2018 National Drosophila Board Agenda, Reports, and Minutes

Wednesday 11 April 2018 3:00 – 6:00 PM
Downtown Marriott Hotel, Philadelphia

Table of Contents for Reports and Discussion Items: **Page**

IMPORTANT NOTE:

Minutes covering the oral presentations and related discussion are included between the written report documents in **BLUE TEXT**. These were prepared by Bruce Edgar (Fly Board President Elect 2018-19) from notes and recordings taken during the meeting. Action Items for follow-up during the year following the meeting are highlighted within these Minutes in **ORANGE TEXT.**

1. 2018 NATIONAL DROSOPHILA BOARD AGENDA

Wednesday 11 April 2018 3:00 – 6:00 PM
Downtown Marriott Hotel, Philadelphia

1. Introduction (Debbie Andrew) 3:00 – 3:05

ADRC

2. Report of the Organizing Committee (Tin Tin Su) **3:05 – 3:15**
3. Treasurer's Report (Michelle Arbeitman) **3:15 – 3:20**
4. Report of the GSA Senior Director (Suzy Brown) **3:20 – 3:25**
5. GSA and the Drosophila Board (Lynn Cooley) **3:25 – 3:30**
6. Sandler Lectureship Committee (Kim McCall) **3:30 – 3:35**
7. Victoria Finnerty Undergraduate Award (Amanda Norvell) **3:35 – 3:40**
8. Image Award (Laura Johnston for David Bilder) **3:40 – 3:45**
9. 2018 & 2019 Fly Meetings (Michael Buszcazak) **3:45 – 3:50**

Discuss action items related to ADRC: 3:50 – 4:00

a. Board needs to nominate the Drosophila person (and two alternatives) for the program committee for the 2020 TAGC meeting in Washington DC. This is someone who can relay and represent the interests of the fly community while still maintaining the vision for TAGC 2020. They are asking us for three nominations [one primary name and two alternates] so that, when GSA looks at nominations from all the communities, they're able to balance biological expertise across the committee.
b. Board should discuss whether the Fly Meeting Organizing Committee should have a mandate regarding diversity and representation of invited speakers and session co-chairs.
c. PIs for the 'New Faculty Forum' were identified this year by asking a question on the registration form about the year in which faculty received their faculty assignment. Is this sufficient to capture all new faculty?
d. Discuss science versus training at ADRC, Fly community versus GSA offerings (see pages 7 and 10 for proposed and current GSA offerings/changes)
e. Discuss child care offerings at ADRC
f. Discuss changes to meeting format to cut meeting costs – charging off site fees, posters being up only ½ duration of meeting
g. Discuss what to do with money in treasury
h. Solvency of Finnerty Award/consider other named awards associated with travel grants

Community

10. Drosophila Board Elections Committee (David Bilder/Laura Johnston) **4:00 – 4:04**
11. Brief update on commercial antibodies project (Bing Zhang/Debbie Andrew) **4:04 - 4:05**
12. Primarily Undergraduate Institutions (Amanda Norvell) **4:05 – 4:15**
13. Advocacy and Communications (Andreas Prokop) **4:15 – 4:25**

Discuss action items related to community: 4:25 – 4:40

a. Idea for more inclusion of non-caucasian ancestry on the fly board
b. Impact of increased registration costs and abstract fees on undergraduate attendees
c. Advocacy and communication

BREAK 4:40 – 5:00

Resources and Projects

14. FlyBase (Norbert Perimon) **5:05 – 5:10**
15. Bloomington Stock Center (Kevin Cook) **5:10 – 5:15**
16. VDRC Stock Center (Lisa Meadows) **5:15 – 5:20**
17. Kyoto Stock Center (Debbie Andrew for Toshiyuki Takano-Shimizu) **5:20 – 5:25**
18. Species Stock Center (Patrick O'Grady) **5:25 – 5:30**
19. Drosophila Gene Disruption Project (Hugo Bellen) **5:30 – 5:35**
20. Harvard Drosophila RNAi Screening Center (Stephanie Mohr) **5:35 – 5:40**
21. Harvard Transgenic RNA Project (Jonathan Zirin) **5:40 – 5:45**
22. Berkeley Drosophila Genome Project (Sue Celniker) **5:45 – 5:50**
23. DGRC (Andrew Zelhof) **5:50 – 5:55**
24. DIS (Jim Thompson) will take any questions we have for him
25. Celeste Berg announces a Larry Sandler Symposium (details in final appendix)

Discuss items related to community resources/projects, as time permits.

ADJOURN

Discussion (Introduction)

Deborah Andrew (current Fly Board President 2017-18) outlined of the Fly Board mission and structure. She also delivered a summary of "state of the fly community", including summaries of the status of the stock centers and resource centers, FlyBase, and all the other topics detailed below in the written reports (see black text in this document).

2. Report of the 2018 Meeting Organizing Committee: Tin Tin Su (chair), Pam Geyer, Giovanni Bosco, Noah Whiteman

The 2018 Organizing Committee was assembled in 2017. Tin Tin Su was invited by Laura Johnston in January 2017 to chair the organizing committee. Tin Tin invited Pam and Gio, and we collectively recruited Noah Whiteman for diverse expertise. The Organizers communicated by email and monthly teleconferences. All decisions were made by consensus following the opportunity for input from all. Suzy Brown at GSA was involved at many stages of planning and participated in conference calls and group emails. In preparing this report, we have modeled it after the 2017 organizing committee report, to make comparisons between the two years easier.

Interaction with the GSA Office

We wish to thank Suzy Brown, Sonia Hall and the GSA office for their assistance and participation in the organization of the meeting. Suzy provided timeline information, data from past meetings, valuable suggestions and points for deliberation. Suzy was responsive to various questions and requests we made. Sonia Hall has been organizing career development events and workshops including the New Faculty (formerly known as Early PI) Forum, a Community Connection Lunch, and workshops on peer-review in publishing. We also benefited from the contributions of Tracey DePellegrin and Cristy Gelling. Thanks!

Timeline and Overview of Meeting Organization

Discussions focused on various aspects of the meeting in the following chronological order: Keynote and Plenary speakers; Platform sessions; Overall program. Outreach and special activities were discussed throughout the planning period. We wanted to generate a program that conveyed exciting and excellent science, with speakers representing the breadth of the Drosophila community in terms of topics, gender, ethnicity, career stage and geographical location. The final program was decided in stages. Plenary speakers were set by **June 2017**. Platforms talks were set by **December 2017**. Types and timing of special events were decided by **February 2018**. As in recent years, only the schedule and lists of talks and posters are in the program book. The abstracts are available online and through the #DROS18 Meeting mobile app.

Keynote Speaker. For the opening night, there was consensus among the Organizers for Keynote Speaker as opposed to a panel discussion. This committee felt it was important to address the gender imbalance seen since 2001 (we did not look further back), where the Keynote Speakers included 11 males and 1 female. Even 5 panel discussions included 19 males and only 4 females. Seven candidate Keynote Speakers were considered, all exceptional senior female scientists. Terry Orr-Weaver was selected by consensus, was invited by email (TTS) and by phone (GB), and she accepted in **June 2017**. The title of her talk is “Research taking flight from foundational biology”.

Plenary Speakers. Nominations for possible plenary speakers were restricted to individuals who had not previously presented a Plenary Talk at the Fly Meeting in the past 10 years. In total, the Organizers identified 46 candidate Plenary Speakers in **April 2017**. In **May 2017**, an independent (blind) vote was held among the four co-Organizers, with 7 candidates receiving 2-3 votes and were placed on the ‘invite’ list. Additionally, 13 received 1 vote each. The merits of these 13 candidates were discussed in a teleconference on May 23, and 5 were chosen by consensus. Plenary speakers were invited by emails sent from the chair. All but one initial of the invitees accepted. The exception was a scientist in India who could not travel due to family obligations. The Organizers replaced this invitee with a short-listed candidate from Japan, in

order to maintain global participation. All invited speakers accepted and committed by **June 2017**.

The 2017 organizers implemented several changes to the format based on the 2016 Meeting Rejuvenation Committee Report (see 2017 report, section on *Major changes/additions to the 2017 Meeting*). For the 2018 meeting, the Organizers decided to make minimal changes to the 2017 format, such that the 2017 format changes had time to mature. Notable 2017 changes that remain in 2018 include the:

- Revised Abstract Categories and Keywords
- PI Early Career Forum (re-named 'New Faculty Forum' in 2018)
- Stand-alone "Techniques & Technology" Platform Session
- Having Platform Sessions (i.e. the number of talks in each) reflect the distribution of abstracts
- Science Slam
- Q&A sessions on peer-review and publishing
- Expectation of fundraising by the Organizers

The 2018 Organizers did make a small number of changes to the format. First, we decided unanimously to treat the Ecdysone Workshop the same as other workshops. This meant that the Ecdysone Workshop organizers had to apply for a workshop slot and the duration of the workshop was limited to 2 hours. Second, the stand-alone "Techniques & Technology" Session was treated as a platform session. As such, speakers were not invited, but were instead selected from abstracts. In addition, the "Techniques & Technology" platform was moved to a Friday slot, because the 2017 session chairs (Hugo Bellen and Julie Simpson) thought Saturday was too late in the meeting to have this session.

