a major reason that more people do not attend on a regular basis. We discussed the two ways to circumvent this issue. The first is to make the meeting cheaper. However we think it would be a bad idea to try to save money in any way that would make the meeting less attractive because this will not help. Airfares are a major cost, and we have no control over that. People have come to expect a certain level of comfort and convenience, and we should keep those. Another way to address this issue would be to raise money for more travel awards. The committee strongly felt this would be a good idea. Any other way of raising more philanthropy would obviously enable many improvements. The Board and Organizers should really put some effort into this.

   B) A second opportunity for improvement that arose from the survey results is that PIs and their trainees would appreciate more opportunities to present their work. One challenge is that this seems to be in direct conflict with another frequent comment, which is that smaller, more specialized, topic-focused meetings are more attractive to many investigators than large organism-focused meetings.

3. Here are our suggestions for adding value to the meeting
   A) For PIs
      i. Social event for PIs/communication with the board

A reception for PIs to meet with the Board (at the hotel, pay ahead with registration) - catch up with colleagues and discussion with Board members. This could be held after the Board meeting and before the opening session.

      ii. Lunch with Postdocs/students (students register ahead of time to have lunch with PIs/speakers from the meeting)

      iii. Make the meeting effective for recruiting students/postdocs (SDB mechanism?) Journal-sponsored “Meet Up lounge?” Market this feature to PIs.

      iv. Add more opportunities to talk

Replace historical session (which has gotten stale) with an up-and-coming PI plenary session and/or make the workshops more prominent. We discussed the need to work in some quality control to the workshops if they become more prominent.

   B) For trainees
      i. Lunch with PIs

      ii. Career development session (non-academic careers)

      iii. Social event (dance party hosted by a company? Zeiss? Genesee?)

iv. Hold a plenary session in which 3-4 Sandler Award finalists speak

v. Create a "big sib" program so new comers know someone

C) For everyone

i. Many people (PIs and students) would appreciate more opportunities to present their work. Yet some people don't like too many concurrent sessions, and the schedule is already so compressed it is hard to find time for social events with lab members, so there are certainly challenges to this. Eliminating the historical session (or holding it only every 5 or 10 years when there is a good reason to do it) is one way to gain another plenary session. Other than that, offering some very short "flash" talks to advertise posters might be an option. Another possibility would be to add a "Doorstep" meeting on a specialized topic for one day or ½ a day prior to the opening of the meeting. ASCB is trying this this year http://www.ascb.org/doorstep/. The Ecdysone Workshop is a micro example of this. But one could hold a Drosophila Neuroscience doorstep meeting or a Cancer Biology of Drosophila meeting or some other topic-oriented meeting. This could change each year to bring a little small/topic-oriented flavor.

ii. Re-vitalize the topics for posters and concurrent sessions (e.g., "mandatory" change of at least 20% of session topics each year)

iii. Introduce a Grad Slam competition along the lines of the one that The University of California holds annually http://www.graddiv.ucsb.edu/profdev/grad-slam. It starts with each campus holding preliminary rounds of competition to identify the best grad student 3-minute presentation about their research. Each campus then holds a final round. The winners from each campus go to a UC wide competition. Leanne and Denise have attended these events and find them inspiring. There is significant prize money attached (the UCSB winner this year won $5,000 and is a fly person).

iv. Better social media presence

We discussed pros and cons of this. Young people might get more engaged. Some people might worry about their unpublished results appearing on Twitter and Facebook. But those are always concerns with or without social media when presenting unpublished work at conferences.

v. Food/drinks at poster sessions

vi. A major benefit of the model organism meeting is the techniques session, which is usually overflowing. This should probably be a plenary session with nothing running concurrently.

Addendum

David Bilder had some questions and suggestions, to which the Committee responded specifically here:

- A sense that senior PIs attend less often, and that this makes it less attractive to postdocs, senior grad students etc. How (besides emphasizing that it is good for the community) can we increase the value to senior PIs? Maybe offer them more Session chair positions?

Between 2006 and 2016 the % of attendees who are PIs has varied between 15 and 20% with no clear trends (see attachment #1 provided by GSA).

- A related idea: is there a way to bring a little of Crete (or the popular Zebrafish PI meeting) to the ADRC? Maybe an evening dinner that is PIs only, with some lightning talks by junior and

senior PIs? It could be pitched as a mentoring/networking session so it doesn't feel exclusive to the other attendees. PIs could sign up for the dinner and have it added to their registration fee.

Denise kind of likes this idea. Howard really does not. We may have to canvas more people to get a sense of whether this is likely to be well received. Alternatively, meeting organizers, if so inclined could simply do an experiment.

- A sense that fewer exciting stories are presented —more published work. This is a trend in all meetings of course but is there a way to incentivize it? Offer an award for best talk (grad student and postdoc categories), stressing unpublished material as a criterion?

The committee did not think that this is a big problem. For many of us keeping up with the published literature is a huge challenge. We are happy to hear intelligent syntheses of published work with a few new ideas thrown in. It is the responsibility of the meeting organizers and session chairs to select speakers who have published something exciting recently so that people are not presenting truly stale stories.

- A sense that we are losing segments such as neuroscience completely. This is largely b/c they have the CSHL meeting, but are there ways to bring them back into the fold? As they don't go to the meeting, they tend to grow apart from being 'fly people' altogether —this is a real loss.
- Are there ways to reach out to other scientific communities to have them come in and appreciate fly work? e.g. an annual invited lecture with a prominent speaker from another model genetic organism, to make links to those communities and stimulate our own?

The committee recognizes that the Neurobiologists created their own meeting, which is of greater value to them than the general fly meeting. Each year neuroscientists are invited to the ADRC meeting to give talks, and they come, but this does not change the fact that the CSH meeting on Drosophila neurobiology is so valuable that they would prefer to go to that. We are not sure we can do anything about that other than attempting to make the fly meeting really good so it is valuable and valued to attend. One possibility is targeting the junior neurobiologists who are very unlikely to get to present at CSH. Another idea is the "Doorstep" meeting as described above.

- Are there ways to make newcomers more welcome, less intimidated? I like the idea of a 'big sibling' matching program where an undergrad or new grad student could sign up to be 'hosted' by a volunteer senior grad student or postdoc with overlapping interests — give them someone to eat with, introduce to other members etc. This would be a good community building exercise

Sure

Survey results have not been included but are available from the committee or Board President.

DISCUSSION: Discussion of the ad hoc committee's report. Although it appears that overall the ADRC meetings remain popular and are in good shape, the Board agreed that it is important to regularly consider ways to keep the ADRC meetings innovative. Ways that this can be accomplished included: more informational/networking opportunities for junior PIs and trainees; ensure that topics of workshops are revisited and changed annually, with at least a 20% change each year; increasing the number of "doorstep" meetings; consider making the Platform session categories arise from the content of submitted abstracts, instead of continuing with "established" categories that may not reflect current trends; try to equalize the ratio of US to European and Asian speakers for invitations (in 2017 8 of 12 speakers are European).

11. Drosophila Board Election Report Amy Bejsovec

The Elections Committee consisted of Amy Bejsovec (Chair), Kristi Wharton, Anthea Letsou, Mark Peifer and Justin Kumar. Kristi and Anthea served last year and will rotate off next year, Mark and Justin were new recruits to the committee and have agreed to serve next year as well. Next year's chair will be Ken Irvine. Amy will remind him to organize the committee next fall and to select two new members to serve 2-year terms.

The Chair solicited nominations from outgoing regional representatives and from the committee, and compiled a list of all nominees, including links to their lab websites. Each member of the Election Committee then ranked the nominations for each open position, from top to bottom, representing their first and last choices. The rank orders from all committee members were added up and used to assemble a final ordered list. The Chair contacted the top-ranked nominees, to persuade them to stand for election, and constructed the final ballot that was then disseminated to the fly community by email (shown below) on Oct. 9th, 2015 with a deadline for voting set for Dec. 11th, 2015. A reminder email was sent on November 11th.

The winners of the election were:
Deborah Andrew, President (2017)
Chris Rushlow, Mid-Atlantic representative (through 2019)
Amy Kiger, California representative (through 2019)
Juan Riesgo-Escovar, Latin America representative (through 2019)
Sarah Bray, Europe representative (through 2019)
Li-Mei Pai, Asia representative (through 2019)

The turnout for this election was unusually high, apparently because some of the votes came from outside of the fly community – the total ballots cast were 1795, compared with fewer than 500 in a typical year. This occurred because one of the candidates forwarded the SurveyMonkey link, which was publicly posted on Flybase, to a number of local colleagues. We received a flood of votes from this region. We were troubled that this gave the candidate an unfair advantage, and so we analyzed the results in a number of ways, including subtracting all of the votes from the region affected, which left a more typical total of 449 ballots. Even without the extra votes, the candidate still won the election. While we appreciate the enthusiasm and ability to communicate with constituents that this event demonstrated, we would like to avoid any appearance of bias in future elections and feel that the voting should be restricted to the fly community.

Election emails and candidate statements are appended to the end of the Agenda (**Appendix 3**).

DISCUSSION: A discussion was held as to whether to restrict the voting in future Fly Board elections, and if so, how this might be done effectively without excluding any interested fly people. Amy proposed that we try two things for next year: 1) state explicitly in the community-wide email that the voting is restricted to those who use Drosophila in their research; 2) ask Flybase not to post the survey link, so that it is only available to those who are on the listserv and receive the email. I suspect that this will not significantly decrease the turnout because the pattern of responses (highest peak after the first email, lower peak at the reminder) suggests that most people who vote do so by clicking on the link in the email. If next year's turnout is low, however, we should revisit this issue and discuss other strategies.

Ken Irvine and others were in favor of posting a Flybase link to the election, with the caveat that it is important that only Fly people vote. The Board discussed ways to ensure that this would be the case. Ideas raised included recognition of voter's IP address and voter registration on Flybase.

RESOLUTION: In the revision to the Charter Ken included the following statement: Only scientists who use Drosophila as a research organism are eligible to vote.

12. Revisions to Fly Board Charter: Ken Irvine

The Charter describing the composition and responsibilities of the Drosophila board has been updated to reflect current practices, and input that was received at the 2016 Janelia Drosophila Resources Conference. A draft revision of the Charter was distributed to all Drosophila board members before preparing this version. Three key points to note:

1. A proposal to include a trainee representative has been included. I would suggest that the elections committee could solicit applications along with the notice of election, and then select a candidate from amongst the applicants, as I don't think it makes sense to have elections for a trainee representative. This proposal will be discussed in Orlando.
2. I tried to develop a flexible proposal for making better use of regional representatives, who previously did not have any responsibilities beyond showing up for the board meeting. This proposal currently adds another responsibility to the President. This proposal will also be discussed in Orlando.
3. Primary function #1 of the Board was modified to expand the advocacy role of the board beyond funding agencies

The complete text is appended at the end of the Agenda (**Appendix 1**).

RESOLUTION: The Board voted unanimously to accept the revised Charter

13. Janelia Drosophila Ecosystem Meeting: David Bilder

Sparked by the revision of the 'White Paper', as well as transitions in leadership and anticipated changes to the funding and organization models for Flybase, a group of Fly Board members organized a meeting to take stock of the current 'Drosophila Research Ecosystem', and identify areas where it can be strengthened. Organizers were Hugo Bellen, David Bilder, Nick Brown, Ken Irvine, Thom Kaufman, Brian Oliver, and Norbert Perrimon. HHMI kindly agreed to host the meeting at Janelia Research Campus on Feb. 18 and 19, 2016. Fly Board officers and regional representatives were invited, as well as a selection of other community and resource leaders worldwide. 40 invitees were able to attend.

In addition to considering the White Paper and the future of Flybase, target questions included: What resources does the Drosophila community need to continue boundary-pushing research? How can new and existing infrastructure – both physical and data - be effectively managed and integrated? How should these be funded for use by the worldwide community? How can Drosophila researchers make the case to funders and the public for their extraordinary impact on fundamental biology and human health?

To address these questions, the meeting had six sessions: Physical Resources; Data Resources; New Technologies; Expansion to Other Communities; Advocacy, Communication, and Community; and FlyBoard and Funding. Each session had brief presentations for context followed by discussion of critical issues. The final meeting sessions were open discussion for the entire group

with an eye towards blue-sky brainstorming of scientific opportunities, as well as specific decisions and initiatives to improve the ecosystem.

A brief list of initiatives other than Flybase/MOD integration and White Paper, and individuals who agreed to take them on, include the below:

- Validated commercial antibody list: Bing Zhang, Thom Kaufman
- Communications and Advocacy (various): Andrea Page-McCaw, Andreas Prokop, Michelle Arbeitman, Sarah Certel, Alexis Nagengast, Gio Bosco
- Community engagement/website: Stephanie Mohr, Andreas Prokop, Scott Hawley
- Fly worker contact list for communication: David Bilder
- Standardized genotypes for published papers to ease curation/annotation: Nick Brown
- Call for community stocks to Bloomington and progress towards a null in every gene: Kevin Cook, Nick Brown
- Revisions to FlyBoard charter: Ken Irvine
- ADRC Innovation ideas: Howard Lipshitz
- Meeting Report: David Bilder

It is hoped that FlyBoard will continue to support, encourage, and monitor the progress of these initiatives, as well as others that have yet to be 'claimed'. It is clear that even the less ambitious initiatives stretch the commitments that Board members already have, and that some initiatives could be enhanced or completed much more easily with modest funding. Discretionary funds for the FlyBoard could have a significant impact on the status of such community improvements, and sources should be explored.

DISCUSSION: It was acknowledged that many young fly researchers actually identify themselves more by research topic than as a "fly person", suggesting a need for ways to integrate new people into the fly "world". The importance of initiatives that will energize community members was also discussed, for example, encouraging local and regional fly meetings to assist in boosting enthusiasm, encouraging PIs to go to Fly meetings (national and regional) and to promote Fly community awareness.

14. Identifying members of the Fly Community: David Bilder

There continues to be a need for effective communication with fly researchers, for instance to inform about resources (new and underappreciated existing resources) and to mobilize energy for advocacy. The latter was anticipated last year and became acute recently when the need to distribute the MOD support letter (see 19 below) arose. As mentioned (some figures are in last year's Board agenda), most researchers are not registered at Flybase, which is the major source of contact emails, and many Flybase addresses are no longer attached to active fly researchers. Recent ADRC attendees are a more updated source but this also covers only a small (and US-biased) subset.

The most sensible approach IMO is to try to maintain a list of fly PIs (and their equivalents in non-academic settings). The logic is that PIs are more stable email- and career-wise than trainees etc. and can be responsible for distributing the information to their own personnel. While this won't allow a count of exact number of community members (perhaps 5-6000? Perhaps 1800 'labs'?), it would be an effective way to communicate with the bulk of the fly community. It has been possible with GSA and others' help to piece together from various sources a list of ~1400 PIs. This will be used for the MOD support letter and perhaps other urgent communications.

If we are serious about maintaining a list of active Drosophila PIs (and I think that we should be), the best approach that I can think of is to have Bloomington and other stock centers ask, on an opt-out permission basis, to add registered PI users to a fly mailing list as they renew their accounts. Probably most Drosophila PIs order at least one stock per year, and the need to maintain the account allows an automatic updating feature. This does not have to be exclusive –it can be interfaced with the ADRC and Flybase tinyletter lists—but it will capture more of the active Drosophila PIs. Currently Bloomington is not set up to do this, but it should be feasible if the FlyBoard and BDSC and other stock center leadership sees fit.

DISCUSSION: The Board discussed various ways to address these issues. In general, it was agreed that Regional Representatives would be a good source of information as each has a list of members from their own area. Other possibilities raised included the formation of a simple *e*-link on stock center orders to remind people to register and yearly web-based solicitation of lab trainees from PIs.

15. Advocacy & Communications: Andrea Page-McCaw

History

In October 2014 Senator Rand Paul made public comments criticizing NIH spending, and included specific criticism of a Drosophila project. The National Drosophila Board had a lively email exchange over how to respond, and this conversation culminated in establishing a Communications Committee in March 2015. Although the formal committee was new, similar conversations and efforts had been initiated over the last decade.

The Communications Committee was one of several structures with similar goals created in the last year. After the Rand Paul incident, some Fly board members raised the possibility of creating a website designed to provide information to the general public and media about Drosophila, and this was established as a different effort. At the Janelia Drosophila Resources workshop in February, two new groups were established, one to work on Community Outreach (led by Andreas Prokop, Stephanie Mohr, and Scott Hawley) and one to work on Advocacy (led by Gio Bosco and Andrea Page-McCaw). Several of the members of these three committees overlap and their efforts have become somewhat merged.

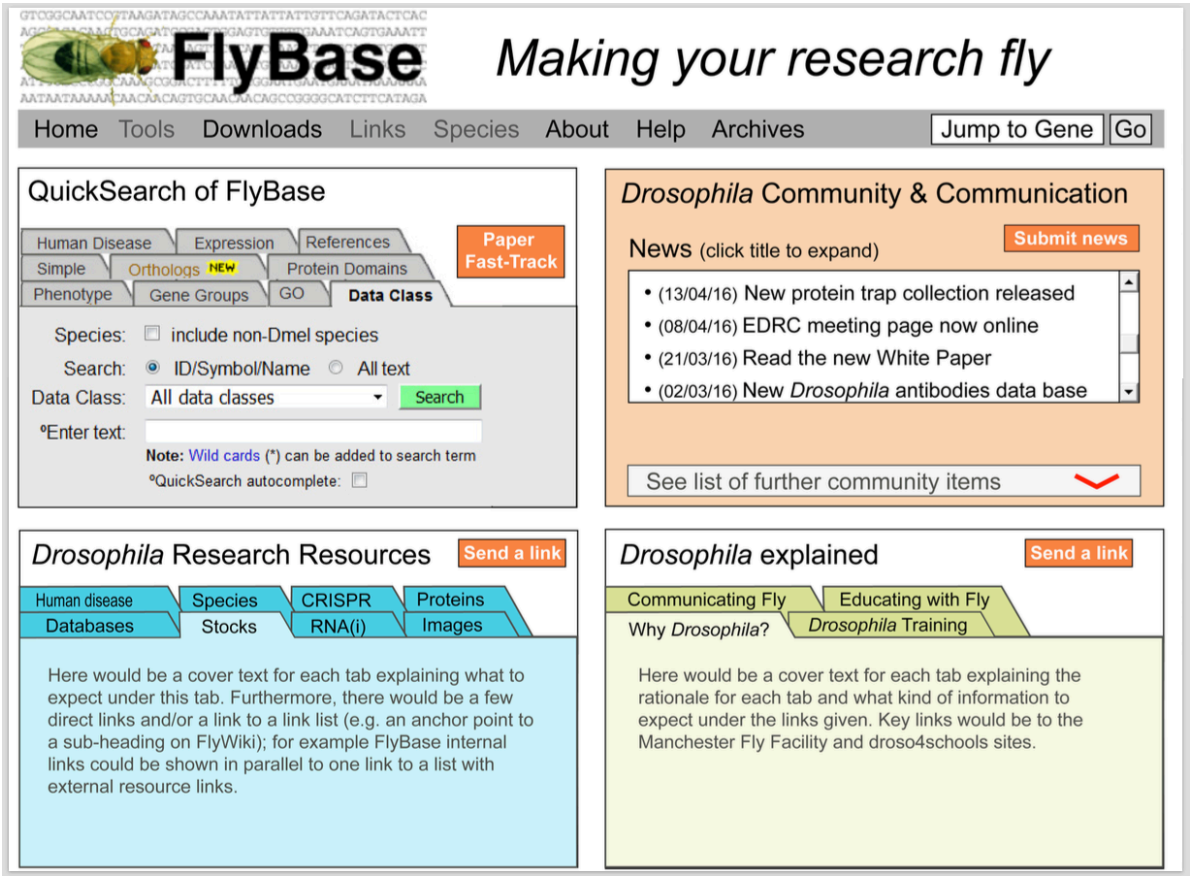
Members

The Communication Committee members are Giovani Bosco, Heather Broihier, Michael Galko, Gary Hime, Stephanie Mohr, Laura Nilson, Andrea Page-McCaw (chair); and graduate student volunteer Saoirse McSharry.
The members of the Advocacy group are Michelle Arbeitman, Gio Bosco, Sarah Certel, Stephanie Mohr, Andrea Page-McCaw, Andreas Prokop.