***Platform sessions*.** In **June-July 2017,** chairs for the Platform Sessions were nominated, discussed and decided by consensus. The chairs were chosen for the scientific excellence but also to ensure diversity across many dimensions including gender, geography and institution type. Chairs were asked to nominate and solicit co-chair positions. This differs from 2017 when the organizing committee selected both co-chairs. In 2018, the chair and co-chair were asked to solicit a junior co-chair, typically a senior post-doc in the lab of the chair or the co-chair. Nearly all chair, co-chair and junior co-chair positions were filled by **August 2017**. As an incentive to early selection, the chair and co-chair were told that they have the option to select their junior co-chair as a speaker in their respective platform session. All but one platform session chairs selected a junior co-chair. All junior co-chairs will be speaking in the session.

The abstract deadline was **November 14, 2017**. From the submitted abstracts, the Organizers allocated the number of talks per Platform Session and sent the co-chairs guidelines for abstract review and talk selection. Co-chairs deliberated and provided ranked lists of selected talks to the Organizers by **December 8, 2017**. The Organizers reviewed the ranked lists to ensure diversity in presenter gender, career stage and individual laboratories represented among Platform sessions. Final Platform talks were assigned by **December 14, 2017**.

***Special Events*.** In **August 2017-February 2018**, the Organizers discussed and decided on special events for the program.

These include:

- Community outreach. Alana O'Reilly was identified as a key local contact. Alana is an Associate Professor at Fox Chase Cancer Center and Scientific Director of

Immersion Science Program for high school students. As a result of discussion, local high school students and teachers are being invited to participate in ADRC. Suzy Brown and GSA are kindly issuing 20 day passes each day, to be distributed by Alana and the teachers to motivated and interested high school students.

- The three 2017 Nobel laureates and Drosophila circadian rhythm researchers were invited to ADRC. Mike Young accepted and will give a 30 min talk on Saturday evening.
- 'FLYght of the Champions' event was established as a community building initiative, which we hope will be continued in future years. In 2018, FLYght of the Champions' will include Nobel laureate Mike Young's address to the community (see bullet point above) poster awards, and the Science Slam.
- Poster awards were moved from Sunday morning to Saturday evening. We felt that having them on Sunday makes them seem like an 'afterthought'.
- Stephanie Mohr will read from her book, *First in Fly* (Harvard University Press, 2018), and hold a Q&A session on Thursday. This free event will occur immediately after a ticketed lunch event.
- 'Year in Review'. An ~15 min review of the accomplishments of the Drosophila community during the year. Pam Geyer will present this review immediately following the plenary session on Thursday morning. She will cover notable awards, induction into national and international societies, and memorials of researchers who passed in the last few months, Mel Green, Fotis Kafatos and Kathy Matthews. GSA sent out calls in its March 2018 newsletter to suggest additional community members to remember but has not received any names as of 03/19/18.

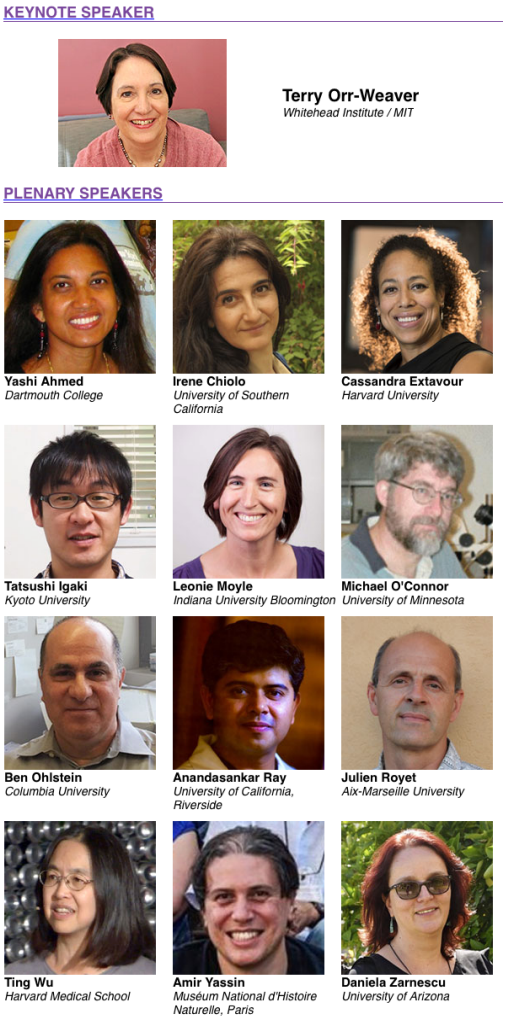
2018 Fly Meeting Registration and trends

Pre-registration is **up by 20% compared to 2017**, with **1343 pre-registrants** as of February 12, 2017. For historical comparison, earlier Fly Meeting pre-registrations were: 1121 (2017), 997 (2016/TAGC), 1517 (2015), 1431 (2014), 1555 (2013), 1537 (2012), 1328 (2011), 1516 (2010), 1383 (2009), 1343 (2008), 1345 (2007).

Compensation for Organizers, speakers and special awards

Free conference registration was granted to the meeting Organizers (4); the Keynote (1) and Plenary Speakers (12); and the Exhibitors that purchased booths. Early registration rate was granted retroactively to one session chair who failed to register on time. Free registration was granted to one junior co-chair who will be between jobs at the time of the meeting. Everyone had to cover their own lodging and travel costs. There were questions about registration and travel compensation from some of the speakers and session chairs. In particular, a potential session chair from South America requested help with registration, travel and lodging but was declined due to lack of funds. This session chair was replaced. The Larry Sandler Award Winner receives complementary airfare, registration, lodging, and GSA lifetime membership. Victoria Finnerty Memorial Fund travel grants were awarded to 7 undergraduate researchers presenting posters.

Detailed description of program components



Opening Session and Keynote Speaker. The 2018 Meeting will follow the traditional program on the first night, with introductions, announcements from GSA, the Sandler lecture and a Keynote lecture. In addition, the Organizers invited Deborah Andrew, Fly Board President, to address the community during the opening remarks. We will also have the GSA president, Lynn Cooley, bestow GSA awards, to one fly person (Mariana Wolfner) and three in other fields.

***Plenary Speakers*.** Plenary Speakers were chosen based on their scientific impact, with an eye towards breadth of topics, ability to engage the audience, and a balance in gender, career stage, and foreign/domestic location. The 2017 report of the organizing committee noted that a concern was raised because 8/12 speakers were non-US-based. In addition, the 2018 Organizers heard concerns about ethnic diversity among the plenary speakers. In selecting 2018 speakers, we remained mindful of the above concerns without deliberately attempting to reach a particular outcome. Notably, the 2018 Plenary speakers are a diverse group that we believe reflect the Drosophila community: 50% female and 50% non-Caucasian. 50% of the speakers are senior investigators (e.g. full professors) and 75% are US-based. Of these speakers, 10 are first-time plenary speakers; the other two spoke in 1997 and 2005.

Abstract Categories and Keywords. The 2017 Organizers made data-based decisions to merge or expand categories, resulting in 19 final abstract categories (versus 17 categories in 2016). The 2018 Organizers kept the 2017 categories and key words, to allow time for maturation and better assessment of impact of the new program. The 19 platform categories were used in defining sections for the posters. The **2018 Abstract Categories** are in **Table 1**.

Submitted abstracts. In total, **889 abstracts** were submitted. Totals in recent years were 716 (2017), 692 (2016/TAGC), 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). Thus, 2018 reflects an **24% increase in abstract submissions over 2017**, in line with a 20% increase in pre-registrations in the same time periods. **In fact, the number of submitted abstracts was so large that late abstract submission was eliminated due to lack of poster board space.** While submitting abstracts, presenters could select a primary and secondary category for talk consideration. There were **429 requests** in the primary category for **164 Platform talks**, which resulted in a **38% success rate.** This was slightly lower than the 39.8% success rate in 2017. The number of total abstracts varied across sessions (see **Table 1**).