Goals and progress

- **"What you can do".** A tangible product of the Communications Committee is the "What You Can Do" slides generated at the 2015 ADRC in Chicago. After Allan Spradling's keynote address, in which he expressed concern about the future of fly research, the audience reacted by asking what individuals can do to help promote Drosophila Research. The committee met several times during the Fly Meeting to produce two "What You Can Do" slides, one to promote research and one to promote funding. These slides were displayed during the platform sessions and closing session at the meeting, were posted on the GSA website, and are still available online at www.tinyurl.com/promoteDros
- **FlyBase homepage.** The related Community Outreach committee proposed a new design for the home page of FlyBase, in the hope it can expand in its role as a community portal. Andreas Prokop, who has already developed substantial outreach content for the Manchester Fly Facility (http://www.flyfacility.ls.manchester.ac.uk), recognized the need for a common, high-traffic portal for dissemination of Drosophila material. At the Janelia meeting, he proposed that the homepages of FlyBase and Bloomington, which already have high traffic volume, be redesigned to be user-friendly for both their original purposes and to offer easy-to-navigate links to additional material. Both organizations were receptive to his idea. Working with a professional web designer, Andreas has submitted two similar templates to FlyBase for consideration (one is below). Content fields can be populated with either material from the Manchester Fly Facility or new content developed by the committee. We have started to write some content.

- **"I Was Fly" list.** Another goal has been to compile a list of fly-friendly experts in various fields



who would be a useful "go-to" resource for quotes and support as needed. This list, called "I Was Fly", is an ongoing effort (5 entries to date). An important question is how this list will be disseminated so that it can be used if/as needed.

- **"Why Drosophila?" Slide Repository.** Michelle Arbeitman on the Advocacy committee has been contacting various fly researchers to ask if they would be willing to share any background slides they have generated that explain why Drosophila is a useful model organism. The slides are stored in a shared Dropbox site, and the collection is in progress.

- **TED talk nominations**. Scott Hawley and Stephanie Mohr, on the Community Outreach committee, note that TED talks would be a straightforward way to promote awareness of Drosophila. There are only a handful of Drosophila TED talks to date, all focusing on neuroscience. Nominations can be done by anyone at the website http://speaker-nominations.ted.com and the nominations populate a database that is mined for all future TED speakers going forward. Members of the committees have nominated at least two fly researchers to date through this process. We encourage the community to nominate engaging Drosophila biologists.

- **Social media.** Stephanie Mohr has been writing a blog entitled "Drosophila Models of Human Disease" http://flydiseasemodels.blogspot.com and posting a twitter feed @smohrfly highlighting Drosophila research and science education. She notes that many fly folks, as well as the GSA, are using social media to promote their research, share resources, build community, share outreach efforts, etc.

- **"Where Did My Medicine Come From?"** Gary Hime has started collecting examples of how discoveries in Drosophila have led to current pharmaceutical therapeutics. Designed for a general, perhaps school-aged, audience, the document describes the drug, the pathway it targets, and how basic science (and fly) research led to this therapy.

- **Political Engagement.** One elusive goal of the committee has been to increase political engagement. Gio Bosco investigated how to make contact with his Congressional representative and reported his takeaways at the Janelia Workshop (in short: make nice with Congressional staffers.) This large goal might be best tackled with a scientific lobbying organization such as GSA or ASCB.

- **Fly video competition.** I was excited to organize a video competition of entertaining/educational fly videos, to be aired at TAGC, with the audience choosing the winner. A number of setbacks derailed me. Our student volunteer thought there would be few entries because it is hard to make a video. Although my own students were excited to make funny/silly videos, the committee was divided about how much the focus should be on entertainment vs. education. Perhaps most importantly, I was unable to find a site to host the videos. Chloe Poston at the GSA advised me twice on possible online resources but I could not establish a site where people could directly upload videos, anyone could watch them, yet we could moderate it (to remove potentially inappropriate content). Finally, there was no cash prize, a standard in similar competitions by other science organizations.

- **Radio shows.** Our student volunteer Saoirse McSharry reached out to Radio Lab and This American Life to suggest Drosophila-based shows. Radio Lab declined; TAL asked for more information and then was silent.

Challenges

There are three main challenges facing these allied committees going forward, and they are somewhat interconnected. The first is identifying the **target audience**(s). There may be benefits to addressing each of many distinct audiences: (1) the receptive public. (2) the hostile, small-government and/or anti-science public. (3) politicians. (4) news media. (5) non-fly scientists, including grant reviewers, textbook authors, and trainees making career decisions choosing fields of study. (6) the NIH. (7) the fly community. Because both the content and the delivery mechanism are different for each of these audiences, it is important to have a clear target. Committee members have different evaluations of where our efforts can be most productive, as did the participants in the Janelia workshop, as do Fly board members.

The second challenge is **time**. The need is great, but since we are all practicing scientists it can be hard to make the time to do what we would like. The Fly board and/or the GSA may want to consider paying someone, in some capacity, to ensure follow-through. However, this person would need clear instruction on the target audience(s).

The third challenge is **distribution**. Several of the deliverables of the committee would need to be disseminated to be useful. What are the means of this dissemination? If one or more website is established, how can content be maintained? This comes back to the idea of a staffer.

DISCUSSION: The Board discussed various ways to address these challenges. A meeting was scheduled for July 14, 2016 in Orlando, with NIH Director Francis Collins and Model Systems Community Leaders (the agenda is included at the end of the Agenda as Appendix 4).

ACTION ITEM: Follow-up on website progress, how to maintain effective communication.

16. Primarily Undergraduate Institutions: Alexis Nagengast

The Primarily Undergraduate Institutions (PUI) associated activities at this year's meeting are similar to previous years but several also include other model organisms. One major change is the splitting of the traditional Drosophila Research and Pedagogy at Primarily Undergraduate Institutions Workshop into two different workshops, both including other model organisms for TAGC. This split was based on feedback from a survey of the fly PUI community given after last year's meeting. The pedagogy workshop (Integrating Research and Teaching) focuses on undergraduate education at all types of institutions and not just PUIs. The undergraduate research workshop (Spotlight on Undergraduate Research using Genetic Research Models) will include eight talks from undergraduate students working with different model organisms. Beth Ruedi, GSA Director of Education and Professional Development, planned additional events and reached out to help make TAGC a productive and positive experience for undergraduate students and their professors/PIs.

Activities at this year's meeting include:

- Undergraduate Student Mixer on Wednesday evening before the Opening General Session.
- Undergraduate Plenary session and workshop for all undergraduate researchers attending the TAGC meeting at 4 pm on Thursday afternoon. This session is also open to the public as part of GSA's outreach program. Beth Reudi will be selecting two speakers that will represent two different communities. Additionally there will be a graduate student panel discussing the process of applying to graduate school and the life of a graduate student.
- Integrating Research and Teaching: Professional Development for Current and Future Faculty Members at 8 am on Saturday.

- Spotlight on Undergraduate Research using Genetic Research Models Workshop at 1:45 pm on Saturday.

There were a few concerns from PUI faculty about the cost of undergraduate registration for this year's meeting ($195 at the early GSA member rate) compared to previous years (~$60). However, many realized that the overall expense was about the same or lower than previous years when factoring in hotel room rates and flight/travel costs. It may be difficult for some PUI faculty to attend both Fly Meetings in Orlando and San Diego because both meetings fall in the same academic year. Our institutional travel funds typically cover one meeting per academic year, which runs from July 1, 2016 to June 30, 2017.

17. White Paper: Ken Irvine

Ken Irvine has spearheaded the writing of a new White Paper, with comments from the FlyBoard and community. The complete text is appended at the end of the Agenda (**Appendix 2**).

RESOLUTION: The Board voted unanimously to accept the White paper

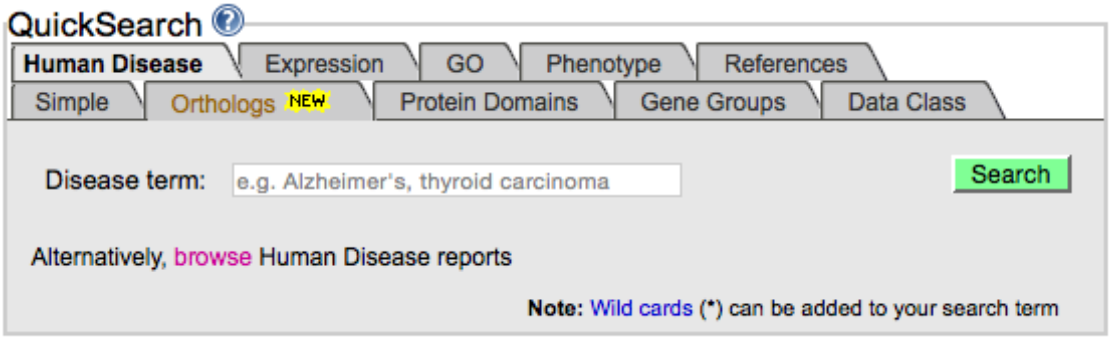
18. FlyBase: Norbert Perrimon

In the last year FlyBase has undergone a set of major changes. The foremost of these was the untimely passing of our PI Bill Gelbart. Bill's leadership since the founding of FlyBase and through the years was instrumental in the project's success. His vision for the utility of FlyBase to foster research in our community resulted in the valuable set of tools that have become a part of our daily lives. He will be missed both by his colleagues at FlyBase and the community at large. Before leaving us Bill approached Norbert Perrimon and asked if he would be willing to take on the leadership of FlyBase. It is our great fortune that Norbert agreed. He has taken on the job with great energy and those of us who have been with FlyBase for some time can attest that he is doing a fantastic job, has brought fresh eyes to the project, and has made important suggestions for improving the look, feel and functionality of the web site. The current PIs of FlyBase are:

Harvard
Norbert Perrimon
Cassandra Extavour
Cambridge
Nick Brown
Indiana University
Thom Kaufman
University of New Mexico
Rich Cripps

A second conspicuous event involves the NHGRI funding of 5 of the Model Organism Databases (MODs, FlyBase, WormBase, MGI, Zfin and SGD). The NHGRI desires two concurrent things to happen: 1. The MODs have been requested to amalgamate into a single web portal that will serve the commonly held data sets using a common set of query tools and a uniform set of output pages and 2. In order to help pay for this amalgamation the budgets of the MODs will be reduced significantly. The PIs of the 5 MODs plus RGD (rat) and GO have come together and formed a consortium (uMOD) in an attempt to affect this request. Their proposed solution will be presented to the NHGRI at a meeting, May 23-24 and the results of that meeting will be summarized at the board meeting in July.

A third important event was the request by NHGRI to make the utility of the MODs including FlyBase more obvious to those involved in the use of model organisms in translational research. Regarding the issues of making FlyBase more relevant to Human Disease models, we have made significant progress. In December, we convened a small focused Human Disease Advisory Committee (Joe Loscalzo, Chair of the Dept. of Medicine, BWH; Dick Maas, Chief of the Division of Genetics, BWH; and Calum MacRae, Chief of Cardiology, BWH) to discuss what information from FlyBase/MODs would be most useful to physician scientists. Based on their recommendations, together with the needs of the model organism communities, and utilizing as a starting point our ongoing efforts to integrate DIOPT orthology tools into FlyBase, we decided to build Gene2Function.org, a web site that will serve as a highly integrated hub to connect MOD-specific resources. As you all know well, the deep annotation of gene functions is scattered at each species-specific database making it slow and difficult to retrieve information on the function of a specific gene in a different species, whether predicted orthologs are associated with human disease(s), and/or to determine the function of the ortholog of a human disease gene in a model organism, etc. With Gene2Function, scientists will be able to query quickly a specific gene or groups of genes from any major model organism and view the orthologous genes from yeast to human on a single “all genes page". As noted, Gene2Function.org is built on DIOPT (http://www.flyrnai.org/cgi-bin/DRSC_orthologs.pl) a tool that predicts orthologous gene relationships from 10 different algorithms and provides a comprehensive view as well as reasonable ranking of prediction confidence of orthologous relationships. From the “all genes



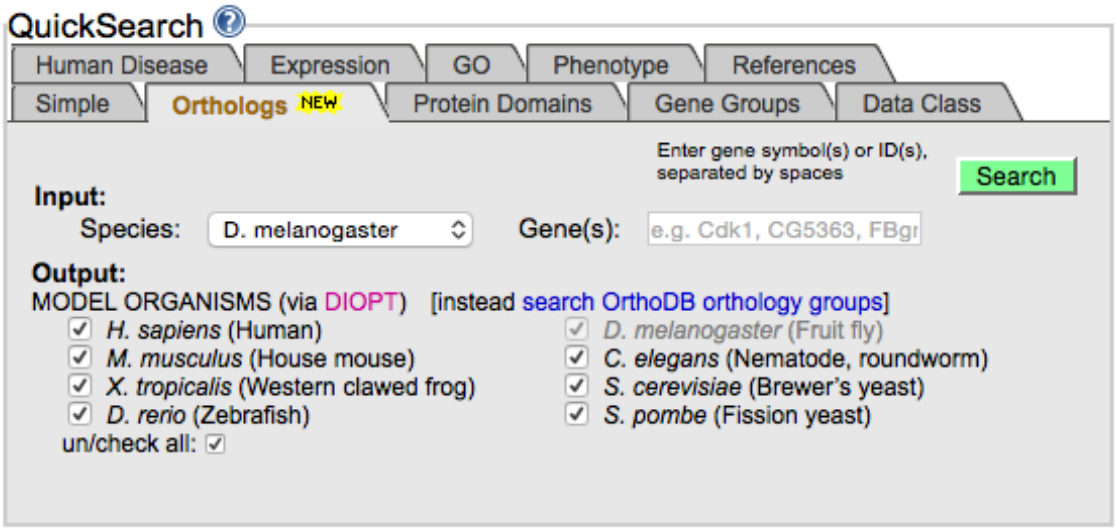
page”, users will be able to easily navigate to detailed gene reports of all the orthologous genes as well as human disease annotation if relevant. In addition, one will be able to query Gene2Function by disease terms and view the associated genes from all the MODs. The goal of Gene2Function is to facilitate studies using model organisms and to make an impact on basic biological insights and translational science. We are making excellent progress with this and should be able to present Version 1 at the upcoming NHGRI meeting in May. We also hope that Gene2Function Version 1 will help us engage in productive discussions with other MODs, in particular at the TAGC meeting in July in Orlando.

In addition to the Gene2Function effort we have added a new Human Disease tab to our Home Page. This tab allows one to search FlyBase by entry of a Disease name and retrive those fly genes that have been annotated as having a Human disease associated orthology or have been used to create a “Humanized” fly model of the disease.

In addition to these projects, we are working on two additional initiatives relevant to Human Diseases. First, in May, FlyBase curators organized a small meeting at Caltech with Human Disease curators from other MODs. The goal was to compare how annotation of Human Diseases is being done across the MODs. A desired outcome is to produce a standardized curation plan that

would facilitate integration. If we are successful, we will consider extending this approach to the curation of other data types across the MODs. Second, we have been working on a "Reagent Table" that we hope journals will use at the time of submission of research papers. The table would be filled in by the authors, submitted as supplementary material and will help identify which reagents were used in the publication. We think that doing this is important for two reasons: 1. It will help curators and PIs identify the exact reagents used in a particular publication, thus accelerating and improving the accuracy of curation and future research based on that paper; and 2. It will help address the issue of "Rigor and Transparency", enforced by the NIH. We shared the "Reagent Table" with other MODs, integrated their comments, and have now approached a number of journals (Cell journals, PLOS journals, ELife, Genetics and G3).

As noted above, FlyBase has recently incorporated orthology data from the DRSC Integrative Ortholog Prediction Tool (DIOPT). This dataset integrates ortholog predictions among nine species (*D. melanogaster*, *H. sapiens* and six other model organisms: mouse, rat, frog, zebrafish, worm, budding and fission yeast) from ten individual tools (Compara, Homologene, Inparanoid, Isobase, OMA, OrthoDB, orthoMCL, Phylome, RoundUp and TreeFam). The DIOPT approach provides a streamlined method for comparison of orthology predictions originating from different algorithms based on sequence homology, phylogenetic trees or functional similarity. DIOPT data are now searchable directly in FlyBase through the new 'Orthologs' tab of our QuickSearch tool, and are shown explicitly within the 'Orthologs' section of *D. melanogaster* Gene Reports. The orthology search tool is now available from a tab on the FlyBase home page.



The results page of a QuickSearch orthology search shows the list of ortholog predictions arranged by species. For each gene, the official gene symbol is shown alongside links to report pages at the relevant species databases, NCBI, Ensembl and/or OMIM. For DIOPT-based searches, the number and list of individual ortholog prediction tools that support a given orthologous gene-pair relationship is given, together with an indication of whether the given ortholog has the highest score for the query gene and whether or not the reciprocal relationship is also true. Links are also given to an alignment between orthologous gene-pairs on the DIOPT site, and to FlyBase Gene Reports where a non-*Drosophila* gene has been expressed transgenically in flies. A similar presentation is used for DIOPT-based data within the 'Orthologs' section of *D. melanogaster* Gene Reports.