The greatest number of abstracts was submitted to “Physiology, metabolism and aging”, with 92 abstracts as a primary choice. The lowest number of abstracts was submitted to “RNA Biology”, with 18 abstracts as primary choice. The corresponding categories from 2017 were “Gene Regulation” (65 abstracts) and “RNA Biology” (14 abstracts). The fraction of abstracts in a given category that requested talks also ranged widely, from 71% in “Stem Cells” to 38% in “Models of Human Disease: Developmental and Physiological Disorders”. This is similar to 2017 when the range was from 72% in “Cell Division and Growth Control” to 33% in “Gametogenesis”). These considerations speak to shifting trends that should be monitored and used to adjust keywords and session topics in the future (see our recommendations below)

Table 1. Categories and abstracts submitted

number of abstracts						
received	request platform	%request platform	selected	% selected	poster	session (primary choice)
43	24	56%	7	29%	36	01. Intracellular Dynamics: Cytoskeleton, Organelles & Trafficking (chair requests Sat-teaching)
68	32	47%	15	47%	53	02. Cell Biology & Signal Transduction (chair requests afternoon slot due to time zone change)
70	27	39%	15	56%	55	03. Cell Division and Growth Control
40	17	43%	8	47%	32	04. Cell Death and Immunity (chair needs to leave after Thursday)
92	42	46%	15	36%	77	05. Physiology, Metabolism & Aging
42	23	55%	7	30%	35	06. Gametogenesis
24	17	71%	7	41%	17	07. Stem Cells
55	26	47%	8	31%	47	08. Neural Development and Physiology
53	26	49%	8	31%	45	09. Neural Circuits and Behavior
59	23	39%	7	30%	52	10. Models of Human Disease: Neurodegeneration and Neurological Disorders
32	12	38%	7	58%	25	11. Models of Human Disease: Developmental and Physiological Disorders
62	31	50%	7	23%	55	12. Evolution & Population Genetics
19	12	63%	4	33%	15	13. Evolution of development, other species
65	37	57%	15	41%	50	14. Patterning, Morphogenesis and Organogenesis
68	33	49%	15	45%	53	15. Regulation of Gene Expression
42	20	48%	7	35%	35	16. Chromatin and Epigenetics
18	12	67%	4	33%	14	17. RNA Biology
27	15	56%	8	53%	19	18. Techniques and Technology
10	0	0%	0	0%	10	19. Educational Initiatives (not talks, only posters)
889	429	48%	164	38%	725	(session 18 will be during the same time as Friday workshops)

Platform Session organization. **Platform Session chairs, co-chairs and junior co-chairs** are listed with affiliation by session in **Table 2**. Three session chairs made scheduling requests based on travel and teaching. These requests were accommodated.

Following abstract submission, the categories were re-organized into 17 Platform Sessions. Five categories that had the most abstracts were given two split sessions (I & II, for a total of 15 talks). Eleven categories were assigned a single session (7-8 talks). Two categories were merged into one session (“RNA Biology” and “Evolution in development, other species” with 4 talks each). “Techniques & Technology” has 8 talks, one fewer than in 2017, to fit into the new time slot on Friday. For “Educational Initiatives”, Suzy Brown informed the Organizers that we need not select abstracts for talks. Instead, these abstracts were considered by Sonia Hall and the Education Committee for GSA-run education-oriented sessions. Sonia tells us that the goal is to have one education workshop and 1 education platform session at each GSA meeting (#17&18, **Table 3**).

The Organizers determined the number of allocated talks to each Platform Session based on the number of submitted abstracts (see **Table 1**). The chairs/co-chairs were asked to generate a ranked list for selected talks with a target number of two more abstracts than the allocated number of talks for that session. The abstracts submitted were reviewed as primary choice, but the chairs/co-chairs were instructed to carefully examine all abstracts in their session and flag abstracts more suitable for the secondary choice either as talks or posters. Multiple such

abstracts were flagged and moved into more appropriate sessions. The chairs/co-chairs were given **2 weeks** from November 21 to December 8 to review and submit their ranked lists of selected abstracts for Platform talks to the Co-Organizers.

The Organizers reviewed their choices and selected final talks by December 14, 2017. In doing so, the Organizers ensured that there was a balance in gender and career stages of the selected abstract speakers within a session. To avoid over-representation of any individual laboratory at the Meeting, the Organizers looked through selected talks for ones from the same laboratory. Only two such examples/labs were found. One lab had two talks but in different sessions, and this was allowed based on a similar practice in 2017. One lab had three talks, but in three different sessions. The Organizers discussed this case and decided to allow it because the PI is an assistant professor and all three talks selected were deemed worthy by the chairs of each session. Having the ranked list of abstracts, we found, was useful for replacing a talk when the speaker withdrew after notification of platform talk assignment.

Table 2. 2018 Drosophila Meeting Platform Sessions & Chairs

Session	Chair	Co-chair	Junior co-chair
01. Intracellular Dynamics: Cytoskeleton, Organelles & Trafficking	Brooke McCartney, Carnegie-Mellon U	Avi Rodal, Brandeis U	Steve DelSignore, Brandeis U
02. Cell Biology & Signal Transduction	Laurel Raftery, U Nevada, Reno	Andrea Page-McCaw, Vanderbilt	Vicki Losick, MDI Biological Labs
03. Cell Division and Growth Control	Laura Johnston, Columbia	Laura Buttitta, U Michigan	Yiqin Ma, U Michigan
04. Cell Death and Immunity	Andreas Bergmann, U Mass Med, Worcester	Eli Arama, Weizmann Institute of Science	Alla Amcheslavsky, U Mass Med, Worcester
05. Physiology, Metabolism & Aging	Stephen Helfand, Brown U	Daniela Drummond-Barbosa, Johns Hopkins	Jackson Taylor, Brown U
06. Gametogenesis	Helen Salz, Case Western U	Prashanth Rangan, SUNY Albany	Nicole Crown, UNC
07. Stem Cells	Hannele Ruohola-Baker, U Washington	Haifan Lin, Yale University	none
08. Neural Development and Physiology	Ramaswami, Mani Ramaswami, Trinity College, Ireland	Quentin Gaudry, U Maryland	Sonia Sen, U Oregon
09. Neural Circuits and Behavior	Marcus Stensmyr, Lund Univ, Sweden	Marco Gallio, Northwestern U	Emanuela Zaharieva, Northwestern U
10. Models of Human Disease: Neurodegeneration and Neurological Disorders	Bing Wei, Stanford	Kanae Ando, Tokyo Metropolitan University	Vafa Bayat, Stanford
11. Models of Human Disease: Developmental and Physiological Disorders	Jun-Yuan Ji, Texas A&M	Hong Xu, NIH-NHLBI	Zhe Chen, NIH
12. Evolution & Population Genetics	Nadia Singh, U Oregon	Dmitri Petrov, Stanford U	Sharon Greenblum, Stanford U
13. Evolution of development, other species	Benjamin Prud'homme, CNRS, Marseille	Virginie Courtier-Orgogozo Institut Jacques Monod	Jack Green, Institut de Biologie du Development. Marseille
14. Patterning, Morphogenesis and Organogenesis	Helen McNeill, U Toronto	Sarah Hughes, U Alberta	Oguz Kanca, Baylor College of Medicine
15. Regulation of Gene Expression	Victoria Meller, Wayne State U	Judy Kasis, NIH	Sandip De, NICHD/NIH
16. Chromatin and Epigenetics	Kami Ahmad, Harvard	Yukiko Yamashita, U Michigan	J. O. Nelson, U Michigan
17. RNA Biology	Bob Duronio, UNC	Greg Matera, UNC	Jim Kemp, UNC
18. Techniques and Technology	Amanda Simcox, Ohio State	Gwyneth Card, HHMI	Ryan Williamson, HHMI

Poster Sessions. There are currently **725 abstracts** scheduled to be presented as posters. As described above, due to the volume of abstracts submitted by the deadline, there is no room (in poster board) for late abstracts. The breakdown of posters by category for the regular abstracts is shown in the **Table 1.**

Poster Awards. A total of up to six poster awards are slated to be given to the top three Graduate student posters (1st, 2nd and 3rd) and the top three Undergraduate posters (1st, 2nd and 3rd). There is no longer a category for postdoctoral poster awards, as many of the judges are the Postdoc trainees functioning as Platform Session co-chairs. Awards will be given based on merit only. The prizes are $500 for 1st place, $300 for 2nd place and $200 for 3rd place.

Based on the recommendations of the 2017 organizers and GSA, posters will be judged initially by the Session junior co-chairs, or co-chairs if no junior co-chairs were available, who will select their best posters. To simplify judging, judges have the option to identify a short list of potential poster award winners for each category (graduate student and undergraduates) based on abstracts for review. 'Best posters' selection will be based on the quality of science and poster design, not on the poster presentation, given the time constraints of the meeting. Junior co-chairs will communicate their recommendations to Noah Whiteman of the 2018 Organizing Committee by Friday at noon. The four Co-Organizers will meet Friday night to determine the poster award winners. Ribbons will be pinned on the winning posters so that attendees can see the winning posters during the poster session on Saturday afternoon. Winners will be recognized by Noah Whiteman during the FLYght of the Champions session on Saturday evening.