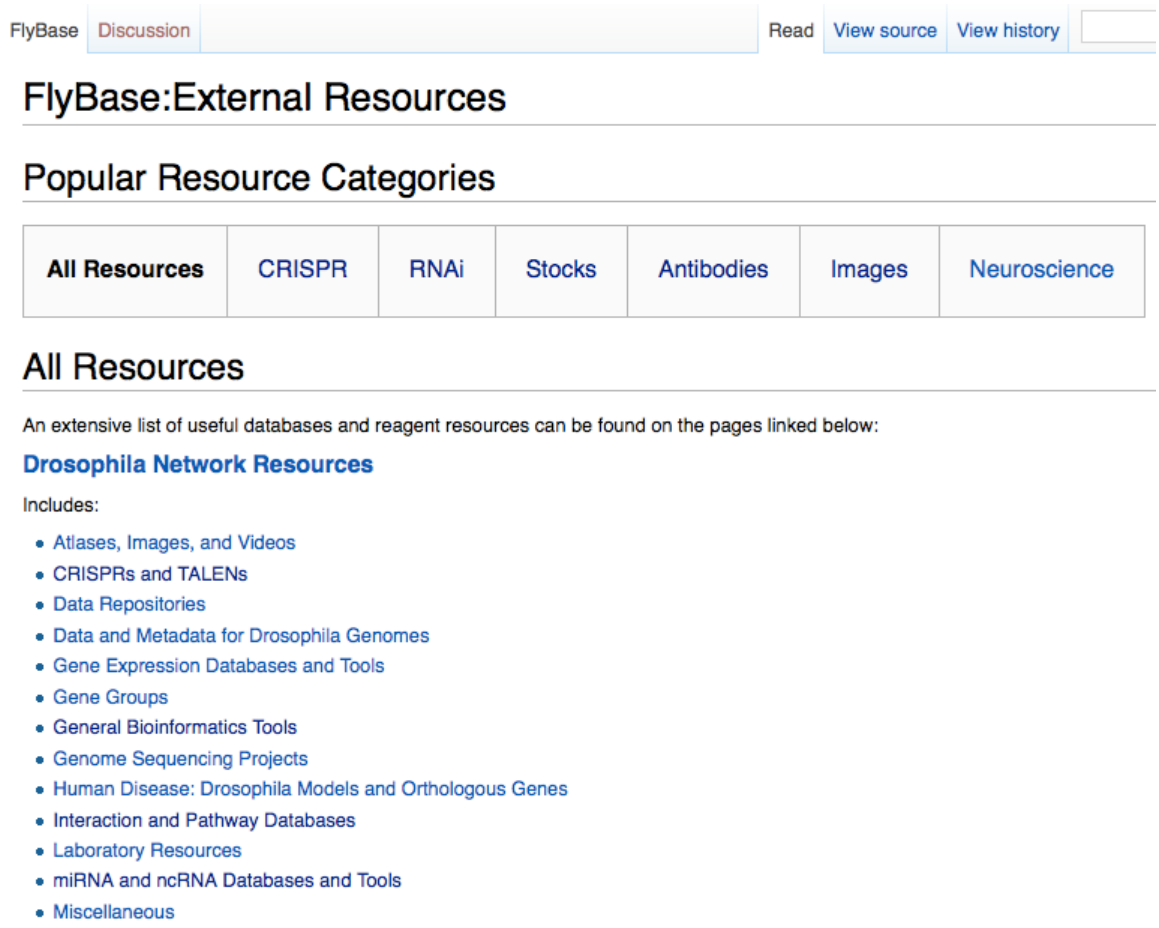
Save results as tsv file Help

Search Term: **dpp** Species: ***Drosophila melanogaster*** **(Fruit fly)** Gene: **dpp** Reports: NCBI FlyBase

Ortholog Gene	Ortholog Gene Reports	Via DIOPT (v5.1.1) Score	Best Score	Best Rev Score	Source	Align	Transgene in Fly
Homo sapiens **(Human)**							
BMP2	NCBI Ensembl HGNC OMIM	7	Yes	Yes (+)	Compara, Homologene, Inparanoid, Isobase, OrthoDB, Phylome, RoundUp	(+)	
BMP4	NCBI Ensembl HGNC OMIM	6	No	Yes (+)	Compara, Inparanoid, OrthoDB, orthoMCL, Phylome, RoundUp	(+)	Yes
GDF1	NCBI HGNC OMIM	1	No	Yes (+)	TreeFam	(+)	
GDF3	NCBI HGNC OMIM	1	No	Yes (+)	TreeFam	(+)	
Mus musculus **(House mouse)**							
Bmp2	NCBI MGI	7	Yes	Yes (+)	Compara, Homologene, Inparanoid, Isobase, OrthoDB, Phylome, RoundUp	(+)	
Bmp4	NCBI MGI	6	No	Yes (+)	Compara, Inparanoid, OrthoDB, orthoMCL, Phylome, RoundUp	(+)	
Gdf1	NCBI MGI	1	No	Yes (+)	TreeFam	(+)	
Gdf3	NCBI MGI	1	No	Yes (+)	TreeFam	(+)	
Xenopus tropicalis **(Western clawed frog)**							
bmp2	NCBI Xenbase	6	Yes	Yes (+)	Compara, Homologene, OMA, OrthoDB, Phylome, RoundUp	(+)	
bmp4	NCBI Xenbase	4	No	Yes (+)	Compara, OrthoDB, Phylome, RoundUp	(+)	
gdf1	NCBI Xenbase	1	No	Yes (+)	TreeFam	(+)	
gdf3	NCBI Xenbase	1	No	Yes (+)	TreeFam	(+)	
Danio rerio **(Zebrafish)**							
bmp2b	NCBI ZFIN	7	Yes	Yes (+)	Compara, Homologene, Inparanoid, OMA, OrthoDB, Phylome, RoundUp	(+)	
bmp2a	NCBI ZFIN	3	No	Yes (+)	Compara, Homologene, OrthoDB	(+)	
bmp4	NCBI ZFIN	3	No	Yes (+)	Compara, OrthoDB, orthoMCL	(+)	
bmp16	NCBI ZFIN	1	No	Yes (+)	Compara	(+)	
gdf3	NCBI ZFIN	1	No	Yes (+)	TreeFam	(+)	
Caenorhabditis elegans **(Nematode, roundworm)**							
dbl-1	NCBI WormBase	3	Yes	Yes (+)	Compara, Isobase, RoundUp	(+)	
tig-2	NCBI WormBase	1	No	No (+)	Inparanoid	(+)	
Saccharomyces cerevisiae **(Brewer's yeast)** - no orthologs found							
Schizosaccharomyces pombe **(Fission yeast)** - no orthologs found							

Another effort during the past few months has been organizing information on FlyBase to make it more user friendly. In many cases, the huge amount of information available at FlyBase was not readily available. Thus, we started implementing a “one stop shop” Resources Section approach with the goal that users should be able to go to FlyBase and open a window that contains all the information (stocks, reagents, protocols, relevant web sites, key publications, etc.) relevant to a specific topic. A number of such Resource pages have been produced and are currently available on FlyBase. These include categories such as RNAi, CRISPR, Stocks, Imaging, Neuroscience, Antibodies. Importantly, we have decided to actively engage the community in helping build these pages. Already, Pavel Tomancak contributed the Resource page on “Imaging”. **We welcome any suggestions and help from the community to build these resources.**

In the works are: miRNA, Methods, Clones and Proteomics. To facilitate the production of these pages, we have contacted experts in the community to help in this effort. For example, Eric Lai’s group is working with FlyBase to annotate miRNA information. miRNA expression levels have been calculated for various cell lines, developmental stages and tissues (44 conditions, consolidated from 277 RNA-Seq experiments). These data will be offered on FlyBase miRNA gene reports, with a detailed view of mature miRNA distribution in GBrowse, and a tool permitting users to find miRNAs by their expression profile. These expression data have also been provided to the DRSC to inform miRNA target prediction, which will be incorporated into FlyBase gene reports of miRNAs and their predicted targets when available. We are also planning on GBrowse track representations of the miRNA expression and target sequence data. Additionally, the Lai group has provided miRNA conservation data that will be displayed in FlyBase gene reports to help users find those miRNAs that are conserved and thus more likely to be biologically relevant.



FlyBase Discussion Read View source View history

FlyBase:External Resources

Popular Resource Categories

All Resources	CRISPR	RNAi	Stocks	Antibodies	Images	Neuroscience

All Resources

An extensive list of useful databases and reagent resources can be found on the pages linked below:

Drosophila Network Resources

Includes:

- Atlases, Images, and Videos
- CRISPRs and TALENs
- Data Repositories
- Data and Metadata for Drosophila Genomes
- Gene Expression Databases and Tools
- Gene Groups
- General Bioinformatics Tools
- Genome Sequencing Projects
- Human Disease: Drosophila Models and Orthologous Genes
- Interaction and Pathway Databases
- Laboratory Resources
- miRNA and ncRNA Databases and Tools
- Miscellaneous

We are also in collaborations with Lucy Cherbas and the DGRC. They have assembled a list of references that use cell lines and made associations to the particular cell line used. FlyBase is incorporating these references into our cell line reports and will carry on the task of identifying the cell lines used in papers. We will enlist the help of authors to identify additional papers by adding a new 'stable *Drosophila* cell line used" flag to the 'Fast Track Your Paper' tool. We will also capture the cell lines used at the time of skim curation of new papers. The cell line identity is a critical piece of information needed by users when evaluating any set of experiments.

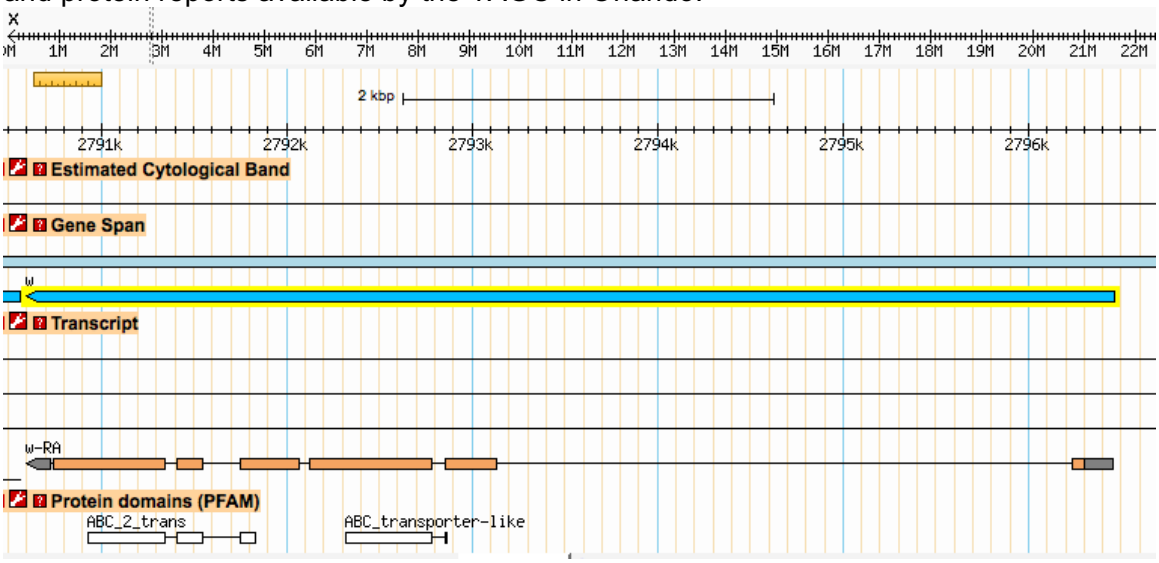
Another noticeable achievement includes creation of six FlyBase video tutorials (and more are being made), these include:

1. "How to cite FlyBase in a publication"
2. "How to find all data related to a gene in FlyBase"
3. "How to generate an excel file of all alleles of a gene"
4. "Author Guidelines in FlyBase."
5. "RNA-Seq Part I: Using GBrowse"
6. "RNA-Seq Part II: Using RNA-Seq Profile Search"

These can be found through our web site at: https://www.youtube.com/channel/UCG-KSNq46vkezAwbrVQojYA/feed.

In addition, we have implemented protein motif data into our database for display. Motif

information obtained from InterPro (specifically the PFAM subset) will be displayed on FlyBase in three places – the protein report where all motifs mapped to a protein isoform are displayed, the gene report where the domains of an exemplar protein (initially the longest) will be used to represent the domain complement of the gene and in Gbrowse where a non-redundant set of motifs for that gene will be shown in the genome context. We have made our implementation flexible so that in the future we can add additional or different sources of motif data and enhance various aspects as needed. In the current release only the GBrowse version is shown. We hope to have the models in the gene and protein reports available by the TAGC in Orlando.



In a project funded by the British Medical Research Council, we are engaging community experts to help us write very brief summaries of fly gene function. Following an initial pilot, the FlyBase PIs have agreed that these summaries should simply briefly report the molecular and biological function of the gene product, using general, non-*Drosophila*-specific language. We have perfected our computational approach to utilize the curated data in FlyBase to identify research papers that have a particular focus on the function of each gene, which then enables us to identify expert authors for each gene. We have started to e-mail authors to request their assistance, with the goal of completing 3000 summaries by October. We are delighted to report that our community has responded very enthusiastically to our requests, so that at the time of writing they have provided key information to guide our summary writing for ~700 genes. Once we have edited summaries for 1,000 genes we will start making them available in the gene reports.

Our ability to pull out the key research papers focused on each gene, based on the data from that paper in FlyBase, will also be used to generate a new summary page for each gene containing the titles and abstracts from these key papers. This will provide an additional way for researchers to rapidly discover what is known about a gene product. As this is a purely computational pipeline, it will be updated in each release, and so reflect the latest literature.

With GSA's help, we have organized a MOD-shared demo-room, centrally located, at the TAGC in Orlando. This allows for two days of one-on-one demonstrations and short scheduled presentations by each of the MODs. FlyBase, WormBase, MGI, Zfin, and

SGD will all have representatives present. We feel it will be beneficial to future collaborations to have members from the 5 MODs in one room.

The DAP program continues to thrive. Of the five post baccalaureate scholars appointed during summer 2015, four applied and were accepted to graduate programs. New scholars will begin this summer. The Frontiers in Genomics class held last semester (with assistance in lead instruction by Bruce Birren of the Broad Institute), went well, and featured guest speakers Kevin White (Institute for Genomics and Systems Biology, University of Chicago) discussing cloud computing and genomic approaches to understanding cancer biology, Danny Park (Harvard University), discussing genomic approaches to understand the spread of emerging diseases; Scott Edwards, (Harvard University) discussing bird phylogenomics; Elaine Mardis (Washington University) discussing cancer genomics; and Thom Kaufman (Indiana University of FlyBase co-PI), discussing evolution of the Hox genes.

Below is a listing of several of the updates, additions and changes made to FlyBase in the last year.

March 30, 2016

- **New orthology data and query tool**
  - FlyBase has incorporated orthology predictions between genes of 8 model organisms from the DRSC Integrative Ortholog Prediction Tool (DIOPT). These DIOPT-derived orthology calls are now shown explicitly within the 'Orthologs' section of *D. melanogaster* Gene Reports, alongside our exisiting orthology set from OrthoDB that is biased towards species closely related to *D. melanogaster*. Both datasets are searchable through the new 'Orthologs' tab of our QuickSearch tool.
- **miRNA annotation set update**
  - The FlyBase miRNA annotation set has been updated to correspond with miRBase release 21. This has added a number of new miRNA annotations for *D. melanogaster* (18), *D. virilis* (60) and *D. pseudoobscura* (1). In addition the remapping of the *D. simulans* miRBase annotations to the new release 2 assembly resulted in the elimination of 16 miRNA gene annotations, primarily removing redundant annotations that were due to assembly artifacts.
- **Systematic nomenclature for *D. melanogaster* tRNA genes**
- We have worked with the Genomic tRNA database (GtRNAdb) to systematically identify and assign informative nomenclature to the ~300 nuclear genes encoding cytoplasmic tRNAs in *D. melanogaster*. These data are best viewed via the new Gene Group page for these genes.
- **P{acman} clones now in GBrowse**
  - PacMan clones from the Chori-321 and Chori-322 libraries can now be viewed in Gbrowse by selecting those tracks from the 'Other reagents' section on the 'Select Tracks' tab of GBrowse.

- *January 14, 2016*
- **External Resources pages**
  - The FlyBase website contains hundreds of links to useful external sites concerning stocks, antibodies, CRISPR, and more. These links have been gathered together and placed on the FlyBase Wiki as several well-organized lists for easy browsing: http://flybase.org/wiki/FlyBase:External_Resources
  - A prominant new button (External Resources) on the FlyBase home page will

take you there, or use the navigation menu at Links → External Resources.

- **New video tutorials**
  - New video tutorials have been made to help you navigate in and use FlyBase. You can find the new videos under Help → Video Tutorials.
- **P{acman} clones**
  - Information on 49422 concordantly mapped P{acman} clones has been added to FlyBase. 12456 of these clones are from the CHORI-321 library (average insert size 83 kb) and 36966 are from the CHORI-322 library (average insert size 21 kb). Construction and characterization of these libraries are described in FBrf0209231. Information on these clones are available in FlyBase in the relevant clone and dataset reports. See the links in the 'External Crossreferences and Linkouts' section of a clone report to determine if a clone is available for purchase from BACPAC resources.
- **Histone modification and TFBS data for embryonic mesoderm: GBrowse tracks**
  - Histone modification data for the embryonic mesoderm are now available (Bonn et al., 2012). These include ChIP-seq genomic occupancy data for H3K4me1, H3K4me3, H3K27Ac, H3K27me3, H3K36me3, H3K79me3 and RNA Pol II (RpII33 subunit) obtained from purified embyronic mesodermal cells. FlyBase offers the ChIP-Seq peak calls in a new GBrowse track, listed under the "Noncoding Features" section of the tracks listing: Histone Modifications - mesoderm (Furlong lab, ChiP-Seq peak calls)
  - ChIP-chip genome binding data for transcription factors key to mesodermal development are now available. Data for 13 transcription factors at various points of embryogenesis (28 samples in all) have been kindly provided by Eileen Furlong's lab (EMBL), comprising several studies: Zinzen et al., 2009, Bonn et al., 2012, Junion et al., 2012, Rembold et al., 2014 and Ciglar et al., 2014. FlyBase offers the ChIP-chip peak calls in a new GBrowse track, listed under the "Noncoding Features" section of the tracks listing: TFBS - mesoderm (Furlong lab, ChiP-chip)

December 12, 2015

- **Community page**
  - Several community-building resources in the FlyBase site have been consolidated into a new Community page. Sign up for our newsletter or Twitter feed, use the FlyBase People database, or visit the FlyBase Forum. Click on the “Join Our Community” button in the FlyBase home page sidebar.

October 28, 2015

- **RNA-Seq tools re-organized**
  - The four most-used tools for access to FlyBase RNA-Seq data: GBrowse, RNA-Seq Profile, RNA-Seq Similarity, and RNA-Seq By Region, have several new entry points. FlyBase users can now find these tools gathered under a single menu heading (Tools ⇒ RNA-Seq Tools), and the QuickSearch Expression tab now has a panel with links to each tool. Each of these access points also has a link to a new RNA-Seq tools summary page, where you can learn more about how and when to use each of these tools, with links to the tools and in-depth help.

November 20, 2015

- ***D. virilis* release incremented**

- At the request of the NCBI, 4 rRNA annotations have been removed from the *D. virilis* genome. The *D. virilis* release number has been incremented to 1.04.

September 3, 2015

- **Fast-Track Your Paper tool upgrade**
  - The FlyBase Fast-Track Your Paper community curation tool has been upgraded. New features of note include being able to upload a list of genes to associate with your paper, 'sessions' so you can go back and change mistakes in a submission, or even take a break and finish entering data later, and more flexibility in ordering data entry tasks.
- **Human Disease Model reports**
  - The FB2015_04 release of FlyBase includes the addition of Human Disease Model reports, which integrate all the disease-related information from multiple reports in FlyBase. These reports highlight the role of systems modeled in flies on research into human disease and the potential impact of the results on translational research. One of the purposes of this report format is to provide a less specialized entry point for non-*Drosophila* researchers and for *Drosophila* researchers newly interested in *Drosophila* disease model systems.
- **GBrowse improvements**
  - Following a recent FlyBase Community Advisory Group survey, several improvements have been made to GBrowse. The default tracks have been updated, a Snapshot feature, allowing you to easily save and view images, has been made more accessible and additional help documentation has been added.
- **Changes to FlyBase home page and navigation**
  - The addition of the new Gene Groups tab to QuickSearch necessitated the partitioning of the QuickSearch tabs into two rows. FlyBase has also restructured the navigation bar and left sidebar.
- **Gene Groups data class additions**
  - FlyBase users can now browse a list of gene groups, or search for Gene Group report pages using the new QuickSearch tab. A new bulk data file is also available here.
- **VDRC Vienna Tiles GBrowse track**
  - FlyBase now offers a GBrowse track to help users browse lines from the VDRC Vienna Tiles (VT) GAL4 collection, listed in the "Other Reagents" section of the GBrowse Track Selection page. The glyphs represent putative enhancers used to generate fly stocks carrying GAL4 transgenic constructs. Clicking the glyph brings up the associated Sequence Feature report - see the "Associated information" section for related genes and constructs (links to stock reports therein): *e.g.*, VT020839. The FlyBase VDRC-VT report offers additional details about the VDRC-VT collection.
  - Report and QuickSearch help revised
- **Improved esyN interactions graphic on gene reports**
  - FlyBase has incorporated a number of improvements to the interactive esyN network graphics. In the gene report, users can now choose to display interactions between neighbors (*i.e.*, interactions between interactors of the gene of interest). To make better sense of complicated networks, three different layout options are available: force directed (default), circle and concentric. These configuration options are shown to the left of the esyN display. FlyBase also now offers esyN displays in the interaction report, where the two subjects of the interaction report are highlighted in pink, and common interactors of the two

factors are highlighted in purple. The force directed, circle and concentric layout options are also available in these interaction report graphics. Please note that these new configuration options do not work in older versions of Safari (v5). FlyBase would like to thank the esyN group (http://www.esyn.org/) for making these new configuration options possible.