Workshops. Based on feedback from attendees at previous Meetings, the 2017 Organizers scheduled two major Workshop Sessions on Thursday night 7:45- 9:45 PM and Friday afternoon 1:45- 3:45 PM, and eliminated the late-night sessions on Saturday. One exception was the Ecdysone Workshop, which took place at the pre-meeting time on Wednesday. The 2018 Organizers have followed the same schedules (except for shortening the Ecdysone Workshop to 2 hours, matching the others). In 2017, there were 11 total Workshops, from nine applications that were received and approved, the Ecdysone Workshop occurred outside of the application process, and a GSA career-oriented Workshop. In 2018, we received 18 applications. Of these, we considered only 11 to be bench research-based; the others were on teaching and career development. **Table 3** lists the 2018 Workshops and those we believe are focused on teaching or career development are in shaded cells. Because the number of bench research-based workshops in 2018 was only two more than the corresponding number (9) in 2017, the Organizers decided to approve all. We also discussed scheduling them in such a way that overlapping interests were minimized. In retrospect, we feel Workshop review and approval was a decision that we should have spent more time on. We make some suggestions for the 2019 organizers below.

		Table 3. 2018 Workshops, in order of presentation	also in 2017?
1	W 2:30-4:30	Ecdysone Workshop	YES
2	Th 7:45-9:45	Drosophila Microbiome	YES
3		Biogenic Amines and Behaviors	YES
4		The Hows and Whys of Drugging Flies – A Chemical Screening Workshop	
5		Autophagy in Development and Disease	
6		Reverse-engineering methods and quantitative analysis of signaling and organogenesis	
7		Building Community Through Mentoring	
8		Overcoming barriers to effectively utilize Drosophila melanogaster in scholarship, research, and teaching at PUIs.	*YES
9		Publishing Genetics Classroom Activities in CourseSource	
10		Advocating Drosophila through using it as an efficient teaching tool	
11	F 1:45-3:45	Functional Genomics Resources from the DRSC & TRiP	
12		Developmental Mechanics	YES
13		Everything you ever wanted to know about sex	YES
14		Feeding Behavior, Nutrition and Metabolism	YES
15		Drosophotoxicology: Examples and opportunities for fly research in toxicological sciences	
16		Spotlight on Undergraduate Research	YES
17	F 2:00-4:00	Professional Development Tool Kit (GSA-presented)	
18	F 6:30-7:30	Exploring Genetics Education (GSA-presented), listed as 'Education' in the program	

*2017 had "Integrating Research and Teaching at PUIs using Drosophila melanogaster as a Model Organism"

workshops considered to be on teaching or career development

Fly Single Cell Atlas. We received a request from the fly single cell RNAseq group (Susan Russo Gelbart, Norbert Perrimon, Thom Kaufman, Gil dos Santos, Brian Oliver) for an

opportunity to present at the conference. The request came after the workshop deadline and approvals. Therefore, we suggested they hold a presentation in the same room as the FlyBase Demo. The organizers believe single cell technology can be quite powerful and there will be interest. The group is happy to do so. This event is now scheduled for 4:05-4:20 on Friday in the FlyBase Demo room.

THE NEXT 4 EVENTS ARE BEING ORGANIZED BY SONIA HALL OF GSA.

New Faculty Forum. This event was created in 2017 as 'Early Career Forum' to address concerns that while certain (senior) generations of fly researchers strongly identify with the Drosophila community and regularly attend the Fly Meeting, the younger generation of PIs have increasing competition for their attention and allegiances to specific topic-related fields and other meetings. This pre-meeting event is designed to provide an opportunity for new faculty (those within the first five years of their appointment) and advanced postdocs to network, learn, and find support, thus fostering community-building while helping young PIs start their career.

The 2017 event was well-attended (49 registered attendants). The 2018 event is being organized by Sonia Hall of GSA. To summarize briefly, the 2018 Forum will occur on Wednesday from 9 am-4:30 pm. Attendees will discuss common challenges and have opportunities to learn about:

- tools and techniques for managing budgets effectively;
- how to be a supportive mentor;
- fostering inclusion;
- the basics of designing and teaching a new course.

The 2018 program has been revised to reflect participant feedback from last year. The focused event will allow attendees to form a strong network of peers with whom they can continue to collaborate, commiserate, and celebrate long after the meeting ends. The forum also features scientific presentations on a diverse array of topics, and a social hour will allow the participants to connect with more established Drosophila researchers. The fee has increased from $50 in 2017 to $100 this year. As of March 14th, there are 32 registrants for 50 available spots. Sonia reports that challenges include the difficulty in recruiting participants because of two concurrent events that would interest new faculty, Ecdysone Workshop (2:30-4:30) and GENETICS peer review workshop I (2:30-4:30).

Community Connections Lunch. This is a ticketed event designed to provide greater visibility for mid-career scientists, create networking opportunities for early & mid-career scientists and foster a sense of community. Round table discussions (10-people per table) will be led by one mid-career attendee and one established investigator. When populating discussion leaders, GSA aimed to have diverse representation of the community. They also looked to provide opportunities to mid-career attendees that were not already present during the meeting. There is room for 180 attendees, 37 of which are discussion leaders; as of March 14, there are 64 registered attendees ($40/person). Sonia reports that the major challenge encountered during the planning of this event was identifying mid-career attendees and their presentation status – speaker, session chair, etc.

GENETICS **Peer Review Workshop**. This two-part event (Wed and Fri 2:30-4:30) provides an introduction to peer reviewing for early career researchers, including graduate students. The workshop will cover best practices and a mock review. Becoming a better reviewer will help the participant become a better author and to hone some of the skills central to scientific success, including critical thinking, evaluating research, providing helpful feedback, and understanding

the mindset and expectations of peer reviewers and editors. Cold beverages and snacks will be provided on both days of the workshop.

Science Slam. We will repeat Science Slam, which was new in 2017. It will take place as a stand-alone event after Mike Young's address, as part of the FLYght of the Champions community-building even on Saturday evening (7:45-10 pm). Sonia reports that representatives from the Early Career Scientist Steering Committee will emcee the event and recruit members of the community to serve as judges. The event is designed to be an informal fun social event. Participants have 3-minutes to show the audience and judges how they would present *Drosophila* to a non-scientific audience "on the fly". There will be no props allowed. Winners will be announced, and awards distributed at the end of the event.

Fundraising
The Organizers generated a fund-raising letter modeled after the one used for a Gordon Research Conference. We planned to send the letter widely to publishers, biotech companies and vendors, but found that the greatest challenge was in knowing whom to send it to. However, it was difficult to identify the appropriate person and his/her contact information by online searches. In the end, the letter was sent to The Royal Society publishers, PloS Biology, Nature, NATURE REVIEWS MOLECULAR CELL BIOLOGY, PloS Genetics, Beckman Coulter, BestGene, Integrated DNA Technologies, NEW ENGLAND BIOLABS, INC, ZYMO RESEARCH CORPORATION. In addition, Tin Tin filled out an online solicitation for Regeneron. The only positive response was from BestGene who donated $3000. Developmental Studies Hybridoma Bank became a sponsor unsolicited. Additionally, GSA sent similar communiques to its list of several hundred potential and existing exhibitors.

Planned assistance to the 2018 Drosophila Conference Organizing Committee
All of the material available to the 2018 Organizers are in a Dropbox folder. The 2019 chair of the organizing committee will be invited to share the folder and will have access to all information. The information includes worksheet templates, tables listing previous speakers and session co-chairs, and templates for solicitation letters sent to potential session chairs, speakers and donors. In addition, a lunch at the Meeting with the current and next year's Organizers is planned for **Saturday** to discuss and answer any questions.

In addition, we have the following **considerations and suggestions for future conferences.**

- In 2017, "Drosophila Models of Human Disease", which had a total of 79 abstracts, was split into two new categories, "Neurodegeneration and Neurological Disorders" and "Developmental and Physiological Disorders." 2018 numbers justify this split; we recommend that the split continues for 2019.
- 2017 organizers recommended re-evaluation of how to best represent Evolution-related sessions. In 2018, "Evolution and Population Genetics" had 62 primary abstracts, whereas "Evolution in Development, other species" had only 19 abstracts. The corresponding numbers were 60 and 19 in 2017. The continued unevenness justifies re-evaluation but we cannot offer specific solutions.
- The 2017 organizers recommended a split of "Regulation of Gene Expression," due to consistently high abstract numbers in this category. But in 2018, whereas "Regulation of Gene Expression" continued to receive a large number of abstracts (68), two other categories received similarly high number of abstracts ("Cell Biology/68" and "Patterning/65"). Therefore, our recommendation would be to not split any of these but to offer two platform sessions to reflect the higher numbers.