◦ *June 26, 2015*
◦ **Protein Domains tab in QuickSearch**
  • The QuickSearch tool on the FlyBase home page has a new tab for searching genes using InterPro protein domain annotations.
◦ **esyN interaction view in gene reports**
  • FlyBase gene reports now include an interactions graphic provided by esyN. The network is interactive, and a linkout goes to the same interaction network at the esyN site, where further configuration and editing is available.
◦ **New reports for non-transposable element based insertions**
◦ FlyBase already produces an Insertion Report for insertions of transposable-element based transgenic constructs, *e.g.* P{GawB}Dll^{em212}. Starting in the fb_2015_03 release, we now also generate an Insertion Report if exogenous DNA is inserted into the genome via non-transposable element-based means. In this case, since no transposable-element ends are present, the ends of the inserted element are designated using 'TI' (for 'transgene insertion') *e.g.* TI{GAL4}.
◦ **RNA-Seq by Region query tool**
  • The new RNA-Seq By Region tool reports the average (per base) expression level for a given genomic region in the modENCODE developmental and tissue RNA-Seq transcriptome profiles. This tool allows one to evaluate the approximate expression level of individual exons, parts of exons, introns and/or intergenic regions. It can be accessed from any FlyBase gene report, in the "High-Throughput Expression Data" sub-section of the "Expression Data" section.
  • Please note that the tool previously called "RNA-Seq Search" has been renamed to "RNA-Seq Profile Search"; FlyBase hopes this change will prevent possible confusion between the two tools.

◦ *March 1, 2015*
◦ **FlyBase newsletter launched**
  • FlyBase users have indicated on surveys that their preferred method of contact is via email. Accordingly, FlyBase will be sending an occasional mailing to our user list, with release announcements, web site updates, and important *Drosophila* community news. Our first such newsletter went out on March 1 of this year.

◦ *May 4, 2015*
◦ **Gene Group reports**
  • FlyBase is introducing new 'Gene Group Reports', which will bring together genes/gene products that are acknowledged to form a biological group, such as members of a gene family (*e.g.* Actins, Wnts), subunits of a protein complex (*e.g.* proteasome, ribosome), or another functional grouping (*e.g.* Ubiquitin E3 ligases). Gene Groups may be searched via the Simple tab of QuickSearch, or navigated to via the new 'Gene Group Membership' section of a Gene Report.
◦ **3 more species genome annotations updated**
  • Annotations generated by NCBI as part of their GNOMON annotation pipeline will replace the CAF1 generated annotations that have not changed since 2006. Three additional species; *D. mojavensis*, *D. virilis* and *D. willistoni* now have

updated GNOMON annotations for a total of 8 species.

- **Gene-level genetic interaction data**
  - A gene-level summary of genetic interaction data for *D. melanogaster* genes is now being computed each release from the allele-level genetic interaction statements captured by FlyBase (this new summary replaces out-of-date gene-level genetic interaction data that was no longer being maintained). The summary gives an overview of the genetic interactions for a gene, complementing the allele-level statements which give a detailed view of each individual interaction.
  - The gene-level genetic interaction data can be accessed in two ways:
  - 1. The 'Summary of Genetic Interactions' section on the Gene Reports contains a table showing the gene-level genetic interaction summary. The table shows which gene(s) have been shown to interact genetically with the gene, together with the nature of the interaction ('enhanceable' or 'suppressible') and the reference(s) from which the data came in each case.
  - 2. A bulk file is accessible through the Precomputed Files page (Files menu ⇒ Current release, "Genetic interaction table" under the Genes section). The format is described here.
- **NIH Expression data plots added to Dpse gene reports**
  - The RNA-seq expression data provided by the Oliver group for *D. pseudoobscura*, and currently displayed in FlyBase GBrowse, can now also be seen in gene reports. Many *D. pseudoobscura* reports now have an expression plot showing these data, similar to those shown on *D. melanogaster* reports for modENCODE expression data.

- *December 2014*
- **Wiki page for FlyBase Community Advisory group**
  - A new Community Advisory Group wiki page has been added, accessible from the Documents section of the homepage. The page includes information about the group, how to join and update your details, and results of the surveys carried out so far.

- *February 24*
- **5 species genome annotations updated**
  - For 5 of the sequenced species; *D. ananassae*, *D. erecta*, *D. pseudoobscura*, *D. simulans* and *D. yakuba*, the CAF1 generated annotations that have not changed since 2006 are being replaced by annotations generated by NCBI as part of their GNOMON annotation pipeline as described in this paper (http://www.ncbi.nlm.nih.gov/core/assets/genome/files/Gnomon-description.pdf), with additional information at http://www.ncbi.nlm.nih.gov/genome/annotation_euk/process/. We have maintained gene, transcript and protein symbol and IDs for GNOMON annotations identified by NCBI as corresponding to existing CAF1 annotations but many models have new identifiers.
- **New reference mitochondrial genome assembly**
  - In FB2015_01, a new *D. melanogaster* mitochondrial genome assembly derived exclusively from the "iso-1" sequenced strain (NCBI KJ947872.2, RefSeq NC_024511.2) replaces the old mitochondrial genome assembly, which was a composite of sequences from various *D. melanogaster* strains. See the current release notes for more details on the new mitochondrial genome assembly.

FlyBase features have been migrated from the old to the new mitochondrial genome assembly. There have been small changes to the nucleotide sequence of the following genes: mt:ATPase6, mt:Cyt-b, mt:ND1-PA, mt:ND4, mt:ND5, mt:lrRNA and mt:ori. The previous mitochondrial assembly continues to be accessible through the archived FlyBase releases.

- **Automatically Generated Summary updated**
  - The '*Comments on Affy2 ProbeSet'* and *'Summary of FlyAtlas Anatomical Expression Data'* sections of the Automatically Generated Summary on the gene reports have been removed. These data are still available elsewhere on the website.

DISCUSSION: It was agreed by all that the loss of Bill Gelbart was immense, but that he made a superlative choice of successor in Norbert Perrimon.

The Board discussed other items to add to FlyBase's scope: better annotation to appeal to physicians and to leverage medical science or disease-based organizations such as the AMA for exposure and resources; the possibility of obtaining funding for FlyBase from private organizations (HHMI, Wellcome, etc), as is currently the practice in Europe; a continually updated reagent and resource category that will assist the new requirement by the NIH and in some journals for standardized resources, including detailed genotypes.

ACTION ITEM: It was generally agreed that the Board should identify and recruit 1-2 people who are willing to determine what the general community feels is important to have included on FlyBase.

19. MOD Support Open Letter: David Bilder

Given the changes initiated by NIH to funding and organization of Flybase and the other Model Organism Databases (MODs), it was thought that a general letter of support for maintaining key but threatened features and overall funding for the MODs, signed by the breadth of scientists who use them, could be constructive. I wrote a draft, coordinated with FlyBase leaders, and took it to leaders of the fish, worm, yeast, and mouse communities. We arrived at a consensus letter that articulates the case for the MODs and the model organisms in general. GSA created a website that allowed collection of signatures, launched on June 21. GSA has also arranged a meeting with Francis Collins at TAGC where community leaders and GSA officers will speak with him about the MODs and model organism funding. We aim to collect as many signatures as possible in order to 'present' the letter to Collins. Model organism community Presidents, Presidents of scientific societies, and Nobel laureates were successfully solicited as highlighted signatories.

Signatures passed 11,000 on July 5th, roughly 1/2 from US-based and 1/3 from NIH-supported researchers. I think that we can take the degree of support as an overwhelming endorsement of the MODs and their community-specific features, and it can also be used to re-emphasize the general value of model organisms to the research community.

One lesson to come from this initiative is the value of coordination amongst model organism communities around common goals. Some but not all of the communities have established FlyBoard-like organizational structures. A formal or informal network

amongst the communities, especially where representative leadership is clear, creates opportunities that otherwise would not exist.

20. Bloomington Stock Center: Kathy Matthews, Kevin Cook, Annette Parks, Thom Kaufman

Stock Holdings as of 5/13/2016

- 59,006 stocks with 62,081 unique genetic components
- 11,424 annotated *D. melanogaster* genes are associated with alleles or constructs in the collection
- 3,333 registered user groups, 1,975 of which ordered stocks in the past year
- 6,679 registered users, 3,031 of whom ordered stocks under their own name in the past year

2015 Use Statistics

- 243,148 samples shipped in 14,180 shipments
- 4.5 orders per stock on average, range 0–142; 69% of stocks ordered at least once, 22% ordered 6 or more times, 12 stocks ordered >100 times, *elav-GAL4* (#8760) was the most popular

Growth

5267 stocks were accessioned in 2015:

- 144 Janelia Farm *lexA* drivers
- 1,014 Gene Disruption Project *Mi{MIC}* insertions
- 1,605 Transgenic RNAi Project stocks
- 476 GFP-tagged proteins from RMCE of *Mi{MIC}* insertions from the GDP
- 724 *P{IT.GAL4}* enhancer trap insertions from the InSITE Project
- 47 Trojan system GAL4 lines from Benjamin White
- 37 ionotropic receptor-GAL4 drivers from John Carlson
- 28 GFP-tagged transcription factors from the modERN Project
- 139 UAS-miRNA sponge constructs from David Van Vactor
- 55 lines for multicolor stochastic cell labeling from Barret Pfeiffer
- 57 *P{Switch2}* insertions from Haig Keshishian
- 157 UAS-miRNA constructs from Steve Cohen
- 125 P element insertions from the GDP
- 659 stocks from other donors

Staff now consists of 47 stock keepers (22 full-time equivalents) and 7 managers/scientists.

Grant Funding We are in year 2 of a 5 year grant from NIH, $432,104 direct costs. Increased income from user fees is paying for growth of the collection.

New Stocks We expect to add 4,000 to 4,600 new stocks in 2016:

- 1,700 Transgenic RNAi Project stocks
- 750 InSITE Project stocks
- 400 UAS-human cDNA lines from the labs of Hugo Bellen and Sue Celniker
- 650–750 lines from the Gene Disruption Project (including 300–400 CRIMICs, 300 T2 GAL4 stocks and 50 tagged protein stocks)
- 500 stocks in all categories from the community at large

Pruning We plan to discard several hundred older P insertions and ~1,900 Janelia GAL4 drivers in 2016.

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

21. VDRC stock center: Lisa Meadows

Vienna Drosophila Resource Center (VDRC), Vienna, Austria

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 Drosophila researchers, both locally and world-wide, and to further develop and expand VDRC resources according to the emerging new technologies and community needs.
Core funding from Austrian Federal Ministry for Science and Research and the City of Vienna currently covers ~30% of total running costs. The remaining 70% of the costs must be recovered from user fees, which have not been increased since June 2014.

Key changes during 2015

1. Acquisition of Tagged FlyFos TransgeneOme (fTRG) library

Donated by Frank Schnorrer (Max Planck Institute of Biochemistry, Martinsried, Germany) and Vijay Raghavan (National Center for Biological Sciences, TIFR, Bangalore, India). This versatile collection consists of 880 transgenic fly lines covering 826 different genes. Each line has been engineered to tag a specific protein with a multi-epitope tag at its C-terminus, for use in a variety of downstream applications including live imaging, subcellular localization studies and interaction proteomics at all stages of Drosophila development.

2. Private stock keeping service extended

The number of stocks maintained on a fee paying basis has increased to ~3000 and a selection of these private stock collections are also publicly available via the 'Other Resources' section, thereby increasing the diversity of the VDRC stock collection.

3. Host institute name change to VBCF

The VDRC host institute changed its name from "Campus Science Support Facilities GmbH" (CSF) to "Vienna Biocenter Core Facilities GmbH" (VBCF). All VDRC services continue exactly as before, with the only change being that invoices are issued by VBCF. All bank details remain unchanged.

Usage Statistics 2015

- Registered users worldwide: **2,463**
- Stocks delivered externally in 2015: **70,672** in **1,771** separate orders
- Total stocks delivered to Drosophila community since 2007: **>1,260,000**

Resources as of May 2016
Total stocks currently available to the community: **35,940**

- 26,585 RNAi lines (16,763 in GD, 9,822 in KK and 177 in the shRNA collection).
- 18 toolkit stocks used for the construction of the RNAi collections.

Collectively, the GD, KK and shRNA 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.

- 8,457 enhancer-GAL4 lines (VTs, Vienna Tiles). Expression patterns annotated in adult brain and embryo. Searchable databases available.
- 880 Tagged FlyFos TransgeneOme (fTRG) lines.
- 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 on a cost recovery basis and also offer a fly food service. See VDRC policy for stock keeping services.

Future
We are in the process of creating some new RNAi lines using shRNA technology, with the ultimate aim of having 2 independent lines per gene. Nearly 200 new shRNA lines are available as of April 2016.

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.

21a. Kyoto Stock Center, Japan: Toshiyuki Takano-Shimizu

The Kyoto Stock Center is currently in good financial shape. They are in discussions with FlyBase about how to contribute. Questions remaining to be resolved for this include exploring what options are available for contribution, how to donate to Flybase, and how to unite the stock center databases.

22. Species Stock Center, UC San Diego: Maxi Richmond

- Stocks held: 1,488 (a decrease from 1,641 in 2014)
- Registered Users: 1,663 (an increase from 1,423 in 2014)
- Shipped in 2015: 1,048 subcultures in 259 shipments (a decrease from 1,137 subcultures in 2014, but an increase from 253 shipments in 2014)
- **Funding:**
    - As of April 2015 the DSSC started Year 1 of a 3-year grant from NSF, which provided $96,775 in direct costs. The annual operating budget for 2015 was $159,050.

    - Revenues for 2015 were $44,730. The deficit was covered by support from UCSD for stock keeper salaries, and the DSSC differential (reserve) account.
- **Sustainability:**
    - The outlook for continued funding for the DSSC is uncertain. The NSF CSBR program that currently funds the DSSC is on hiatus for fiscal year 2017 for re-evaluation.
    - On 25May16 NSF released an update that a biennial competition for CSBR proposals would commence in 2017, no additional program changes were announced but are anticipated
    - Community support for the DSSC (and living collections in general) is crucial right now
    - We asked our users to respond to the NSF hiatus, and many submitted feedback to NSF highlighting the importance of the collection
    - We have requested support from FASEB, the GSA, Fly Board, and the living collections community in the form of feedback to NSF
    - If current NSF funding restrictions continue major changes will be needed to keep the DSSC sustainable.
- **Growth:**
    - Due to the limited funding, the DSSC has only allowed new accessions of stocks if others could be pruned.
        - Twenty stocks (17 of which were new species to the collection) from Ary Hoffmann and Michelle Schiffer (University of Melbourne) were added to the collection
- **Personnel**
    - Stock keeping staff consists of 7 undergraduate part-time employees providing 1.25 full time equivalent (FTE). Management staff is 1.25 employees.
- **Costs:**
    - Stock center daily operations and stock maintenance accounts for ~87% of costs
        - Average annual maintenance cost per stock: ~$96.92
- **Cost recovery:**
    - Price per stock: $35
    - 20 ug genomic DNA: $127
    - Special services/requests: $135/hour
- **New stocks:**
    - We are currently not in a position to add more than 20 new stocks in the current year, and will be selective choosing high value stocks with genome sequences or other outstanding characteristics.
- **Pruning:** We continuously evaluate usage of stocks and remove any that are not commonly ordered. We decreased the collection by 153 stocks in 2015.
    - Eight mutant *D. buzzatii* stocks were de-accessioned due to lack of use and mite contamination.
    - Twenty-one stocks were lost due to reproductive failure and/or bacterial contamination.
    - The remaining stocks pruned from the collection were deemed low value based on minimal demand
- **Future**

- The DSSC will be changing directorship from Therese Markow to Patrick O'Grady, and will be moving to UC Berkeley at the beginning of 2017.
- Staff will be reduced to 1 full-time Curatorial Assistant in addition to 1.25 FTE equivalent of undergraduate stock keepers.
- Both Teri and Maxi are willing to serve on the Scientific Advisory Board during and after the transition.

- **Scientific Advisory Board**
  - Patrick O'Grady (University of California, Berkeley)
  - Harmit Malik (Fred Hutchinson Cancer Research Center)
  - Sean Carroll (University of Wisconsin, Madison)
  - Steve Schaeffer (Penn State)

DISCUSSION: Maxi Richmond is working with officials at the NSF to deal with the DSSC funding uncertainty. In addition, she is serving on the Shared Resource Center of FASEB in order to communicate shared resources. David Bilder asked if and how FlyBoard could help with funding issues. It was agreed that the next FlyBoard president, Laura Johnston, will coordinate with Maxi and the NSF to identify ways the FlyBoard can assist the DSSC. It was pointed out that the NSF is "in crisis" with respect to living stock collections, and that there appears to be a general lack of interest for funding MOD infrastructure.

ACTION ITEM: The FlyBoard is available to provide as much assistance as needed to the DSSC in their communications and negotiations with the NSF.

23. Drosophila Gene Disruption Project (2003-2019): Bellen, Perrimon, Hoskins, Spradling Laboratories

Since its inception, the Gene Disruption Project (GDP) has strived to provide publicly available strains that facilitate access to the Drosophila genome and all its regulatory and coding elements. Our goal during the most recent past 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 genes *in vivo* (Figure 1; Venken et al., 2011). The GDP generated about 17,500 MiMIC strains and selected 7,400 insertions, including ~2,850 known protein coding genes, for public distribution by the Bloomington Drosophila Stock Center (Venken et al., 2011; Nagarkar-Jaiswal et al., 2015b). During the more than twenty years mutants were generated using transposition, we also characterized transposon specificity as a side benefit (Bellen et al. 2011; Spradling et al. 2011).

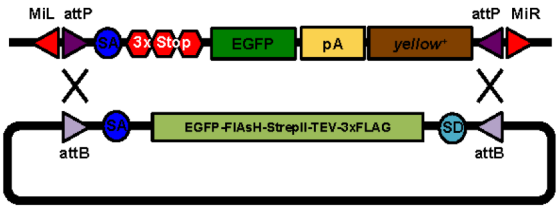


Figure 1. Key features of the MiMIC TE. Minos ends (MiL/MiR) for random genomic integration and attP sites flank a mutagenic gene trap, EGFP and *yellow*$^{+}$ markers. DNA of any design between attB sites (in this case a "reporter" exon) can be swapped by RMCE, replacing *yellow*$^{+}$. Splice acceptor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

One of the major attractions of the MiMIC system is its potential to generate functional GFP fusions of 70% of the Drosophila protein coding genes. The GDP MiMIC insertions which are present in coding introns allow us to generate an artificial exon that encodes EGFP-FlAsH-StrepII-TEV-3xFLAG fusion proteins (Figure 1). Almost all tagged genes/proteins allow determination of precise protein distribution as well as purification strategies using nanobodies against GFP such as immunoprecipitation (IP) of proteins (Neumüller et al., 2012), chromatin IP for DNA-associated proteins, and IP-mass spectroscopy (Zhang et al, 2013). We showed that 77% of internally-tagged proteins are functional, and that more than 90% can be imaged in unfixed tissues in third instar larvae. Moreover, the tagged mRNAs can be knocked down by RNAi against GFP (iGFPi) (Neumüller et al., 2012; Nagarkar-Jaiswal et al., 2015b) and the tagged proteins can be efficiently knocked down by deGradFP technology (Caussinus et al., 2011; Nagarkar-Jaiswal et al., 2015b). 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 about 2,000 genes that contain intronic MiMICS (Nagarkar-Jaiswal et al., 2015b). Additionally, we developed a system whereby the conversion is carried out through genetic crosses instead of injections (Nagarkar-Jaiswal et al., 2015a). The donor MiMIC insertion stocks (on X, 2, and 3) have been made available to the BDSC. This large-scale generation of protein tags by the GDP provides a major resource for the Drosophila community (Nagarkar-Jaiswal et al., 2015a,b) and we have presently generated tagged insertions in ~600 genes, almost all of which have been deposited in the BDSC. Our website at http://flypush.imgen.bcm.tmc.edu/pscreen/rmce documents the expression pattern in third instar nervous system as well as other available information.

Funding support for the GDP (NIGMS R01 GM06785) was renewed in 2015 and is now in its second year (year 14). We continue to utilize the MiMIC collection as the foundation for our projects. 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 donor cassette to insert an artificial exon that encodes the T2A-GAL4 in MiMICs inserted in coding introns. This creates a null allele and leads to the production of GAL4 protein in the endogenous expression pattern, permitting numerous elegant manipulations. We have created and validated insertions for 150 genes using the T2A-Gal4 RMCE donor and will soon begin depositing them in BDSC. We plan on tagging about 2,000 genes with GFP and T2-GAL4 using a new set of vectors that we have developed.

Another aim to expand the GDP collection is by inserting a small MiMIC-like swappable insertion cassette into 3,500 genes that currently have no MiMIC insertion using CRISPR (a.k.a. CRIMIC) (Lee et al., in preparation). Our original vector design had a success rate of about 50% and we are currently performing vector redesign in order to improve the technology and meet our goals. We have prioritized 3,000 of 3,500 target genes based on their potential roles in human disease. So far we have obtained insertions in about 100 genes that were not previously tagged by MiMICs using this technology. We aim to vastly expand this collection in the next 4 years.

Creating a library of UAS-human cDNAs tagged with HA
(Celniker and Bellen laboratories)

We applied for R24 funding from ORIP (NIH resources) to promote the integration of human and fly biology. We were recently awarded this grant and will start in June 2016. The goal of this new project is to create 9,000 human full-length cDNAs that have fly homologs in a UAS-cDNA-HA vector (Bishof et al., 2014). We will also generate 1,500 transgenic flies that carry these constructs. We have already cloned 200 human cDNAs in this vector and have created transgenic flies for these 200 genes. They will be deposited in the BDSC this summer.

References

Bellen HJ, Levis RW, He Y, Carlson JW, Evans-Holm M, Bae E, Kim J, Metaxakis A, Savakis C, Schulze KL, Hoskins RA, Spradling AC (2011) The Drosophila Gene Disruption Project: progress using transposons with distinctive site-specificities. *Genetics* 188:731-745.

Bischof J, Sheils EM, Björklund and Basler, K. (2014) Generation of a transgenic ORFeome library in *Drosophila. Nat Comm.* 9:1607-1620.

Caussinus E, Kanca O, Affolter M (2011) Fluorescent fusion protein knockout mediated by anti-GFP nanobody. *Nature Structural and Molecular Biology* 19:117-121.

Diao F, et al. (2015) Plug-and-play genetic access to Drosophila cell types using exchangeable exon cassettes. *Cell Reports* 10:1410-1421.

Gnerer JP, et al. (2015) Gene-specific cell labeling using MiMIC transposons. *Nucleic Acids Research* 43: e56.

Lee PT, et al. (2016) Integration of MiMICs by CRIPSR: CRIMIC, a versatile mutagenesis and tagging method. (In preparation).

Nagarkar-Jaiswal S, DeLuca SZ, Lee PT, Lin WW, Pan H, Zuo Z, Lv J, Spradling AC, Bellen HJ (2015a) A genetic toolkit for tagging intronic MiMIC containing genes. eLife 4:e08469.

Nagarkar-Jaiswal S, Lee PT, Campbell ME, Chen K, Anguiano-Zarate S, Cantu Gutierrez M, Busby T, Lin WW, He Y, Schulze KL, Booth BW, Evans-Holm M, Venken KJ, Levis RW, Spradling AC, Hoskins RA, Bellen HJ (2015b) A library of MiMICs allows tagging of genes and reversible spatial and temporal knockdown of proteins in Drosophila. eLife 4:e05338.

Neumüller RA, Wirtz-Peitz F, Lee S, Kwon Y, Buckner M, Hoskins RA, Venken KJ, Bellen HJ, Mohr E, Perrimon N (2012) Stringent analysis of gene function and protein-protein interactions using fluorescently tagged genes. *Genetics* 190:931-940.

Spradling AC, Bellen HJ, Hoskins RA (2011) Drosophila *P* elements preferentially transpose to replication origins. *Proceedings of the National Academy of Sciences USA* 108:15948-15953.

Venken KJT, Schulze KL, Haelterman NA, Pan H, He Y, Evans-Holm M, Carlson JW, Levis RW, Spradling AC, Hoskins RA, Bellen HJ (2011) MiMIC: a highly versatile

transposon insertion resource for engineering *Drosophila melanogaster* genes. *Nature Methods* 8:737-743.

Zhang K, Li Z, Jaiswal M, Bayat V, Xiong B, Sandoval H, Charng W-L, David G, Haueter C, Yamamoto S, Graham B. and Bellen HJ (2013) The C8ORF38 homologue Sicily is a cytosolic chaperone for a mitochondrial complex I subunit. *Journal of Cell Biology* 200:807-820.

24. Harvard Drosophila RNAi Screening Center: Stephanie Mohr

1. DRSC R01 renewal

We express our deep gratitude to the board and broader community for support of our NIH R01 renewal application. We were renewed (funded through 11/30/2019 to N. Perrimon, PI). We look forward to continued service to the community in the area of RNAi reagents, high-throughput screens, and beyond.

2. New name, new phase

We are restructuring the DRSC & TRiP to create a more integrated team and website. As part of this, we are changing the name of the facility to DRSC-Functional Genomics Resources (DRSC-FGR). In addition to continuing support for the now mature RNAi technology and state-of-the-art high-throughput screens, we are also expanding into CRISPR technologies for both cell-based and in vivo applications (see sections ***3-5*** below). The name change also reflects expansion of our suite of bioinformatics tools over the past several years, which has thrived in large part due to the contributions of Dr. Claire Yanhui Hu, our Director of Bioinformatics, and includes tools useful to researchers working in the fly and other systems (see section ***6***). We will all miss Dr. Liz Perkins and appreciate her many years of hard work on behalf of the community. At the same time, we are pleased to welcome Dr. Jonathan Zirin as Assistant Director of the DRSC/TRiP. Jonathan is now the point-of-contact for community inquiries relevant to TRiP fly stocks and nominations.

Our new website, done in collaboration with Harvard Web Publishing, provides us with an updated, flexible, content-managed site. We hope the new site will help researchers find the resources they are looking for—and some they didn't know about before but are glad to find. Continuing our commitment to being responsive to the community, the upgrade includes a single, more informative contacts page for DRSC & TRiP leaders and staff, as well as contact information on specific pages to help ensure that questions reach the right folks. The URL for the home page, protocol pages, other information pages, etc. will change. The URLs for the online tools (e.g. DIOPT, UP-TORR) will not. The Director's Blog www.flyrnai.blogspot.com will cease to be updated and will be replaced with a multi-author "News" feed integrated within the new site.

3. Cell-based screening and reagents

3.A. Screening trends. The DRSC has offered genome-wide cell-based RNAi screening since 2003. Back then, when researchers did not typically have access to either screening equipment or dsRNA libraries, N. Perrimon and colleagues created the center to fill that need. Over time it has been increasingly common for folks to have access to high-throughput screening equipment at their own institutions. In response to this, we shifted our model, and began shipping everything from single templates for

dsRNA production to custom and pre-made large-scale libraries for screening off-site, in addition to continued offering of on-site screening. We will continue our support for on-site and off-site screening—researchers continue to get in touch about planned screens. At the same time, we have begun focusing an increasing proportion of our resources on development of new technologies, including in the area of CRISPR technologies, continuing our mission to make cutting-edge technologies and reagent libraries available to the broadest possible relevant research community.

3.B. dsRNA libraries for cell screening.

Table 1: Reagent libraries at the DRSC

Library	***Type of reagent***
Genome-wide (DRSC 2.0)	dsRNA
"FDA" (see ***3.C.***)	dsRNA
Autophagy-related	dsRNA
GPCRs	dsRNA
Kinases & Phosphatases	dsRNA
Membrane-bound organelle-related	dsRNA
RNA Binding Proteins	dsRNA
Transcription Factors & DNA Binding	dsRNA
Transmembrane domain-containing	dsRNA
Ubiquitin-related	dsRNA
miRNA sponges (for loss of miRNA function screens)	Plasmid DNA
UAS-miRNAs (for gain of miRNA function screens)	Plasmid DNA
TRiP VALIUM shRNAs ("FDA" and broader collection) (***3.D.***)	Plasmid DNA
Custom library (96-well format)	dsRNA
'Cherry-pick' of template (1 or lots)	Linear DNA template for IVT
CRISPR gRNA library for pooled screens (***4.B.)***	*In process*—pooled plasmid library

IVT, in vitro transcription for dsRNA production.

3.C. New "FDA" dsRNA library. In the past year, we built a new focused cell-based RNAi library, designed by Perrimon lab postdoc Ben Housden, which we call the "FDA library," that targets *Drosophila* orthologs of human genes for which there is a known FDA-approved small molecule inhibitor or other type of interactor. The library is being used for a series of screens where the positive 'hits' in the screen correspond to drug target candidates. Our expectation is that using this library will accelerate the process of identifying candidate drugs that can be used to perform further relevant cell-based and in vivo assays. We applied our optimized design rules in building the library, including no experimental dsRNAs in the outermost two wells and 2-3 unique dsRNAs per gene.

3.D. New use of TRiP shRNAs as a cell screening reagent. Recently, Perrimon lab postdoc Ben Housden has been working out a novel way to use the TRIP VALIUM shRNA plasmid collection as a cell-screening reagent. A source of Gal4 is co-transfected. The researcher is also co-transfecting UAS-GFP to monitor uptake of the shRNA. This gives an advantage over the dsRNA approach, as it allows for tracking of what cells get the RNAi reagent vs. not, including via FACS analysis. We recently re-arrayed and amplified this collection, applying the same "FDA" filter and with 3 designs per gene. The

shRNA approach is particularly promising for applications not amenable to dsRNA-based screening.

4. Cell-based CRISPR technologies in fly cells

4.A. Single-gene knockout cells. We continue to work on cell-based knockouts using CRISPR technology. We would like to offer this as a service but the technology is not robust enough at this time to predict outcomes, production costs, and time-lines reliably. With the CRISPR knockout cell lines we have made, we have seen successful application of 'omics approaches (screening and RNAseq). We recently hired a full-time technician who is focusing on improving the CRISPR knockout cell line production pipeline and isolating specific cell lines. Anyone interested in a custom CRISPR modified cell line should feel free to contact us about a collaboration or for additional protocol information.

4.B. CRISPR pooled screening in fly cells. In mammalian cells, RNAi reagents and now CRISPR libraries are commonly used for pooled screens. The most common approach to this is lentiviral infection at a low multiplicity of infection (biasing to one event per genome) and use of a next-generation sequencing approach to determine what reagent sequences are enriched or depleted in selected cells vs. the starting population. The main barrier to doing this in fly cells has been the lack of a system comparable to the lentiviral system, in which cells with single inserts integrated into the genome can be generated efficiently, such that positive 'hits' in the screen can be identified using next-generation sequencing. Work in the Perrimon lab led by postdoc Ram Viswanatha has overcome this barrier and make CRISPR pooled screening approachable in fly cells. The Perrimon lab is currently working to scale up the approach. We see this as a key technology to bring to the DRSC and make available to the community. Anyone interested in CRISPR pooled screening should contact us about a collaboration.

5. Updated support for high-content imaging

A big draw for visitors and local screeners is the ability to perform automated confocal screens at our facility. We recently secured funds from HHMI and Harvard Medical School to replace our 10-year-old, expensive-to-maintain PerkinElmer Opera with a GE InCell 6000 automated confocal system. The new instrument supports more formats (microscope slides and 6-, 12-, 24-, 96- and 384-well format plates). This opens the door to moderate and high-throughput confocal image-based screens of embryos, larvae, and tissues. At the same time, we will be able to continue to support automated confocal cell-based screens.

6. DRSC Online Tools

Below we summarize our newest, newly updated, and most popular online tools for reagent identification and data mining, analysis, and visualization. We continue to develop new tools and analyses.

Table 2: Selected subset of our most popular online tools and newest tools.

Name	***URL***	***Purpose***
GLAD[1]	http://www.flyrnai.org/tools/glad/web/	View curated gene lists
DGET[2]	http://www.flyrnai.org/tools/dget/web/	Mine expression data
MIST[2]	http://fgr.hms.harvard.edu/ProteinSearch/	Visualization of molecular interactions

DIOPT[3]	http://www.flyrnai.org/diopt	Search for orthologs
DIOPT-DIST[3]	http://www.flyrnai.org/diopt-dist	Search for human orthologs and diseases
Find CRISPRs 2	http://www.flyrnai.org/crispr2/	Find and evaluate gRNA designs
UP-TORR	http://www.flyrnai.org/up-torr	Identify RNAi reagents
RSVP	http://www.flyrnai.org/rsvp	Validation data for RNAi fly stocks
FlyPrimerBank	http://www.flyrnai.org/flyprimerbank	qPCR primers
ScreenSummary	http://www.flyrnai.org/screensummary	View cell RNAi screens and data sets

[1] New this year—see section ***10. Publications.***
[2] New this year—publications forthcoming.
[3] Rat newly added this year (in addition to support for yeasts, mouse, human, worm, fly, fish, frog).

7. Drosophila protocols portal
We have been working on an online portal for search and view of protocols for *Drosophila* research. We have a prototype site at http://www.flyrnai.org/tools/protocols/web/. The most relevant comparison seems a simple Google search (feedback from postdocs also suggests that many folks search for protocol info at ResearchGate). Comparison with Google sets a high bar. We are working to identify ways that a protocols portal can add value. The site centralizes resources distributed across the web, including publications, lab web pages, *Drosophila* Information Service technical tips, and YouTube videos. A search with "media" or "dissection" shows off what we see as the best of what the portal currently offers (a search with "food" shows a limitation of our current annotations). The records were human-curated and primarily include recent publications. Our longer term plans include: (a) add automated import of protocol publications from PubMed based on 'smart' searches; (b) incorporate feedback; (c) explore what additional resources should be added to the site; (d) consider implementing a user-added protocol option; and (e) transfer management to FlyBase or another host. Please contact Stephanie with any critical feedback and/or protocol resources you think should be added. We consider this very much a draft work-in-progress that will be driven by community interest.

8. Workshop at TAGC meeting
We are hosting a workshop on Functional Genomics Screening at TAGC. The emphasis will be on cross-species studies. Speakers: Susan Dutcher, Brenda Andrews, Norbert Perrimon, and Calum MacRae.

9. Summary of next directions
In the near future we plan to:

- Launch a re-organized and updated DRSC-Functional Genomics Resources website
- Continue support of on-site and off-site RNAi screening
- Facilitate CRISPR studies (cell lines, pooled screens, improved online tool)
- Upgrade to a GE InCell 6000 automated confocal microscope

10. Publications May 2015-May 2016

DRSC Bioinformatics

1. Hu Y, Comjean A, Perkins LA, Perrimon N, Mohr SE. **GLAD: an Online Database of Gene List Annotation for Drosophila.** J Genomics 2015, July 1; 3:75-81. PMID: 26157507
2. Vinayagam A, Gibson TE, Lee HJ, Yilmazel B, Roesel C, Hu Y, Kwon Y, Sharma A, Liu YY, Perrimon N, Barabási AL. **Controllability analysis of the directed human protein interaction network identifies disease genes and drug targets.** Proc Natl Acad Sci U S A. 2016 May 3;113(18):4976-81. PMID: 27091990.

Cell-based screens

1. Zanotto-Filho A, Dashnamoorthy R, Loranc E de Souza LH, Moreira JC, Suresh U, Chen Y, Bishop AJ. **Combined Gene Expression and RNAi Screening to Identify Alkylation Damage Survival Pathways from Fly to Human**. PLoS One. 2016 Apr 21. PMID: 27100653
2. J. Zanet, E. Benrabah, T. Li, A. Pélissier-Monier, H. Chanut-Delalande, B. Ronsin, H. J. Bellen, F. Payre, S. Plaza. **Pri sORF peptides induce selective proteasome-mediated protein processing**. Science 18 September 2015: vol. 349 no. 6254. PMID: 26383956
3. Helenius IT, Haake RJ, Kwon YJ, Hu JA, Krupinski T, Casalino-Matsuda SM, Sporn PH, Sznajder JI, Beitel GJ. **Identification of Drosophila Zfh2 as a Mediator of Hypercapnic Immune Regulation by a Genome-Wide RNA Interference Screen**. J Immunol. 2015 Dec 7. pii: 1501708. PMID: 26643480
4. Housden BE, Valvezan AJ, Kelley C, Sopko R, Hu Y, Roesel C, Lin S, Buckner M, Tao R, Yilmazel B, Mohr SE, Manning BD, Perrimon N. **Identification of potential drug targets for tuberous sclerosis complex by synthetic screens combining CRISPR-based knockouts with RNAi**. Sci. Signal. 08 Sep 2015: Vol. 8, Issue 393, pp. rs9. PMID: 26350902
5. Stephanie E. Mohr, Yanhui Hu, Kirstin Rudd, Michael Buckner, Quentin Gilly, Blake Foster, Katarzyna Sierzputowska, Aram Comjean, Bing Ye. **Reagent and data resources for investigation of RNA binding protein functions in *Drosophila melanogaster* cultured cells.** G3: Genes, Genomes, Genetics. July 20, 2015. PMID: 26199285
6. Dopie J, Rajakylä EK, Joensuu MS, Huet G, Ferrantelli E, Xie T, Jäälinoja H, Jokitalo E, Vartiainen MK. **Genome-wide RNAi screen for nuclear actin reveals a network of cofilin regulators.** Cell Sci. 2015 May 28. pii: jcs.169441. PMID: 26021350

25. Harvard Transgenic RNAi Project: Jonathan Zirin

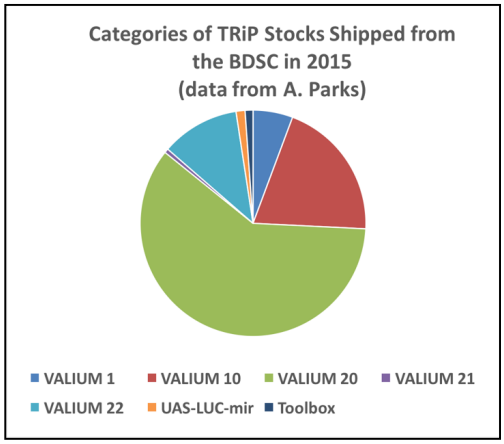
Assistant Director DRSC/TRiP (May 16, 2016)

The Transgenic RNAi Project (the TRiP: supported by NIGMS R01-GM08494; N. Perrimon, PI) is entering a new phase, as it completes its fourth and final year of its second round of funding (ends June 2016). The TRiP competing continuation proposal to the NIH has received a favorable score. We thank the board for their continued support of our venture, and are optimistic that new grant funding will be secured. At that time the TRiP will diversify to include the existing TRiP-RNAi project and the new TRiP-CRISPR project (described below). The goal of both projects is to generate high quality community resources utilizing our established and proven TRiP platform. The TRiP recently published a complete description of the TRiP platform, the TRiP-RNAi project and all reagents generated (Perkins et al. 2015).

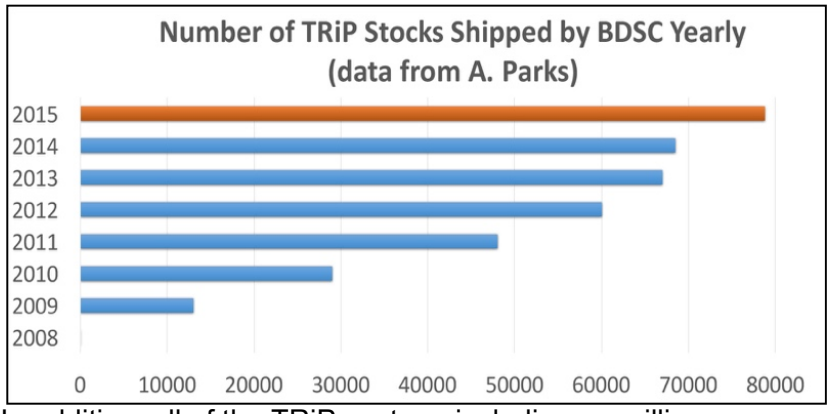
As always, all transgenic stocks are sent to the BDSC for distribution to the fly community.