- The 2017 organizers recommended that “RNA Biology”, which has had low abstract numbers over the years, be merged with another or even incorporated into “Gene Expression”. We support that recommendation and suggest pairing “RNA Biology” with another low-abstract session, “Evolution of Development”, as a viable option.
- “Physiology, Metabolism and Aging” received the highest number of submissions: 92 abstracts. Yet, the number of requests for platform talks in this session was low, such that the final % selected for platform talks was 36% and not different from the overall average of 38%. We recommend watching this category in the future and splitting as needed into two categories.
- Suzy Brown alerted the Organizers about a Twitter thread complaining about the lack of microbiota-related keywords and categories. One of the Organizers, Noah Whiteman, tweeted with the explanation that we are adhering to recently updated keywords and categories from 2017. We suggest considering the addition of these keywords in the future.
- Include a ‘PI name’ category in abstract submission. This will help the organization committee recognize abstracts from the same lab rather than to do time-consuming detective work by googling or similar. The ‘Institution’ category, currently in place, was partially helpful but we ran into several instances of multiple PI/labs from the same institution.
- With the elimination of the late-night Saturday workshop sessions, workshop requests are becoming harder to accommodate. Additionally, there are several workshops that have become institutionalized (Ecdysone, sex, feeding, PUI, etc.). We suggest the 2019 organizers consider better ways to review and approve Workshops. For example, some workshops could be every other year.
- Sonia reports that challenges in organizing the New Faculty Forum include the difficulty in recruiting participants because of two concurrent events that would interest new faculty, Ecdysone Workshop (2:30-4:30) and GENETICS peer review workshop I (2:30-4:30). We suggest that GSA and 2019 organizers considering holding the New Faculty Forum from 8:30 am-2:30 pm instead of 9 am-4:30 pm. This would avoid the conflict and may increase participation in NFF.

ACTION ITEMS FOR THE BOARD

- Board should discuss whether the Fly Meeting Organizing Committee should have a mandate regarding diversity and representation of invited speakers and session co-chairs.
- PIs for the ‘New Faculty Forum’ were identified this year by asking a question on the registration form about the year in which faculty received their faculty assignment. Is this sufficient to capture all new faculty?

Discussion (59th Annual Drosophila Research Conference; ADRC)

Tin Tin Su reported on the ADRC 2018 program. Dr. Su reported that the organizers had great interactions with GSA. One goal for 2018 was to invite speakers that represent the full spectrum of diversity of *Drosophila* researchers better. We think we achieved this to a large degree by starting out with diverse pools of possible speakers. There were more women and minorities as plenary and keynote speakers this year. We had a similar structure to the program this year as at the last meeting. Registration was up 20%, a good sign. The topics of the concurrent sessions are continually changing. This year the physiology and metabolism new sessions, reflecting increased interest and activity in these fields. New special events have been added. Nobel laureates have been invited for a special event. Community outreach efforts in the program are extensive. There is a special new session to commemorate fly researchers who have passed away. Day passes for high school teachers have been made available.

Diversity: Tin Tin Su commented positively on the career stage diversity of the 2018 program. Mark Peifer (Fly Board president elect-elect) proposed that the Fly Board should endorse ensuring diversity in ADRC speakers as a goal and/or guideline. There was extensive discussion amongst many Board members on the issue of maintaining diversity in the speaker selection for ADRC. The discussion resolved that diversity should include Gender, Ethnicity, Career Stage and other qualities, and that speakers should represent the full diversity spectrum of the entire Fly community. N. Whiteman commented that the 2018 ADRC committee did consider diversity, as well as topics, when setting up the program. The topic of European representation at ADRC was also discussed. How many European speakers are appropriate? Several members commented that several years back, ADRC had a large number of European plenary speakers that was an inappropriate representation. Others commented that this was a chance occurrence and has not been repeated. Sarah Bray commented that international representation is important, and that the European Fly Meeting (EDRC) meets only every 2nd year. Bruce Edgar commented that ADRC is perceived by many as the main Fly meeting for the entire world, not just for North America, and that we should remain inclusive. The European and Asian Drosophila conferences are smaller and more regional. Mark Peifer commented that we need to make a conscious effort to ensure diversity. Tin Tin Su commented that there is no need to compromise quality to ensure diversity; it is easily possible to achieve both aims. Thom Kauffmann commented that it is better to build bridges, not walls. Allan Spradling commented that the Fly Board should define the appropriate proportion of non-North American speakers at ADRC. The Australian Rep to the Fly Board offered to help identify Australian speakers. Pam Geyer commented that the organizers (for 2018) did reach out to the Fly Board International reps to get suggestions from other continents for speakers. Other opinions were offered. It was generally agreed that striving for balanced diversity amongst the presenters is an important goal to maintain, however no specific resolution was made or approved. Mark Peifer has followed up by organizing a poll of Fly Board members to try to publish a statement on diversity as an approved guideline. At writing, this poll was still in progress.

New faculty at ADRC, etc.: In further discussion, Tin Tin Su noted that we need to identify "new faculty" in ADRC registration, to get them to attend the new faculty forum. Suzi Brown (GSA) volunteered: "Will do." Laura Johnston noted that the new faculty forum, although it is very popular, is early in the morning on the first day of ADRC, and is therefore expensive because it requires attendees to fly a day earlier and book an extra hotel night.
D. Andrew volunteered that ADRC "should not be all science all the time." Where is the balance between science and non-science in the ADRC program? GSA mainly organizes training opportunities in the ADRC program. Events do cost significantly. Tracy Depellegrin (GSA) said that GSA needs to be more communicative with the ADRC organizing committee about community & training events. This year we have done this with the ADRC program. Community & career events are not scheduled during scientific sessions. GSA is trying to get feedback on value for these events too.
Pam Geyer: One issue is ADRC attendance, which has diminished a bit. What gets people to come back? Networking, time/events/meeting, colleagues, the people attendees meet, and opportunities. Attendance is not just because of good science talks. Pam thinks there is now a nice blend of science and non-science. Mark Peifer proposed to do a survey to determine why attendees come to ADRC and what they value. Do they value the non-scientific events a lot? Debbie Andrew noted that we will already have exit polls from ADRC 2018, but it's not a bad idea to get more data from attendees. Celeste Berg: It's good to have organized science networking events (assigned meals w/ speakers/attendees etc.).

Child Care at ADRC: Suzy Brown (GSA) said that GSA can provide funding for childcare to help, and also has information. Care.com is used by ACSB. We could use this too. A lactation

room is available at ADRC. Having a committee to make recommendations for family support for all GSA meetings will be good. It was resolved that such a committee is to be formed. We would like volunteers for this committee. Mark Peifer: ACSB has the whole thing laid out on their meeting website, but ADRC does not. We should have child-care options on the ADRC website and also included with the registration materials. ACSB gives childcare awards for meeting attendance. After some discussion, Julie Brill is nominated to chair a child-care committee (from GSA) to help improve child care and family options at the next ADRC (2019).

3. Treasurer's Report 2018 Michelle Arbeitman

Summary of Finnerty, Sandler and Drosophila Reserve Fund balances over several years.

Vicky Finnerty Memorial Fund				
	Contributions	Transfers from Meetings	Awards	Fund Balance
2011	3,726	-		3,726
2012	4,102	6,000	5,178	8,650
2013	-	6,000	7,150	7,500
2014	3,960	6,000	8,940	8,520
2015	1,324	6,000	4,705	11,139
2016	886	6,000	3,795	14,230
2017	1,500	6,000	3,844	17,886
2018*	700	6,000	4,945	19,641

*contributions ytd as of 2/28

2018 Awards: 10, totaling $4945
5 @ $599
3 @ $450
2 @ $300

Drosophila Reserve				
Meeting Year	Location	Net Income	Fund Balance	# Meeting Attendees
1993	San Diego	$ 17,105	$ 25,964	1165
1994	Chicago	2,800	27,946	1222
1995	Atlanta	8,417	36,363	1103
1996	San Diego	15,035	51,398	1423
1997	Chicago	31,663	83,061	1382
1998	Washington	21,522	104,583	1378
1999	Seattle	(6,053)	98,530	1366
2000	Pittsburgh]	(56,060)	42,470	1183
2001	Washington	71,656	114,126	1627
2002	San Diego	60,661	174,787	1552
2003	Chicago	(22,993)	151,794	1603
2004	Washington	23,026	174,820	1617
2005	San Diego	89,943	264,763	1515
2006	Houston	6,196	270,959	1402
2007	Philadelphia	16,663	287,622	1507
2008	San Diego	(5,410)	282,212	1447
2009	Chicago	(47,935)	234,277	1506
2010	Washington	27,082	261,359	1668
2011	San Diego	64,471	325,830	1541
2012*	Chicago	(81,484)	244,346	1537
2013	Washington	2,921	247,267	1555
2014	San Diego	6,982	254,249	1431
2015	Chicago	(21,457)	232,793	1569
2016	Orlando	(11,000)	221,793	1066
2017	San Diego	(56,463)	165,330	1205