The TRiP-RNAi Project. The TRiP-RNAi project will continue to make RNAi stocks for nominations received from the community and to maintain and improve the current library of TRiP RNAi stocks available at the BDSC. The TRiP facility, established at Harvard Medical School in September 2008, has generated approximately **~12,805** Fly stocks, with **~1,946** in production and **~42** nominated. These completed stocks, in production and nominated represent **~10,116** unique FBgns which we calculate covers **73%** of the genes in the fly genome (**83%** of highly conserved genes).

TRiP RNAi Stocks at BDSC					
Generation	**Vector**	**Hairpin**	**# Stocks**	**Use in**	**Ref**
1st Generation	VALIUM1	dsRNA	678	soma	14
	VALIUM10	dsRNA	1808	soma	13
2nd Generation	VALIUM20	shRNA	7509	soma, germline	12
	VALIUM21	shRNA	96	soma, germline	12
	VALIUM22	shRNA	1607	soma, germline	12



We are producing the lines with the help of 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. All completed stocks are annotated on the TRiP website 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 and the THFC at Tsinghua University, in China.



In addition to the TRiP RNAi stocks (see Table), the TRiP, via the BDSC, 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 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. 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 (Bejarano et al., 2012). In addition, we advised the VDRC with the design of their new UAS-RNAi lines using short hairpin microRNA (shRNA) (http://stockcenter.vdrc.at/control/about_shrna). As the TRiP continues to expand its collection of RNAi stocks, nominations continue to be received from the fly community.

In 2015 the BDSC sent **78,801** subcultures of TRiP stocks (**890** of these were Toolbox and **1,015** were UAS-LUC-mir stocks) to **1,322** different user groups in **41** countries (A. Parks, personal communication). As of May 11, 2016 there were **11,697** TRiP stocks in distribution at the BDSC and the TRiP expects to send **1700-2000** new RNAi stocks to Bloomington in 2016.

Gene Categories. In line with the DRSC online database of **Gene List Annotation for Drosophila** (GLAD) (Hu et al., 2015), the TRiP stock collection is now organized by sets of specific gene categories; e.g., protein kinases, protein phosophatases, transcription factors and transcriptional regulators, secreted proteins, membrane receptors. Additionally, with support from ORIP/NCRR R24 RR032668 to N. Perrimon, we assembled a TRiP collection representing *Drosophila* orthologs of genes associated with human diseases, the **Human Disease TRiP Project** (HuDis-TRiP). The HuDis project has generated TRiP RNAi stocks for 2,246 Drosophila orthologs of human disease-associated genes. These include 92.4% coverage for 670 high-confidence Drosophila orthologs of high-confidence disease-associated human genes. Our preliminary characterization of these high-confidence HuDis lines involves crossing each line to a set of 10 Gal4 drivers, then analyzing whole animal and tissue/organ specific phenotypes. We are continuing to generate HuDis lines at HMS via the RNAi production pipeline.

Validation of the TRiP lines. The TRiP continues its curation of reagents via the **RNAi Stock Validation and Phenotypes Project** (RSVP) at HMS, 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 Lab Postdoc, who 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% (Sopko et al. 2014). 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 addition to TRiP stocks, RSVP includes results curated by FlyBase for other major stock collections, such as phenotypes associated with VDRC fly stocks. Currently on the RSVP there are 8,334 data entries for 5,202 TRiP lines representing 3,735 fly genes. In addition, the RSVP contains 23,451 data entries extracted from FlyBase for 17,782 RNAi lines representing 11,346 genes.

The TRiP-CRISPR Project. With new funding from the NIH, the TRiP will transition from predominantly RNAi fly stock production to development of new resources based on CRISPR technology. We have started to build a genome scale collection of ~9,000 transgenic sgRNA fly lines, providing powerful, versatile and transformative tools for the fly community. This resource will allow activation, repression and generation of

mutations of the targeted genes. This new resource will leverage the existing transgenic RNAi platform to produce the stocks, making them available at the Bloomington *Drosophila* Stock Center (BDSC), and curating information on the quality of reagents via the TRiP website. As we build the new CRISPR collection, we will encourage and receive gene target nominations from the community.

CRISPR/Cas9 Toolbox. Along with the sgRNA lines targeting individual genes, we are producing a TRiP-CRISPR/CAS9 Toolbox set of Gal4/Gal80ts/UAS stocks that will allow spatial and temporal expression of Cas9 proteins with dead nuclease activity (dCas9), fused to either transcriptional activators (dCas9-a) or repressors (dCas9-i), which can be used for gene activation and repression in cells expressing the sgRNAs. Additional wild type Cas9 toolbox stocks will also be available for generating mutant mosaics in the soma, or generating small deletions and modifications in the germline. 46 TRiP CRISPR/CAS9 Toolbox lines are complete and will soon be made available at the BDSC.

References and TRiP publications

1. Jodoin JN, Coravos JS, Chanet S, Vasquez CG, Tworoger M, Kingston ER, Perkins LA, Perrimon N, Martin AC. Stable force balance between epithelial cells arises from F-actin turnover. Dev Cell. 2015 Dec 21;35(6):685-97. doi: 10.1016/j.devcel.2015.11.018. Epub 2015 Dec 10.
2. Perkins LA, Holderbaum L, Tao R, Hu Y, Sopko R, McCall K, Yang-Zhou D, Flockhart I, Binari R, Shim HS, Miller A, Housden A, Foos M, Randkelv S, Kelley C, Namgyal P, Villalta C, Liu LP, Jiang X, Huan-Huan Q, Wang X, Fujiyama A, Toyoda A, Ayers K, Blum A, Czech B, Neumuller R, Yan D, Cavallaro A, Hibbard K, Hall D, Cooley L, Hannon GJ, Lehmann R, Parks A, Mohr SE, Ueda R, Kondo S, Ni JQ, Perrimon N. The Transgenic RNAi Project at Harvard Medical School: Resources and Validation. Genetics. 2015 Nov;201(3):843-52. doi: 10.1534/genetics.115.180208. Epub 2015 Aug 28.
3. Hu Y, Comjean A, Perkins LA, Perrimon N, Mohr SE. GLAD: an Online Database of Gene List Annotation for Drosophila. J Genomics 2015, July 1; 3:75-81. PMID: 26157507
4. Sopko R, Foos M, Vinayagam A, Zhai B, Binari R, Hu Y, Randklev S, Perkins LA, Gygi S, and Perrimon N. Combining genetic perturbations and proteomics to examine kinase-phosphatase networks in Drosophila embryos. Developmental Cell 2014. doi: 10.1016/j.devcel.2014.07.027.
5. Yan D, Neumüller RA, Buckner M, Ayers K, Li H, Hu Y, Yang-Zhou D, Pan L, Wang X, Kelley C, Vinayagam A, Binari R, Randklev S, Perkins LA, Xie T, Cooley L, Perrimon N. A regulatory network of Drosophila germline stem cell self-renewal. Dev Cell. 2014 Feb 24;28(4):459-73. doi: 10.1016/j.devcel.2014.01.020.
6. Shulman JM, Imboywa S, Giagtzoglou N, Powers MP, Hu Y, Devenport D, Chipendo P, Chibnik LB, Diamond A, Perrimon N, Brown NH, De Jager PL, Feany MB. Functional screening in Drosophila identifies Alzheimer's disease susceptibility genes and implicates Tau-mediated mechanisms. Hum Mol Genet. 2014 Feb 15;23(4):870-7. doi: 10.1093/hmg/ddt478. Epub 2013 Sep 25.
7. Hu, Y., Roesel, C., Flockhart, I., Perkins, L., Perrimon, N. and Mohr, S.E. (2013). UP-TORR: online tool for accurate and up-to-date annotation of RNAi reagents. Genetics, 195(1): 37-45. doi: 10. 1534/genetics.113.151340. Epub 2013 Jun 21.
8. Hu, Y., Sopko, R., Foos, M., Kelley, C., Flockhart, I., Ammeux, N., Wang, X., Perkins, L., Perrimon, N. and Mohr, S. (2013) FlyPrimerBank: An Online Database for

Drosophila Gene Expression Analysis and Knockdown Evaluation of RNAi Reagents. G3 (Bethesda), 3(9): 1607-16.
9. Bergwitz C, Wee MJ, Sinha S, Huang J, DeRobertis C, Mensah LB, Cohen J, Friedman A, Kulkarni M, Hu Y, Vinayagam A, Schnall-Levin M, Berger B, Perkins LA, Mohr SE, Perrimon N. Genetic determinants of phosphate response in Drosophila. PLoS One. 2013;8(3):e56753.
10. Staller MV, Yan D, Randklev S, Bragdon MD, Wunderlich ZB, Tao R, Perkins LA, Depace AH, Perrimon N . Depleting gene activities in early Drosophila embryos with the "maternal-Gal4-shRNA" system. Genetics. 2013 Jan;193(1):51-61. doi: 10.1534/genetics.112.144915.
11. Bejarano, F., Bortolamiol-Becet, D., Dai, Q., Sun, K., Saj, A., Chou, Y.T., Raleigh, D.R., Kim, K., Ni, J.Q., Duan, H., Yang, J.S., Fulga, T.A., Van Vactor, D., Perrimon, N., Lai, E.C. (2012). A genomewide transgenic resource for conditional expression of Drosophila microRNAs. 2012, Development 139(15): 2821—2831.
12. Ni J-Q, Zhou R, Czech B, Liu L-P, Holderbaum L, Yang-Zhou D, Kim H-S, Tao, R., Handler D, Karpowicz P, Binari R, Booker M, Brennecke J, Perkins LA, Hannon GJ and Perrimon N (2011). A genome-scale shmiR resource for Drosophila transgenic RNAi in both the germline and soma. Nature Methods 8, 405-407.
13. Ni J-Q, Liu L-P, Binari R, Hardy R, Shim H-S, Cavallaro A, Booker M, Pfeiffer B, Markstein M, Wang H, Villalta C, Laverty T, Perkins L, and Perrimon N (2009). A Drosophila resource of transgenic RNAi lines for neurogenetics. Genetics, 182(4): 1089-1100.
14. Ni J-Q, Markstein M, Binari R, Pfeiffer B, Liu L-P, Villalta C, Booker M, Perkins LA, and Perrimon N (2008). Vector and Parameters for Targeted Transgenic RNAi in Drosophila melanogaster. Nature Methods 5, 49-51.

26. Berkeley Drosophila Genome Project: Susan Celniker, Ann Hammonds, Ken Wan, Erwin Frise

A. Introduction

The BDGP was established in 1992 to sequence the *Drosophila melanogaster* genome. Now in our twenty-fourth 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. Release 6 was made public last year (GenBank and FlyBase) and we hope to integrate PacBio sequencing to produce the next version of the genome sequence. 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 mapped 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

After completion of the Release 6 genome sequence, our efforts to improve the genome are centered around incorporating the PacBio long-read whole genome shotgun assembly (MHAP) into Release 6 with the goal of producing an integrated consensus assembly that will become Release 7.

C. cDNA Clone Resources

The Gateway expression-ready clone collection to be used to generate a Y2H map (Mohr, Perrrimon, Vidal, Celniker) has been sequenced using a pooling and random shotgun strategy using one lane of the Illumina HiSeq. We are in the process of submitting the sequence to GenBank as full-length cDNA clones when they are finished and as ESTs when they are incomplete.

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.

*Not colony purified

Collection	Vector	Promoter	N-term Tag	C-term Tag	ORF Stop Codon?	System	Past year (2/2015-2/2016)	Total
XO	pDNR-Dual	T7	--	6xHN	No	*E. coli*	96	10330
XS	pDNR-Dual	T7	--	--	Yes	*E. coli*	58	10470
MXO	pMK33-CTAP-BD	Metallothionein	--	TAP	No	Cell culture	0	1961
FMO	pMK33-CFH-BD	Metallothionein	--	Flag-HA	No	Cell culture	95	10146
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*	743	10664
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
ECD	pECIA2	Metallothionein	--	HRV 3C Protease Cleavage site; Fc; V5; 6xHN	No	Cell culture	0	207
ECD	pECIA14	Metallothionein	--	HRV 3C Protease Cleavage site; Pentameric rat COMP helix; Alkaline Phosphatase; Flag; 6xHN	No	Cell culture	0	207

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
ECD	414	414

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. Our homepage includes a separate browse tab for the CRM experiments to improve accessibility. We are in the final stages of releasing a new version of the gene report pages. The improved gene reports will include graphical summaries of the stage specific organ system annotations and a graphical representation of the associated modENCODE RNA-seq data. The updated version also will allow searches by all known gene name synonyms and human ortholog names. We continue to add new search and discovery tools based on computational image and annotation analysis. We have recently published an advanced method for modeling spatially local gene interactions and networks with our dataset. 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, can be accessed at http://insitu.fruitfly.org/som. We are active participants in the development of image analysis within the open source image analysis platform FIJI (fiji.sc). We are starting to use our recently finished open source microscope automation software for automated slide loading and imaging with commodity hardware. To date annotated experiments for 7938 genes, documented with over 123,000 images, have been deposited into the public database.

E. ENCODE model organism Project – modERN (Bob Waterston, Susan Celniker, Kevin White, Valerie Reinke and Mark Gerstein)
The ENCODE model organism project is an independent R01 submitted to complete the study of fly and worm transcription factors (those defined as having a currently recognized DNA-binding domain) determining their genomic DNA binding sites in animals using the ChiP-Seq assay as was perfected in ENCODE. The application was funded and started in August 2014. To date the Celniker lab has produced 256 transgenic GFP tagged-TF fly lines and deposited 150 at the Bloomington Stock Center. Another 40 are ready to ship to Bloomington and the remaining 60 are in the process of being balanced. The White Lab has performed ChiP-Seq for 218 lines, 14 from ModENCODE, 214 from modERN. The data is being processed through the ENCODE pipeline and is being distributed through the ENCODE DCC.

F. 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 submit clones to the DGRC molecular stock center for distribution to the community.

G. 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.

H. Funding

The BDGP is funded almost exclusively by NIH grants (NIGMS). An R01 (SEC) funds the spatiotemporal gene expression studies and was renewed last year 2015. Image analysis research for the spatiotemporal expression studies is funded through an NIH BISTI grant to Erwin Frise. The competitive renewal was resubmitted February, 2016. We are also funded under subcontracts from Harvard University (Perrimon, PI, Celniker, co-PI) to construct ORF clones for Y2H studies, 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 and just recently from Baylor College of Medicine (Bellen, PI, Celniker, co-PI) to construct human ORF clones for expression in flies.

27. DGRC: Andrew Zelhof

Key Changes:

In the current year, both Drs. Peter and Lucy Cherbas have officially retired from the DGRC and we thank the Cherbas' vision, dedication, and hardwork in generating a resource for the distribution of cellular and molecular reagents as well as expanding the utilization of Drosophila cell lines in research. Even though Peter and Lucy have given up their official titles, they will both continue to assist and advise the new leadership of the DGRC. Andrew Zelhof (Biology Department, Indiana University) was asked, accepted and has been appointed the Director of the DGRC.

Personnel:

Lei Gong, Associate Director of Cell Resources
Kris Klueg, Associate Director of DNA Resources
Johnny Roberts, Project Scientist
Vanessa Worthy, Project Scientist

Rolf Rockliff, Fiscal Officer
Kara Erdel, Customer Support
Chris Hemmerich, Database Specialists

Peter Cherbas, Associate Scientist
Lucy Cherbas, Associate Scientist

Use Statistics:

1. Vectors products shipped – 3322 (2014) and 2934 (2015) and 1828 (Jan. –June 2016)
2. Cell line products shipped – 321 (2014) and 482 (2015) and 267 (Jan. –June 2016)

New and Future:

1. The addition of Chris Garcia's "Extracellular Interactome" collection.
2. The addition of FlyBi Drosophila ORFeome vFB5.52 Collection – 10K ORFs in pDONR223 Gateway vector.
3. 18 cell lines with phi31 docking sites for recombinase-mediated cassette

exchange (DGRC and Simcox labs)
4. CRISPR vectors (O'Connor-Giles Lab)
5. Vectors for cell line recombinase-mediated cassette exchange.
6. Integration of cell line usage in publications with Flybase.
7. In the process of hiring of an Associate Director of Resource Development. Immediately, he/she will continue to direct and develop the use of CRISPR technology to add epitope tags to genes in specific cell lines.

Grant Funding: NIH P40OD010949 - We are in year 4 of a 5 year grant from NIH. Both the direct costs and program income currently support our activities.

Pruning:
According to NIH guidelines all collections and cell lines have been backed up. However, due to the potential for limitations in the space required to house the reagents we need to continuously examine the usage of each collection.

We will begin to evaluate the retention of the following collections:
1. Drosophila Species ESTs: The *Drosophila* Species Collections comprise ESTs/cDNAs from five different species libraries generated by AgenCourt as part of the *Drosophila* Species Consortium genome sequencing project. The libraries include: D. virilis D. ananassae D. mojavensis D. erecta D. grimshawi. These clones have not been fully characterized and may or may not be full length. We received these clones "as is" from the AgenCourt.
2. *Drosophila Species Fosmids:* The DGRC houses the fosmids generated in the *Drosophila* Species Sequencing Project for D. virilis, D. ananassae, D. mojavensis, D. erecta, or D. grimshawi,
In both above cases, there is no easy way to search for clones — end sequences are listed in the NCBI trace archives but community members cannot search by gene name and even if they try to search through an alignment, they will only pull something up if it matches the end sequence.
We had one order for a few species clones in the past three years (2014) and one order for several fosmids about 2.5 years ago.
3. The Curagen yeast 2-hybrid collection. We had four orders in the last three years. The portal associated with it no longer exists - the company that collaborated on it housed the portal (searchable database) for several years and they eventually pulled it down.

Publications:
1. Diverse Hormone Responses in 41 Independent Drosophila Cell Lines. Stoiber M, Celniker S, Cherbas L, Brown B, Cherbas P. G3 (Bethesda). 2016 Jan 15;6(3):683-94. PMID: 26772746

2. Tools for Targeted Genome Engineering of established Drosophila Cell Lines. Cherbas L, Hackney J, Gong L, Salzer C, Mauser E, Zhang D, Cherbas P. Genetics. 2015 Dec;201(4):1307-18. PMID:26450921

Scientific Advisory Board:
Susan Parkhurst, Fred Hutchinson Cancer Research Center (chair)
John Abrams, University of Texas Southwestern Medical Center, Dallas
Deborah Andrew, John Hopkins School of Medicine

Spyros Artavanis-Tsakonas, Harvard Medical School
Stephen Rogers, University of North Carolina, Chapel Hill

28. DIS: Jim Thompson

In response to our annual "Call for Papers" in the fall, a tradition that is at least 50 years old, researchers world-wide are invited to share information and resources in Drosophila Information Service. Volume 98 (2015) of DIS, published in January, is in one way a transition volume. At the recommendation of the Board several years ago, DIS began developing a freely-accessible web site and reducing the number of its printed copies. Available on www.ou.edu/journals/dis for the past several years, access has been very good. But some institutional libraries and research labs still like to have a printed volume. Thus, beginning with Volume 98, Lulu.com will prepare and distribute printed copies on demand. This will improve efficiency by reducing time and cost. Articles will, of course, also be accessible free of cost on our website. In addition, we are expanding our coverage of published articles in the FlyBase publications database.

We already have several accepted submissions for the 2016 issue of Dros. Inf. Serv., Volume 99. These will be uploaded to our website as "2016 in press" soon. Submissions are accepted at any time, with the firm deadline of 31 December for each calendar year volume. Manuscripts are preferred electronically in MSWord and can be sent to jthompson@ou.edu. James N. Thompson, jr., Department of Biology, University of Oklahoma, Norman, OK 73019.

APPENDICES.

APPENDIX 1:

Full text of proposed revised Charter:
Rules of Charter

Preamble
Over time, the Drosophila research community has experienced significant expansion. New activities, with potentially dramatic impact on the community as a whole, have been initiated by various individuals. In recognition of these facts and to ensure and facilitate inter-communal communication, some changes to the Drosophila Board are warranted. The present document embodies these changes and provides a historical framework for the benefit of newer community members.