* $20K transferred to Sandler Fund

Ending reserve balance available for investment: $165,330

Larry Sandler Fund					
	Investment Gain/transfer	Travel Expenses	Other Expenses	Net Income	Fund Balance
1993				1,417	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	1,076	1,208	37	(169)	28,640
2006	1,963	469	15	1,479	30,119
2007	2,187	501	15	1,671	31,790
2008	(859)	441	20	(1,320)	30,470
2009	1,198	768		430	30,900
2010	947	1,482		(535)	30,365
2011	555	420		135	30,500
2012*	23,821	826		22,995	53,495
2013	6,847	1,171		5,676	59,171
2014	4,865	580		4,285	63,456
2015	369	428		(59)	63,397
2016	5,716	709		5,007	68,404
2017	8,201	1,014	112	7,075	75,479
2018				-	75,479

Includes $20,000 transfer from meeting fund

Flyboard vote on investing Fly community money

The Fly community has ~$165,330.00 that was previously a reserve fund needed to insure the costs of the annual meeting. The GSA has recently reorganized meeting procedures and the Fly community no longer needs to have money in place to insure our meetings. Following discussions, the current, recent past, and future Presidents along with the Treasurer have recommended that the community invest this money in a low fee Vanguard fund, and then use the earnings to support travel awards for trainees. The GSA will handle the account and report to the Treasurer each year for the board meeting. According to GSA, award amounts of $600.00 or more will incur taxes on the recipient, so we recommend ~$599.00 for each award. Currently, the meeting organizers select Finnerty travel award winners, so these additional travel awards can also be chosen by the meeting organizers. Alternatively, this could become part of the president's responsibilities for the year she/he serves.

The President, President-elect, President-elect-elect, past-President, past-past President and Treasurer will decide on a travel award application process and work with GSA on getting an announcement and submission directions online. Any other use of the invested reserve money and investment return money must be brought to the Flyboard by the President and agreed to by majority vote.

To Consider at a later date: The Finnerty undergraduate travel award will run out of funds in three years, based on the average amount awarded in previous years, without additional investment. Some of the reserve fund investment returns can be used to bolster this award. There are other ideas for naming travel awards that can also be considered.

An email ballot will be sent to the Full Fly board. Feedback on the proposed ballot is requested within two weeks after the fly meeting. Please contact michelle.arbeitman@med.fsu.edu. This vote will include all Fly board members, including ex officio members.

Ballot:

1) The investment should be in a low-fee Vanguard fund that is (see below for examples of fund allocations):
   a) Low to moderate risk
   b) Moderate to high risk

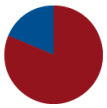
2) The travel awards will be for
   a) Undergraduate students, graduate students and post-docs
   b) Only graduate students
   c) Only graduate students and post-docs

3) The amount used for travel awards each year will be $8000-$9000. This assumes an average 5% annual return on investment.
   a) Agree to spend $8000-$9000/year
   b) Disagree to spend $8000-$9000/year

4) If the invested reserve fund goes below $150,000, travel awards will not be issued until the reserve funds returns to $150,000.
   a) Agree
   b) Disagree

5) Please provide comments/feedback/suggestions.

Which LifeStrategy Fund is best for you?

	LifeStrategy Income Fund	LifeStrategy Conservative Growth Fund	LifeStrategy Moderate Growth Fund	LifeStrategy Growth Fund
For investors who:	Care most about current income. Accept the limited growth potential that comes with limited exposure to stock market risk. Get details on LifeStrategy Income Fund	Care more about current income than long-term growth. Want some growth potential but with less exposure to stock market risk. Get details on LifeStrategy Conservative Growth Fund	Care more about long-term growth than current income. Want more growth potential and accept added exposure to stock market risk. Get details on LifeStrategy Moderate Growth Fund	Care most about long-term growth. Accept significant exposure to stock market risk in exchange for more growth potential. Get details on LifeStrategy Growth Fund
Investment time horizon	3 to 5 years	More than 5 years	More than 5 years	More than 5 years
Risk	1 **2** 3 4 5 Low to moderate	1 2 **3** 4 5 Moderate	1 2 **3** 4 5 Moderate to high	1 2 3 **4** 5 High
Target allocation	 20% stocks 80% bonds	 40% stocks 60% bonds	 60% stocks 40% bonds	 80% stocks 20% bonds
	INVEST NOW	INVEST NOW	INVEST NOW	INVEST NOW

*Vanguard LifeStrategy Funds average expense ratio: 0.14%. Average is asset-weighted. Source: Vanguard as of December 31, 2016. Industry average expense ratio for comparable life-cycle funds: 0.77%. Industry average excludes Vanguard. Source: Lipper, a Thomson Reuters Company, as of December 31, 2015.

All investing is subject to risk, including the possible loss of the money you invest. Diversification does not ensure a profit or protect against a loss.

Each LifeStrategy Fund invests in four broadly diversified Vanguard funds and is subject to the risks associated with those underlying funds.

Discussion and Action Items

Michelle Arbeitmann gave the Treasurer's Report. There is a new cost structure. We (the Fly Board and Community) now have 165K$ to invest; since GSA covers ADRC meetings now this balance has been returned to the fly community. These funds will be invested and the income will be used for travel awards, as previously agreed by the Fly Board. Michelle would like feedback on investment options and who the recipients of travel awards should be. This was discussed amongst the Board by email, and an electronic ballot was later distributed to poll the Board on their opinions about investment choice options. The funding for the Finnerty award for travel was discussed. Proceeds from the investment will be used for this. Debbie Andrew proposed to re-name the Finnerty travel award after other important Drosophilists who've died recently, so that donations could be given in their names.

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

Fiduciary Responsibility

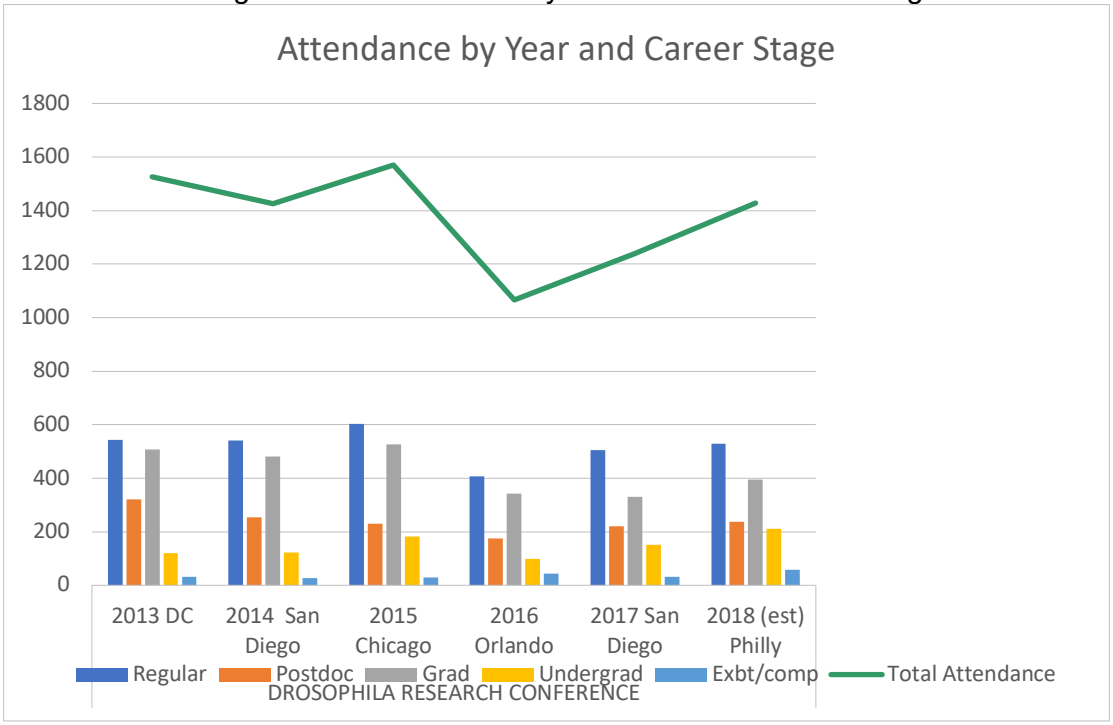
After some pretty significant financial losses for the Drosophila Conference, the GSA Board mandated that the Drosophila Conference be managed in the same fiscally responsible way that all of the other GSA conferences are managed Although those losses were absorbed by a fairly healthy conference reserve, it was not a sustainable model for the meeting and in fact the reserves had gone down more than 50% in the last several years. It was felt that rather than using the reserves to cover losses, this money should be in the hands of the community to use as they see fit for travel awards, special projects, etc. and the society would take on the financial risk and be responsible for operating the meeting in the black. These changes were critical to the future of the meeting. The Fly Board was notified of these changes in September and GSA's Executive Director, Tracey DePellegrin and other staff worked with then GSA Board President Lynn Cooley, FlyBoard current and former Presidents Debbie Andrew and Laura Johnston to make sure everyone was aware that other than the financial side of things, nothing was changing. The community and organizers were still in charge of the programming and, the reserves no longer had to be maintained for potential conference losses. GSA can still manage the reserves if that's what the Fly Board decides is the best plan of action. Fly Board Treasurer Michelle Arbeitman (who could not be part of some of the earlier conversations due to the devastation from Hurricane Irma) is working with Mary Adams (GSA's Controller) and others regarding the reserves.