A Short History of the Drosophila Board
The Drosophila community has held an annual research conference for more than 50 years. In the early days of the group, the community was small and less than a hundred individuals would attend these meetings, which could therefore be organized in an informal fashion. In the late 1970s and early 1980s, however, the community had grown to such an extent that attendance at the conference was typically over 1000 individuals. Consequently, organization of the conference became an overwhelming task for any one individual, and the University dormitory housing traditionally used for the meetings

became inadequate. Furthermore, meeting registration fees exceeded expenditure, and moneys began to accumulate. As the number of conference attendees and as the fund increased, and when the housing for the conference was moved to commercial hotels, questions of personal liability began to trouble the individual organizers. It was at this point that Linda Hall and Dan Lindsley suggested the creation of a Drosophila Board and drew up an agreement with the Genetics Society of America's administrative offices to run the annual meetings. The agreement with the GSA offered two advantages: (1) the administrative details would be handled by professionals, and meeting cancellation insurance could be more readily obtained, (2) the Drosophila fund could be held in trust by the GSA to help defray meeting costs, while avoiding IRS problems for individual scientific program organizers. When, following his untimely death, the Larry Sandler Memorial Lecture Fund was established, the GSA agreed to set up and manage a separate account for this fund.

During the first few years, the Board was made up of individuals who had been actively involved in organizing previous conferences with an attempt to include members from across the U.S. and Canada so that the board would represent the interests of the entire North American Drosophila research community. More recently, International representatives were added to facilitate communication and coordination of Drosophila resource efforts throughout the world.

Composition of the Drosophila Board
The Drosophila Board is a representative group of working scientists who use Drosophila as their primary model organism.

The Board meets once a year in conjunction with the North American Drosophila Research Conference. Additional business is conducted by email, and, if necessary, by telephone or video conferences.

Officers
The Drosophila Board will have a President, elected by the community, who will serve for one year as President elect and for one year as President. To ensure long-term memory of the Board, the President will serve three additional years, as "past-President", "past-past President" then "Member-At-Large" in sequential years. The President-elect and Past Presidents will be actively involved in providing leadership to the Fly Board by providing assistance, advice, and counsel to the President.

The Drosophila Board will have an elected Treasurer who will serve for three years.

Regional Representatives
The Board consists of one elected Representative from each of the following regions of the U.S. and Canada:

New England	(Maine, Vermont, New Hampshire, Massachusetts, Connecticut, Rhode Island)
Mid-Atlantic	(Downstate New York, New Jersey, Eastern Pennsylvania, Delaware, West Virginia, Washington D.C., Maryland, Virginia)
Southeast	(North Carolina, South Carolina, Georgia, Florida, Alabama, Mississippi, Kentucky, Tennessee, Louisiana, Puerto Rico)
Midwest	(Minnesota, Wisconsin, Iowa, Illinois, Indiana, Missouri)
Great Lakes	(Upstate New York, Ohio, Western Pennsylvania, Michigan)
Heartland	(Colorado, Kansas, Nebraska, North Dakota, South Dakota, New Mexico, Texas, Arizor Oklahoma, Arkansas)

Mountain (Oregon, Washington, Idaho, Montana, Wyoming, Utah, Nevada, Alaska)
California (California, Hawaii)
Canada (Canada)

In addition, there will be a representative for:
Primarily Undergraduate Institutions (U.S.)

as well as International Representatives from each of the following regions:
Australia/Oceania
Asia
Europe
Latin America

These delegates will be elected, and serve for a term of three years. If it is not possible to find two interested candidates in a region, a single candidate may instead be appointed by the board. The board is open to potential changes in international representation, or differences in the manner of selection of international representatives.

There shall also be a Trainee Representative (Senior graduate student or Post-doctoral researcher), who shall serve for a term of 2 years. The Trainee representative shall be selected by a committee of board members.

***Ex officio* members**
The following individuals from the research community (or their designated representative) are invited to serve on the Board as ex officio members:
- The Director of FlyBase, and the chair of the FlyBase SAB
- The Director of the Berkeley Drosophila Genome Project
- The Director of the Bloomington Stock Center
- The Directors of other major national and international Drosophila stock centers, including the Drosophila Species Stock Center, the VDRC, and the Kyoto DGGR
- The Chairs of the Stock Center Advisory Committees
- The Director of the DGRC
- The Directors of the DRSC/TRiP
- The PI of the Drosophila Gene Disruption Project
- The Director of the Transgenic RNAi Project
- The Editor of DIS
- The current chair of the Sandler Memorial Lectureship selection committee
- The current chair or a representative of the Image Award Committee
- The Chairs of the Scientific Organizing committee of the previous, current, and upcoming North American National Drosophila Research Conference.
- Leaders of other Drosophila community resource projects and centers, by invitation of the President
- Any Drosophila researchers serving on the board of the GSA

The Board's discussion of community issues benefit from input from the entire community. It is the responsibility of the Regional Representatives to canvass Drosophila researchers residing in their regions so input can be obtained on major issues of concern. Advice from the *ex officio* members is invaluable and will be solicited on all Board issues. However, the Officers, including the Treasurer, and Regional Representatives, as the elected officials of the Board, constitute its voting body.

Elections
The "past-past President" will be responsible for organizing the election of the President, Treasurer, and the Regional Representatives. A nomination committee will be formed to name two delegates for each position to be elected. Delegates living in the different regions are chosen to ensure diversity and broad representation on the Board, but everyone in the Drosophila research community may vote for the all the open positions, including any of the regional representatives who are on the ballot that year. Only scientists who use Drosophila as a research organism are eligible to vote. Elections will be held October to December. The newly elected Representatives begin their term in the following spring at the annual meeting. Regional representatives whose terms are expiring serve until the annual board meeting, and are invited to attend the board meeting in the year their terms expire as ex-officio members.

Responsibilities of the Drosophila Board
The primary functions of the Board are:
1 To serve as advocates for the Drosophila research community and represent community interests to funding agencies, other scientific organizations, and the general public.
2 To facilitate a free and productive relationship between the research community, the administrators of FlyBase, leaders of community resource and information projects, and the Directors of the Stock Centers.
3 To insure a successful annual North American Drosophila Research Conference. The Board selects the venue, based on recommendations from GSA. The President-elect appoints the chair of the Scientific Organizing committee for the next meeting to be organized (2-3 years in advance).
4 To administer the meeting fund of the Drosophila research community.
5 To administer awards, including the Larry Sandler Memorial Lecture fund, undergraduate travel awards, including the Victoria Finnerty Award, and the Image Award.

Responsibilities of the Drosophila Board Presidents:

President-elect elect – Attends the first meeting after being elected, to observe

President-elect
(1) Takes the minutes at board meeting, circulates the minutes to the board by email so that they can be approved and posted on Flybase in a timely fashion.
(2) Chooses the meeting organizers for the next Fly meeting to be planned.

President
(3) Presides over the board meeting: solicits reports from the meeting organizers, GSA director, Treasurer, Sandler committee chair, Finnerty award chair, Image Award chair, Elections committee, Communications committee, and all of the community resources and projects.
(4) Writes “FlyNews” newsletter, updates fly community on resources, meetings, and other news, distributed ~ twice/year.
(5) May be responsible for organizing writing of the next White Paper.
(6) Writes letters of support for resource project proposals, on behalf of the fly community. These normally cite community support for the goals of the project by referring to the White Paper

(7) Updates the lists of plenary speakers, historical speakers, session chairs, Sandler award winners and selection committees, and sends copies to the next meeting organizers.
(8) Reminds past-past-president that they need to run the next election in September.
(9) Addresses, with help and support of the Fly board, any other matters arising that affect the fly community.

Past-president
(10) Aids current president and attends next meeting for continuity.

Past-past president
(11) Selects and chairs Election Committee for the board, and organizes elections. Include in board meeting report the master list of board members, with their term limits. Submit this to Flybase.

Responsibilities of the Regional Representatives:
To effectively carry out the responsibilities of the *Drosophila* Board, standing committees may be formed, and each regional representative is encouraged to serve on at least one committee. These committees can also include non-board members. Possible committees could include:

Advocacy: Develop and implement plans to advocate for *Drosophila* Research.

White Paper: Review and approve or update White Paper.

Infrastructure: Develop recommendations for new resources that would benefit the Drosophila community. Review annual reports of community resources that report to the Fly Board.

Community: Develop plans to enhance communication and exchange of information and resources among Drosophila researchers

Fly Meeting: Review organization of the North American Drosophila Conference, make recommendations for changes

SAB: Support oversight of Drosophila resources and resource projects by serving on Scientific Advisory Boards.

The incoming President shall determine which committees need to be formed and encourage regional representatives to choose an appropriate assignment.

Meeting Site
The site of the annual Drosophila Research Conference will rotate in the following order: East, West, Center of the U.S.

This charter was prepared for the Board by Th. Kaufman and J. Lucchesi and was revised by the Board at its meetings on March 31, 1993, at the Town & Country Hotel, San Diego, CA, on April 5, 1995, at the Westin Peachtree, Atlanta, GA, by an electronic vote in February 2003, on March 20, 2003 at Chicago on March 23, 2004 at Washington D.C, and July 2016 in Orlando FL.

APPENDIX 2:
Drosophila White Paper

The first Drosophila White Paper was written in 1999. Revisions to this document were made in 2001, 2003, 2005, 2007, 2009 and 2012. The 2001 - 2012 versions are available at: http://flybase.org/wiki/FlyBase:Fly_Board. Here, the Drosophila Board of Directors presents an updated White Paper identifying and prioritizing current and future needs of the Drosophila research community, based on input from community leaders and comments received from community members.

Part I *Drosophila* as an experimental system for research: past, present, and future

Drosophila melanogaster is a leading animal model for biomedical research and understanding the basic biology of animal systems. Lessons acquired from studies in *Drosophila* directly impact our understanding of evolutionarily distant metazoans, including humans and other vertebrates, as well as invertebrates such as mosquitoes that are of medical or agricultural importance.

Our understanding of the basic principles of genetics, including the nature of the gene, genetic linkage, meiotic chromosome segregation, and recombination, all arose from studies in *Drosophila*. Pioneering studies that linked molecular lesions in the genome with mutant phenotypes led to the identification of many proteins that play essential, conserved roles in development and physiology. For example, many of the components of systems that cells use to communicate with each other and respond to their environment, including the Notch, Wnt, Hedgehog, Hippo, and Toll signaling pathways, and Trp channels, were first discovered and characterized in *Drosophila*. Components of these pathways are now recognized as central contributing factors to major human diseases including cancer, cardiovascular disease, and neurological disorders, and drugs targeting these pathways are in use or in clinical trials today. Thus *Drosophila* research provides an essential pipeline for discovery of drug targets and, in some cases, direct identification of lead compounds and drugs.

Drosophila research has defined not only molecules and pathways but also fundamental biological processes, including the innate immune response, stem cell determination and maintenance, cell and tissue polarity, growth control, pattern formation, organ morphogenesis and physiology, circadian rhythms, sensory biology and animal behavior, learning and memory, neuronal pathfinding, and synaptic transmission. *Drosophila* thus serves as an outstanding organism for understanding animal biology and modeling human disease, including identifying molecular mechanisms and new therapeutic strategies. The enormous contributions of *Drosophila* research have been acknowledged in part through recognition of many *Drosophila* researchers with major scientific prizes, including several Nobel prizes.

Drosophila will, with adequate funding, continue to play a key role in future research, providing insights into both fundamental biological processes and human disease, as *Drosophila* presents a unique and overwhelming combination of strengths as an experimental model. These include the wealth of information accumulated during a century of research on its genetics, development, physiology, ecology, and evolution, a vigorous and collaborative community of researchers, relatively low maintenance costs, short generation time, simple genome, and an extensive and accessible toolkit that provides diverse strategies for manipulation and visualization of gene function. The unique position of *Drosophila* as a complex, yet easily manipulated and analyzed, animal model makes it well suited for a broad range of studies including investigations of organ

development and physiology, neural function across scales from molecules to neural networks to behaviors, transcriptional regulation including *cis*-regulation, nuclear architecture, gene regulatory networks, and epigenetics, and the genetic basis of complex traits. *Drosophila* studies also provide insight into the importance of gene-gene interactions, and powerful tools to identify genes and pathways relevant to orthologous complex traits in humans, gene-environment interactions, including interaction between the microbiome and animal physiology, metabolomics and pharmacogenetics, and identification and characterization of human disease genes. In addition, the genus *Drosophila* has been a key model system for understanding population biology, the molecular basis of speciation, and evolution. *Drosophila* also serves as the closest genetic model for the major insect vectors of disease, including as *Anopheles gambiae* (malaria), *Aedes aegypti* (zika, dengue fever, yellow fever), and *Culex pipiens* (West Nile fever), as well as many agriculturally important insects, including pollinators such as honeybees, and pests that include many species of beetles and aphids.

The ability of *Drosophila* research to continue to pioneer our understanding of general principles underlying the biology of animals including humans depends both on the availability of funding, and on continual reassessment of the resources necessary to support *Drosophila* research. We prioritize continued funding of investigator-initiated research into both basic and applied problems in biological sciences. We also encourage better integration of *Drosophila* researchers during the planning stages of larger projects, much like our community's participation in the Genome and ENCODE projects. We encourage support for community identified shared resources, as outlined in this document.

Part II Maximizing contributions of *Drosophila* research

Here, we outline current resource priorities of the *Drosophila* research community, in order of importance.

1) Informatics Resources for *Drosophila* Research

To ensure that *Drosophila* continues to play its essential role in both basic and translational biomedical research, it is crucial that there be a central bioinformatics resource that captures, organizes and presents core information on *Drosophila* genomics and genetics, both from the primary literature and from large-scale data- and resource-generation projects. The primary resource for this is currently Flybase, and there is universal agreement that continued support for the curated resources exemplified in Flybase is essential to all *Drosophila* research. Key informatics resources include genome and transcriptome sequence information, up-to-date gene annotations, the characterization of mutant phenotypes, RNA and protein expression profiles, and interacting gene, protein, RNA and small molecule networks, and catalogs of *Drosophila* stocks and molecular reagents, as well as databases for new classes of information such as gene expression atlases, neural connectivity, and metabolomics. Whereas capture of some classes of information from the literature may be automated, organizing and presenting most classes of information requires manual curation. All these data classes require community input, direction and oversight. Generic genetics and genomics databases are not a viable substitute.

To enhance the accessibility and utility of *Drosophila* bioinformatic resources, both for *Drosophila* researchers and for those working with other systems, it is essential to link resources dedicated to *Drosophila* with those dedicated to other organisms. Evolution is a powerful genomics tool that informs research on organisms throughout the tree of life. Nascent interactions among databases supporting the well-established model systems and human genomic and genetic disease information must be

strengthened and made more accessible. Not only will this promote more rapid progress in *Drosophila* research, it will significantly enhance progress in functional genomics overall by promoting cross-talk among scientists working in different fields. Up-to-date and well-organized electronic databases are essential conduits to translate information from *Drosophila* research to other areas of study, including the study of human biology, genetic disease and biomedicine, cellular responses to infectious pathogens, and dipteran disease vectors. Maintaining a current and organized database requires not only an investment in effectively linking databases, while preserving their essential and diverse contents, but also creating interfaces that make them accessible to varied user groups. At the same time, it is essential that the unique classes of information fundamental to *Drosophila* research be preserved and enhanced so that these databases continue to benefit future research. We are concerned about fragmented NIH policy on database support and the lack of international efforts to support this infrastructure. Our community would like to play a more active role in establishing these programs, rather than having decisions imposed on us.

2) Resources for analysis of genes and phenotypes

Resources that facilitate functional analysis of genes and phenotypes are a high priority for *Drosophila* researchers. A powerful advantage of *Drosophila* as a model system lies in the wide repertoire of genetic manipulations that are possible; continued enhancement of this genetic toolkit should include expanding the set of genes with loss-of-function mutations, including null alleles created by gene deletion or disruption for genes not already represented in existing mutant collections, and resources that facilitate replacement of genomic loci with allelic variants. CRISPR/Cas9 technology makes it possible to target any gene, and an expanded collection of mutations that covers most or all genes, including genes without large ORFs (encoding peptides or small RNAs), and hence underrepresented in gene disruption collections, will be a valuable resource for a wide range of studies. Development of genetic resources should advance strategies and genome-wide resources for manipulating the activity and expression of genes with tight spatial and temporal control, including expression of wild-type or variant alleles, and fly lines that enable targeted knock-out or knock-down of gene expression. This can be done through RNAi, strategies based on CRISPR/Cas9 and its derivatives, or protein degradation strategies, in combination with independent systems for spatial and temporal manipulation of expression (*e.g.* GAL4, LexA, QF) to allow conditional and reversible removal of genes, mRNA or proteins in any tissue at any time. Insertional mutations created by targeting GAL4 or LexA to knock down gene function, combined with expression of cDNAs under GAL4 or LexA control, will enable proper spatial and temporal expression for rescue experiments, including expressing altered genes for structure-function studies, expressing tagged proteins for analysis of protein localization, and expressing homologous genes from humans or other species.

We support continued development of tools to study human genes and their disease variants in *Drosophila*, facilitating emerging strategies in precision medicine, and accelerating characterization of undiagnosed diseases. Creation of a library of human cDNAs in fly-ready vectors allows all researchers to quickly obtain, modify and study human genes, and we advocate creation of a collection of transgenic fly stocks that carry tagged UAS-human cDNAs. This will permit testing of function of human genes in *Drosophila*, and provide a basis for the functional testing of human disease variants, an increasingly common need in medical genomics.

We advocate support of community facilities and resources for high-throughput screening, including RNAi or CRISPR/Cas9-based screening, and pharmacological screening, both in cell lines and in whole animals. While the ability to analyze genes and

phenotypes *in vivo*, in an intact animal, is a particular strength of *Drosophila*, some classes of experiments can be more easily performed on cultured cells, and expanding the collection of available *Drosophila* cell lines to include more diverse cell and tissue types, and improving on methods to culture cells and tissues *in vitro*, will facilitate live imaging studies, and biochemical and pharmacological characterization and screening of cells and tissues.

We advocate for resources that enable, enhance and expand physiological and phenotypic characterization of *Drosophila*. These will provide a deeper understanding of responses to environmental perturbations, gene-environment interactions, and polygenic traits. This should include annotation of the *Drosophila* metabolome, and the establishment of standardized protocols and resources to permit comparisons of the metabolome across tissues, genotypes, and species. It should also include analysis of the *Drosophila* microbiome and its contribution to physiology, including resources to characterize microbiomes from diverse genetic backgrounds and environments.

Tools and resources to determine expression patterns of *Drosophila* RNAs and proteins at high temporal and spatial resolution, together with sub-cellular localization profiles, provide essential insights into function and valuable markers for phenotypic characterization. To extend the expression analysis tool-kit, we advocate two complementary approaches: the creation of collections of tagged genes and the production of antibodies against *Drosophila* proteins. Antibodies are a foundational resource in molecular biology, as they enable the study of protein localization, modifications, and interactions, *in situ,* with genes under endogenous regulatory controls, without any potential for impairment of gene function by tags. A repository of highly specific, high affinity, and sustainable antibodies will be a valuable resource, and in addition to immunization, synthetic techniques, including recombinant antibodies, nucleic acid aptamers and non-immunoglobulin protein scaffolds should be expanded. Tags are needed as an efficient, reliable, and inexpensive way to study protein localization and characterize protein function, given current limitations of antibody resources. Limited sets of tagged genes are currently available, but broader gene sets need to be generated, along with stable fly lines, and the activity of tagged proteins needs to be confirmed by genetic rescue experiments. These collections should include tagging endogenous genes with markers (*e.g.* GFP) at their genomic loci, without disrupting gene function, to assess expression patterns of genes and subcellular localization of proteins in wild-type and mutant backgrounds, and provide reagents for GFP-based knock-down or immunoprecipitation experiments. Collections of tagged transgenes carrying tagged cDNAs (*e.g.* UAS-cDNA-tag) can also be used for localization and interaction studies, and are valuable for structure-function studies and comparisons to human UAS-cDNA collections. Many genes produce multiple transcript isoforms via RNA processing mechanisms, including regulated alternative splicing, and future analysis of expression patterns should include the spatial and temporal distribution of alternative transcripts and protein isoforms.