GSA Conferences Staff/Structure:

In 2016 GSA recruited and hired Tracey DePellegrin as the new Executive Director. Tracey is new to the ED position but not to GSA (and probably most of you) as she had been successfully managing the GSA journals for many years. Tracey recognized that GSA can and should be a better partner with the communities. Also, for the conferences, we had untapped resources on staff that could be involved with conferences and make them even more valuable for our communities. In addition, Sonia Hall was hired as the Director, Engagement and Development. Sonia is developing many programs for GSA that will be rolled out, in whole or in part, and included at all GSA Conferences to enhance the meeting while not taking away from any of the scientific content. Cristy Gelling, who also had worked with Tracey at the journals, moved to the position of Communications Director where she has made a real difference in the look and feel of all conference communications from websites to promotion to social media. Suzy Brown is still the main contact for the Drosophila conference but now Tracey, Sonia and Cristy participate

on conference calls with the organizers too to help better understand their vision and figure out how to best implement that vision.

59th Annual Drosophila Research Conference
Currently there are 1,433 people registered for the conference. While we don't anticipate that number will go up too much, it represents an increase of over 200 people from last year year's final attendance figure. This chart shows you the recent attendance figures for the meeting.



Some Logistical Notes:
The size of our block of sleeping rooms and the ratio of sleeping rooms to meeting space are two of the most important factors that impact our ability to have lower sleeping room rates and favorable pricing on expenses such as coffee (as many as 600 gallons of coffee and tea combined are consumed at a typical Drosophila meeting costing as much as $60,000 or more). With the merger of two major hotel chains, it is a sellers' market. So while typically it would be wise to book at least five years out for a meeting of this size, in the current climate it is prudent to wait and let things re-adjust. However, some things that may be necessary in the future are having posters go up and down which will reduce the amount of space needed making us a better fit for more hotels; going to second or third tier cities where you may sacrifice slightly on convenience in terms of air access but prices, including sleeping room costs, are more reasonable; being flexible with dates and pattern so that we can find a good fit enabling the hotel to give us a better deal. The selection of any location will be at the discretion of the Fly Board based on recommendations from GSA.

You may remember from last year's meeting there was some discussion around people not staying in the conference hotel and possibly charging a fee if you do not stay in the conference hotel. While some groups do that and we will keep it as a possible option, we want to be careful about how something like this is implemented – especially if someone is staying elsewhere because their budget is tight. But we haven't ruled out the possibility of having a surcharge for those who choose to stay elsewhere. We want to gather some more data first. Many of the things that impact registration fees and sleeping room rates are tied to our ability to pick up our contracted block. This year we were lucky that we were able to adjust our block 18 months out to lower our commitment.

You may have noticed for the past several years we have had a lactation/nursing mother's room and will do so again this year. GSA has also formed a committee to investigate other ways that we can help families fully participate in meetings even though they have young children. Travel awards are one way of doing that where need based awards are provided for a family to decide what they want to do – bring a caregiver with them; get additional help in their own home while they travel; etc. We will also be looking into on-site childcare. We welcome your feedback.

FUTURE CONFERENCES

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

2020 – TAGC/61st Annual Drosophila Research Conference: April 22-26, The Gaylord National Resort & Convention Center, Metro Washington, DC. $189.

2021-62nd Annual Drosophila Research Conference: Town & Country Resort and Conference Center San Diego, CA Dates/rates tbd

Registrations - 2018

	Number
Regular GSA Members	463
Regular NonMembers	65
Postdoc GSA Members	198
Postdoc Nonmembers	39
Grad Student GSA Members	336
Grad Student Nonmembers	59
Undergrad GSA Members	184
Undergrad Nonmembers	28
Complimentary	57*
Early/Regular	**1,433**

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

Registrants by Country

United States	1190	Hungary	3
Canada	50	Ireland	3
United Kingdom	26	Norway	3
Japan	23	Argentina	2
China	18	Chile	2
France	18	Denmark	1
Germany	9	Finland	1
South Korea	9	Lebanon	1
Taiwan	9	Netherlands	1
Spain	8	Portugal	1
India	7	Russian Federation	1
Sweden	7	Slovakia	1
Australia	6	United Arab Emirates	1
Brazil	6		
Singapore	6		
Switzerland	5		
Austria	4		
Israel	4		
Mexico	4		
Czech Republic	3		

DISCUSSION AND ACTION ITEMS

Suzi Brown gave the GSA Directors report. Suzi noted that the GSA needed to take financial control of ADRC to break even w/ ADRC. The meeting was in financial jeopardy before. GSA has this year changed ADRC registration pricing, and changed staff structure to increase community help. One GSA goal is to make the ADRC meeting accessible to women, parents & families. This is important for ensuring diversity. The Fly Board discussed charging fees to participants that stay at other locations (to subsidize hotel bookings at main venue), but no resolution was reached. Suzi reported that advance booking priorities are changing. ADRC is currently booked through 2021, in San Diego.

Discussion: none.

5. GSA AND THE DROSOPHILA BOARD (LYNN COOLEY)

Lynn Cooley – President of GSA 2017-18 - presented. Lynn reported that GSA has a new executive director – Tracy Depellegrin – and introduced her. This change in leadership will help GSA to better serve the needs of its members. The GSA board is re-considering priorities of GSA. Suggestions for priorities of GSA are welcome from the Fly Board and model organism communities. A Fly Board member will now to attend the GSA meeting (Laura Johnston did in 2017).Generally, this will be the Fly Board President from the previous year. More communication between GSA and the Fly community is needed. Family friendly conferences: there is a new GSA childcare committee chaired by Susan Dutcher. This committee will address how to make conferences more family friendly. A new meeting is being sponsored by GSA: Population, Evolutionary, and Quantitative Genetics (PEQG; held 5/2016 in Madison WI). It's already oversubscribed. The next Allied Genetics Conference (TAGC) meeting, combining multiple model organism model systems, will be held in 2020 in suburban Washington DC. (see Future Conferences, p22).

Discussion: none.

6. Larry Sandler Award Committee Report (Kim McCall)

Committee members:
Kim McCall, Boston University (Chair)
Barbara Mellone, University of Connecticut
Daniel Barbash, Cornell University
Susan Tsunoda, Colorado State University
Michael Buszczak, University of Texas Southwestern

Chair 2019:
Daniel Barbash, Cornell University

Total 2018 Nominees: 19
Total Male Nominees: 10 Total Male advisors: 14.5
Total Female Nominees: 9 Total Female advisors: 4.5

Winner:
Lucy Liu (Ph.D. mentor: Dr. Hugo Bellen). Dr. Liu obtained her Ph.D. in Neuroscience in 2017 from Baylor College of Medicine. She is currently a postdoc with Dr. Norbert Perrimon at

Harvard Medical School. Dr. Liu received a number of awards from her graduate work including the Harold M. Weintraub Student Award in 2017. For her thesis, Dr. Liu investigated cellular mechanisms involved in neurodegeneration, following up from previous work in the Bellen lab demonstrating that several neurodegenerative mutants accumulated lipid droplets in glial cells. Using fly genetics, biochemistry and microscopy, Dr. Liu dissected the pathway leading from dysfunctional mitochondria to elevated ROS, activation of JNK and SREBP, culminating in lipid droplet accumulation. She showed that inhibition of ROS or JNK was sufficient to reduce lipid accumulation and delay neurodegeneration. Dr. Liu went on to investigate the mechanisms of lipid transfer between neurons and glia using a genetic approach in flies and a murine neuron-glia co-culture model. She found that glial-derived lactate is transferred to neurons and promotes lipogenesis in the presence of ROS. The lipid is then transferred to glia through APOD in flies, or APOE in mammals. By analyzing human APOE in flies, Dr. Liu determined that the APOE4 variant associated with increased risk of Alzheimer's Disease is defective in lipid transfer. The work from her thesis is published in three first author papers in Cell (2015), Seminars in Cell & Developmental Biology (2017) and Cell Metabolism (2017). Altogether her work has demonstrated novel findings highly relevant to understanding neuron-glia metabolic interactions and neurodegenerative disorders in humans.