Support for functional analysis of the *Drosophila* genes and phenotypes must be coupled to bioinformatic efforts that will establish atlases and databases of the resulting data sets, and make them accessible to all researchers, as described above in part 1. It must also be coupled to mechanisms for making available tools and resources widely available, as described below in parts 3 and 4.

3) *Drosophila Stock Centers*

Stock centers that provide universal access to genetically defined stocks are essential for all *Drosophila* research and they remain a high priority for infrastructure funding. They are complex operations that are heavily used by the national and

international fly communities. For example, the Bloomington Drosophila Stock Center, the repository for *Drosophila melanogaster* strains funded by NIH, maintains more than 59,000 genetically distinct stocks and distributed 243,148 samples to approximately 2,000 laboratories during 2015. These centers, whether general or specialized in scope, distribute the "core" stocks necessary for genetic experimentation in *Drosophila*.

Stock centers must have the physical ability to maintain the large number and variety of stocks needed for contemporary genetics research in a safe and reliable manner, and, to retain relevance and impact, they also need the management capacity to assure that collection contents adjust to changing research needs. Stock centers must keep valuable existing stocks while acquiring new stocks from researchers and integrating with or leading large-scale resource development projects. To maximize the benefit of maintaining the strains, stock centers must provide information that will promote their experimental use by integrating stock information into online model organism databases such as FlyBase, emphasizing website development and maintenance, and having staff available for consultation. These efforts to provide information on stock applications are particularly important to investigators new to *Drosophila* research, such as those wishing to pursue discoveries made in vertebrates using the sophisticated genetic approaches available in flies. Stock centers must also have the capacity to deal with the regulatory challenges associated with the distribution of live animals and the administrative challenges of acquiring large proportions of operating budgets from user fees.

We urge funding agencies to recognize that the viability and vitality of stock centers depends on the appropriate balance between grant support and user-generated income. Cost-recovery programs have enabled stock centers to expand beyond the limits of grant funding, but, as public resources important to scientific progress, stock centers need the security and stability provided by continued public investment and oversight. The continued success of stock centers will depend on agencies giving them flexibility in determining staffing, the structures of cost-recovery programs and the uses of fee income. We strongly believe that healthy partnerships between stocks centers and funding agencies will continue to be a key factor in the success of *Drosophila* as a research organism.

4) Molecular and Cell line Stock Centers

Molecular and cell-line stock centers provide the community with access to an expanding set of key resources at affordable costs, enhance research capabilities, enable efficient use of resources, and facilitate exchange of materials. It is important to maintain reliable, central repositories that are able to distribute key reagents to the scientific community expeditiously as it can relieve individual labs of this responsibility and afford the end user with a dependable timeline for receiving materials. A central repository also ensures that these valuable resources are not degraded or lost, and provides technical guidance and ready access to reliable, relevant protocols. In addition, the importance of a molecular stock center is magnified by NIH guidelines that require investigators to make materials widely available and that emphasize reproducibility.

Key resources to be maintained and distributed include cDNA clones and transformation vectors, as well as collections of full-length cDNA and genomic clones for expression in flies, in cell lines, and in yeast or bacteria. Molecular reagents for manipulation of gene expression (*e.g.* by RNAi or CRISPR/Cas9) also need to be maintained and distributed. A molecular stock center needs to be able to accept both resources generated by large-scale project, as well as donations from individual labs. A reliable, centralized repository of *Drosophila* cell lines also needs to be maintained. Support for antibody repositories is also invaluable. Some *Drosophila* monoclonal

antibodies are available from the NIH-supported Developmental Studies Hybridoma Bank, but support for storage and distribution of polyclonal antisera, and antibody reagents created by other techniques such as phage display, would also be valuable.

APPENDIX 3:
Election emails and candidate statements

On October 9, Flybase sent out the following email to their mailing list:

Dear Drosophila researcher,
It is time to cast your vote for new members of the National Drosophila Board of Directors. The Board plays an important role in the Drosophila research community, so please take a few moments 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 fly 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 13 regional representatives: 8 from the U.S. and one each from Canada, Latin America, Europe, Asia and Australia/Oceania, and one representative for primarily undergraduate institutions, all of whom serve 3-year terms. The Board is led by three elected officers: a President, a President-Elect and a Treasurer. In addition, the Board has ex officio members, including past-Presidents, meeting organizers and representatives of the Drosophila community resource centers. For more information about the Board and the summaries of the annual Board meetings see: http://flybase.org/wiki/FlyBase:Fly_Board.

This year we are electing the President-elect, who will serve as President starting with the fly meeting in 2017. We are also electing representatives for the Mid-Atlantic and California regions, and international representives for Asia, Europe and Latin America, who will serve 3-year terms starting with the fly meeting in July 2016.

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

(insert survey link)

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 11, 2015.

Thank you,
Drosophila Board Election Committee
Amy Bejsovec (Chair)
Kristi Wharton
Anthea Letsou
Mark Peifer
Justin Kumar

President-elect (Vote for ONE)

Deborah Andrew
The Johns Hopkins University School of Medicine
Deborah Andrew grew up in Florida and attended the University of Central Florida, where she received a Bachelor's Degree in Fresh Water Ecology and Master's Degree in Genetics. It was during her Master's research with David Kuhn that she developed her lifelong passion for Drosophila research. Debbie's doctoral training was with Bruce Baker and James Posakony at the University of California, San Diego, where she studied Drosophila sex determination. She was a post-doctoral fellow with Matthew Scott, at the University of Colorado, Boulder and at Stanford University. In Matt's lab, Debbie began studies on Drosophila organ development, which she has continued since joining the Cell Biology Department at Johns Hopkins in 1993. Debbie is best known for her studies of the salivary gland and trachea, uncovering molecular/cellular pathways governing organ specification, morphogenesis and tissue-specific gene expression. Debbie has been an active member of the Drosophila community, serving as the Mid-Atlantic representative to the Drosophila Board from 1994–1997, as a member of the elections board from 2010-2011, as Treasurer of the Drosophila Board from 2013–2016, as a member of the Drosophila Genomics Resource Center advisory board since 2013, and as co-organizer of the 2010 Drosophila meeting in Washington D.C.

Helen McNeill
University of Toronto
Helen McNeill received her PhD from Stanford University, studying E-cadherin and cell polarity with W. James Nelson. She began to study Drosophila genetics, and the genetic control of planar cell polarity (PCP) with Michael Simon (also at Stanford University). She started her independent lab in London, England, at Cancer Research UK, where her group worked on PCP control by the transcription factor Mirror, and the coordination of growth and the timing of differentiation by the Insulin Receptor Signaling pathway. Helen moved to the Lunenfeld-Tanenbaum Research Institute at Mount Sinai Hospital in Toronto, Canada in 2005, where she is a Senior Investigator, and Professor of Molecular Genetics at the University of Toronto. Her group currently investigates Fat cadherins in PCP and growth control in flies, mice and hydra. Helen was previously a representative from Canada to the Drosophila Board of Directors, and has helped organize Keystone meetings (2013, 2015), Gordon Research Conferences (2010, 2012) and the Canadian fly meeting (2011). She was Director of the Developmental Biology Program of Toronto (2007-2013), and is active in training new scientists, and promoting research using model organisms.

Mid-Atlantic (Vote for ONE)

Chris Rushlow
New York University
Chris Rushlow received her PhD in Genetics with Arthur Chovnick at the University of Connecticut, then began her postdoc training in developmental biology first with Dr. David Ish-Horowicz at the Imperial Cancer Research Fund in London and then with Dr. Michael Levine at Columbia University. Since 1991 Chris has been running her own lab, first at the Roche Institute of Molecular Biology and then at New York University where she is currently a Professor of Biology. Chris's major research interest is transcriptional programming and reprogramming with a particular focus on regulation of zygotic-genome activation in the early Drosophila embryo. Chris has been an active member of

the fly community for several decades, promoting research in fly genetics and genomics, and training future generation scholars through activities such as mentoring students in her lab including undergraduate and graduate (Master and PhD), as well as high school students through the ARISE summer program for New York City high school under-represented groups."

Amita Sehgal
University of Pennsylvania
Amita Sehgal is the John Herr Musser Professor of Neuroscience and Investigator of the Howard Hughes Medical Institute at the University of Pennsylvania. Amita received her Ph.D. from the Weill Graduate School of Cornell University and conducted her postdoctoral work with Dr. Michael Young at Rockefeller University. She has received many awards and honors, including election to the National Academy of Medicine and the American Academy of Arts and Sciences. Amita's research focuses on the genetic basis of circadian rhythms and sleep. She and her collaborators developed a Drosophila model for sleep, which has become popular worldwide and has expanded the spectrum of neural processes and behavioral interactions that can be studied in Drosophila. Amita is a strong advocate of Drosophila research and participates in the fly community in many ways, which include generation of lines as part of a consortium and talks at fly meetings She co-organized the Neurobiology of Drosophila meeting at Cold Spring Harbor in 2007.

California (Vote for ONE)

Amy Kiger
University of California, San Diego
Amy Kiger received her BA in Biology from Wellesley College, and after graduation, conducted her first fly research as a technician in Michael Young's group at Rockefeller University (and has continued in the fly field ever since). Amy obtained her PhD in Developmental Biology at Stanford School of Medicine as a Howard Hughes Predoctoral Fellow in Dr. Margaret Fuller's laboratory, where she described genetic control of germ line stem cells. She did her postdoctoral research as a Jane Coffin Childs Fellow with Dr. Norbert Perrimon at Harvard Medical School, where she addressed cell biology questions with the advancement of new RNAi methodologies. Since 2004, Amy has led her own lab in the Section of Cell & Developmental Biology at the University of California, San Diego. Amy's research investigates membrane trafficking control of cellular remodeling, including mechanisms of endosomal and autophagic regulation required for immune and muscle cell functions. Amy is an active member in the local and national fly communities. She organizes the San Diego fly meetings, has chaired sessions at national fly meetings, written reviews on fly research methods and contributions in cell biology, and trained dozens of new fly researchers in her laboratory. Amy is a dedicated educator, who advocates and instructs on the use of flies and other model organisms (including their importance in cell biology fields) in her ongoing roles in both the academic and research settings.

Kavita Arora
University of California-Irvine
Kavita Arora received her PhD in Neurobiology with Dr. Obaid Siddiqi at the Tata Institute of Fundamental Research in Bombay, where she studied neurogenetics of chemosensory behavior in Drosophila. She then joined Dr. Christiane Nüsslein-Volhard's lab at the Max-Planck Institute of Developmental Biology in Tübingen for her

postdoctoral training. She continued her postdoctoral work with Dr. Michael Levine at Columbia University, New York and Dr. Michael O'Connor at the University of California Irvine. Since 1995 Kavita has had her own lab at the University of California Irvine, where she is currently professor and Vice-Chair in the Department of Developmental and Cell Biology. Kavita's major research interest is TGF-beta signal transduction and integration of signaling inputs from multiple pathways in embryonic patterning, regulation of neuronal behavior, and energy homeostasis. Kavita is an active member of the fly community. She co-organized the Annual Drosophila Conference in San Diego in 2003, and for the last decade has co-organized the annual Southern California fly meeting. At UCI she helped develop and facilitates a Postdoc Mentorship Program. She is on the editorial board of genesis, and is committed to promoting genetics research and education at both the undergraduate and graduate levels.

Latin America (Vote for ONE)

Helena Araujo
Federal University of Rio de Janeiro
Helena Araujo graduated with a bachelor's degree in Biology at the Federal University of Brasilia (UnB), Brazil and has a PhD in Molecular Biology from the Federal University of Rio de Janeiro (UFRJ). She received training in the fly field during her postdoc at the University of California in San Diego (UCSD), working with Dr. Ethan Bier on fly development. Since 2001 Helena has been running her own lab at the Institute of Biomedical Sciences, UFRJ. Helena's major research interest is on the role of morphogens in Drosophila development, especially during embryogenesis and development of the wing. Helena is an active member of the Developmental Biology community in Latin America, organizing meetings in the field and promoting research on the fly. She is committed to training the next generation of Brazilian scientists on the genetics and development of model organisms. She also works for scientific awareness of the great public by producing fly comics.

Juan R. Riesgo-Escovar
Mexican National Autonomous University
Juan R. Riesgo-Escovar received his primary and college education in Mexico and graduated with a special mention and medal from the Mexican National Autonomous University, as he got the highest grade of his class for a perfect 10/10 grade average. Juan entered the fly field for his graduate studies with Dr. John Carlson. After receiving his MSc and PhD in Biology at Yale University, Juan did his postdoc training with Dr. Ernst Hafen at the University of Zürich in Switzerland. Since 1998 Juan has been running his own lab at the Neurobiology Institute, part of the Mexican National Autonomous University, where he is an associate professor. In 2004 he was awarded the Young Researcher Prize at his University. Juan's major research interests are developmental biology, signaling, and Drosophila diversity. Juan has been an active member of the fly community, promoting research using model organisms and training future generation scholars through activities such as organizing Developmental Biology meetings (both national and international), and serving in boards of community organizations.

Asia (Vote for ONE)

Li-Mei Pai
Chang Gung University

Li-Mei Pai received her graduate training and obtained a Master degree in Department of Microbiology and Immunology at National Yang Ming University, Taiwan. She then embarked on studies in the fly field and began her Ph.D training with Dr. Mark Peifer at the University of North Carolina. Later on, she continued her postdoc training in Dr. Trudi Schupbach's lab at Princeton University. Since 2001 Li-Mei has been running her own lab at Chang Gung University in Taiwan. Her major research interests include egg development, vesicle trafficking, and metabolism and fertility. She has been an active member of the academic community, including the Genetics Society of America, American Society of Cell Biology, society of Developmental Biology in Asia, and the fly community in Taiwan. She has been promoting research using model organisms and training future generation scholars through activities such as co-directing the summer course at National Taiwan University for the fly community in Taiwan, and co-organizing the first Asia Drosophila conference, and participating in Asia Developmental Biology conferences.

Kwang-Wook Choi
Korea Advanced Institute of Science and Technology
Kwang-Wook Choi grew up in Korea and graduated with BS and MS from the Seoul National University. After receiving his PhD in fly neurobiology with Dr. William (Chip) Quinn at Princeton, Kwang had his postdoctoral training in eye development with Dr. Seymour Benzer at Caltech. From 1995 to 2008, Kwang was a professor at the Baylor College of Medicine. Since his return to Korea in 2008, he has been a professor in the Department of Biological Sciences at KAIST. His research interest is in growth control, pattern formation, cell polarity, and more. Kwang has been an active member of the fly community, promoting interaction among Drosophila scientists in the Asia-Pacific region. He co-organized the 2nd Asia-Pacific Drosophila Research Conference (APDRC), and is currently serving as chair of the Asia-Pacific Drosophila Board.

Europe (Vote for ONE)

Sarah Bray,
University of Cambridge, UK.
Sarah Bray graduated from University of Cambridge where she continued for her PhD research, investigating the regulation of protein synthesis in sea urchins with Dr Tim Hunt. Attracted by the powerful transgenic approaches that were being pioneered in Drosophila, she joined the group of Dr Jay Hirsh at Harvard Medical School for her post-doc to study the regulation of Dopa decarboxylase. It was shortly after arriving in USA that Sarah attended her first Annual Drosophila Conference (in Charlottesville), which cemented her enthusiasm for working with flies and also initiated many friendships. Sarah subsequently worked with Dr Fotis Kafatos at Harvard University, where she continued her studies on gene regulation and neurogenesis that paved the way for her subsequent research focus on Notch signaling. Returning to the UK to take up a position in University of Cambridge in 1991, Sarah has been running her own group since then, investigating aspects of cell signaling and gene regulation in development, primarily in the context of the Notch pathway. She is currently Professor of Developmental Biology and is an elected member of EMBO and a Fellow of the Academy of Medical Sciences. Sarah has been an active member of the fly community since the early days of her post-doc, and seeks to promote research using model organisms through her roles on funding panels. She has been involved in organizing the biannual EMBO Conference on the Molecular and Developmental Biology of Drosophila (and is currently Co-chair of the organizing committee), is a frequent participant and session chair at the USA fly

meetings, and strives to encourage the next generation of researchers at all levels through teaching and mentoring programs.

Antonio Jacinto
CEDOC - Chronic Diseases Research Center
NOVA Medical School, Lisbon, Portugal

Antonio Jacinto received his primary and college education in Sintra and Lisbon, Portugal, and graduated in Biochemistry at the University of Lisbon in 1993. He got his PhD in Genetics and Developmental Biology in 1999 from the University of London with Prof. Phillip Ingham, for work on the Hedgehog pathway in flies. His Post Doctoral training was at University College London with Prof. Paul Martin, where he established Drosophila as a model system for epithelial repair. Antonio started his independent research group in 2002 at the Gulbenkian Institute of Science, Oeiras, Portugal, and moved to the Institute of Molecular Medicine, Lisbon, in 2004. Since 2011 he has been running his lab in CEDOC - Chronic Diseases Research Center, Lisbon, where he his now the institute's Director. Antonio´s main research interests are on tissue repair and regeneration and his approaches normally involve advanced imaging and genetics. Antonio is an active member of the fly community, promoting the use of animal models in biomedical research, training future generation of researchers and medical doctors, and participating and organising meetings where flies have the central stage. Antonio has played a particularly important role in developing the fly community in Portugal by encouraging colleagues to start Drosophila labs in Portugal and more recently by recruiting fly PIs for the institute that he directs.

Appendix 4. Collins GSA Agenda

Meeting with Francis Collins and Model System Community Leaders
Sponsored by the Genetics Society of America
July 14, 2016 at 10:00 am, Orlando, FL, **Los Angeles Room**, Orlando Marriott

Participants:

Hugo Bellen, Baylor College of Medicine, HHMI, Drosophila community resources
David Bilder, UC Berkeley, President Drosophila Board of Directors
Judith Blake, The Jackson Laboratory, PI Mouse Genome Database (MGD) and Gene Ontology (GO)
Mike Cherry, Stanford, PI yeast database (SGD) and Gene Ontology (GO)
Andrew Chisholm, UC San Diego, President Worm Board of Directors (WormBoard)
Lynn Cooley, Yale, Vice President GSA
Stan Fields, University of Washington, HHMI, President GSA
Mary Mullins, University of Pennsylvania, Vice President International Zebrafish Society
Norbert Perrimon, Harvard, HHMI, PI FlyBase
Jasper Rine, HHMI Professor, UC Berkeley, Past President GSA
Paul Sternberg, Caltech, HHMI, PI WormBase and Gene Ontology (GO)
Monte Westerfield, University of Oregon, PI zebrafish database (ZFIN)

Agenda

1. Model organism databases (MODs) (brief intro from Jasper Rine)
Community anxiety about the plans in NHGRI to integrate databases is high. These databases are repositories of many kinds of information essential to research projects, but not necessarily the same types of information in each database. A merger that results in data loss or degradation of our ability to use the data would be a huge setback.

How can the community best work with the NIH to ensure information resources are maintained?

Will other NIH institutes participate in funding the Alliance of Genome Resources (MODs and Gene Ontology)?

2. Funding for model system research (brief intro from Hugo Bellen)

Despite encouraging and welcome statements from NIH about their support of model system research, information about levels of funding for model organism-based projects is hard to find.

Can the NIH track the data on funding for model system research and provide these data on their website?

Funding for research projects using model systems is concentrated in NIGMS.

How can interest and support for model system research be spread to other institutes? For example, partnerships with disease-focused investigators?

The number of R01 grants to Drosophila projects has declined 30%, and reductions in other model systems have also occurred.

Can the number of R01 grants to model system projects be increased?

Anecdotal comments suggest many study sections in CSR are dismissive of research proposals using model systems.

Can CSR train their SROs, study section chairs and study section members to recognize the value of model system research?

The Model Organisms for Biomedical Research website is moribund.

Can the NIH reactivate their trans-NIH working group on model organisms?