Runners up:
Rory Coleman, Columbia University, New York (Ph.D. mentor: Gary Struhl)
Samuel Walker, Champalimaud Centre for the Unknown, Portugal (Ph.D. mentor: Carlos Ribeiro)

Notes on process:
Of the 19 nominees, the committee selected 4 finalists for which the whole PhD thesis was evaluated. The final discussion was carried out over a Skype meeting.

2018 Nominees:

Nominee	Gender	Thesis advisor	Gender
Emily Behrmann	F	Paul Schmidt	M
Heidi Bretscher	F	Donald Fox	M
Ugo Cappucci	M	Sergio Pimpinelli	M
Courtney Choutka	F	Sharon Gorski	F
Rory Coleman	M	Gary Struhl	M
Eduardo Dupim	M	Antonio Carvalho	M
Zachary Fuller	M	Stephen Schaeffer	M
Yogesh Goyal	M	Stanislav Shvartsman, Trudi Schüpbach	M/F
Kelsey Hazegh	F	Tania Reis	F
Adam Isabella	M	Sally Horne-Badovinac	F
Nadja Katheder	F	Tor Erik Rusten	M
Lucy Liu	F	Hugo Bellen	M
Michael Meers	M	Gregory Matera	M
Shan Meltzer	F	Yuh Nung Jan	M
Sarah Neuman	F	Arash Bashirullah	M
Nicholas Rizzo	M	Amy Bejsovec	F
Upasana Shokal	F	Ioannis Eleftherianos	M
Benjamin Stormo	M	Donald Fox	M
Samuel Walker	M	Carlos Ribeiro	M

Kim McCall presented the work of the Larry Sandler Award Committee. There were 9 & 10 female & male nominees, respectively. The committee read four Theses in full. Rory Pullman – Columbia & Samual Walker – Portugal were chosen as runners up. Lucy Lu was chosen as the 2018 winner. Lucy did her PhD in the Bellen Lab, at Baylor University. Lucy presented her lovely work in the first session at the 2018 ADRC.

Discussion: none.

7. Finnerty Undergraduate Travel Award Committee (Amanda Norvell)

Alexis Nagengast, the previous PUI representative to the Board, graciously served as Chair of the Award Committee this year. This year we received 25 applications for the Victoria Finnerty (VF) Undergraduate Travel Award and funded the top 10 for a total of $4945. Applications were markedly increased this year, nearly double the 13 received for the 2017 meeting. In order to maximize the number of students who received funding, money was awarded on a sliding scale, with a maximum amount of $599 because recipients do not have to pay taxes on amounts less than $600.

The awardees are:

- Elizabeth Hemenway (Poster #440, University of Missouri-Kansas City, $599
- Emily Rivard (Poster #649), College of the Holy Cross, $599
- Oandy Naranjo (Poster #311), Boston University, $599
- Yonatan Schwartz (Poster #431), Yeshiva University, $599
- Leah Anderson, (Poster #697), The Ohio State University, $599
- Jingxian Liu (Poster #682), Cornell University, $450
- Karam Khateeb (Poster #519), University of Wisconsin-Madison, $450
- Nicholas Bulthuis (Poster #553) Loyola University, $450
- Rose Besen-McNally (Poster #222), College of the Atlantic, $300
- Katie Tiemeyer (Poster #338), Boston University, $300

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), Sarah Certel, Justin DiAngelo, Amanda Norvell and Matthew Wawersik.

Discussion: none.

8. Image Award (David Bilder – Laura Johnston reported)

After 14 years, David Bilder is stepping down as Chair of the Committee. Nasser Rusan has agreed to take over as Chair for next year. Nasser has constituted a new committee, which this year included Nancy Bonini, Don Fox, and Mia Levine as well.

This year's competition had 68 total submissions, including 18 videos.

The winners this year were:

Nikos Karaiskos, for his image illustrating mapping of *Drosophila* embryonic cells by single cell RNA-Seq.

Asako Tsubouchi, for her video reconstructing converging primary and secondary somatosensory neurons in the brain.

The runner-ups were:

Peng Jin, for his image 'Cryo-EM map of the *Drosophila* mechano-transduction channel NOMPC'

Erica K. Shannon, for her video of damage-induced Ca++ waves in the pupal notum.

Nasser Rusan announced that he will make the Image Award presentation at the 2018 ADRC meeting. Nasser will add new members to the committee from Europe and Asia for 2018-19. Nasser will establish a Twitter account and take other measures to get more submissions next year.

Discussion: none.

9. 2019-2020 Fly meetings (Michael Buszczak)
The 2019 ADRC organizers are Michael Buszczak, Helmut Krämer, Rachel Cox, and Harmit Malik.

The organizers plan to study the platform sessions at the 2018 meeting, before deciding on whether changes are needed. The 2018 meeting includes a number of relatively new sessions that were first introduced to the program in 2017. These were largely based on suggestions made by the 2016 Meeting Rejuvenation Committee Report and include a new PI forum, a PI Happy Hour, a stand-alone technique session and a Science Slam. The organizers will monitor how these additions work in their second year and decide whether they are appropriate to keep in 2019.

The 2018 organizers have made a number of outstanding suggestions in their meeting report, particularly in regards to the organization of the concurrent platform sessions. All of these ideas will be kept in mind during the course of putting together the 2019 meeting. As in years past, the organizers will aim to put together a program that reflects the diversity of both the science being studied and the community as a whole.

We are currently considering a list of speaker suggestions. Our plan is to get the sessions and invited speakers sorted out within three weeks after the 2018 meeting.

Discussion (ADRC 2019)

Michael Buzsczak discussed the 2019 ADRC meeting. He has organized a committee. Michael will take suggestions for speakers now. One priority is to emphasize diversity in the speaker program.

Debbie Andrew asked the Board to please ask questions following the presentation, especially if the question is not listed in the Agenda for later discussion. Celeste Berg noted that more and more senior PIs are presenting and wishes more students and postdocs present at ADRC, including ADRC 2018. Tin Tin Su commented that session chairs were encouraged to have students and postdocs speak, and that overall they are highly represented in the ADRC 2018 program. The program was reviewed at a second level for broad representation of career stage, after it was proposed. Pam Geyer commented that session organizers were given the opportunity to have a co-chair for their session, and that many of these were early stage career investigators that were given the option to speak, and that many chose to. Tin Tin Su comments that this is a justifiable perk for serving as a session co-chair, especially for early stage PIs, and that the chairs received no financial support for organizing or attending the meeting, though they did a lot of the work. D. Andrew noted that for ADRC 2019 it is up to the organizers how to handle this issue. Later in the meeting, Tin Tin Su noted that the 2018 ADRC speaker program consists of 20% faculty presentations, 30% posdoc presentations, and 40% student presentations, representing a good breadth of representation of career stage.

TAGC 2020 (Tracey Depelligrin)

We are excited to announce the date and location for TAGC 2020, GSA's multi-community meeting: **April 22–26, 2020**, **in the Washington, DC metro area**. TAGC 2020 promises to be even bigger and better than TAGC 2016! We're planning a stimulating meeting spanning a broad range of genetics.

Who's participating?
The Yeast, Drosophila, *C. elegans* Development (cell biology and gene expression meeting), Xenopus, Mammalian Genetics, and Population, Quantitative, and Evolutionary Genetics (PEQG) communities will also be participating—and we hope the zebrafish and ciliates communities will also be joining us.

When and Where?
Our outstanding venue is just outside Washington, DC: the Gaylord Resort and Convention Center at National Harbor. This state-of-the-art conference facility offers many amenities with excellent nearby dining and lodging choices. It's just 8 miles from Capitol Hill and the historic sights of downtown DC.

How will this meeting be different from TAGC16?
The overwhelming response from TAGC16 participants surveyed (87%) was that GSA should hold this meeting again, but with more topic-driven (theme-based) programming that spans community boundaries. So for TAGC 2020, we're planning on a roughly 50/50 split between organism-specific sessions and organism-spanning sessions. The organism-specific scientific programming will be determined by each community's Program Committee; the organism-spanning (topic-driven) scientific programming will be the responsibility of the TAGC Program Committee. The TAGC Program Committee will work with each community's Program Committee to ensure optimal integration of the two programs.

What will be similar to TAGC16?
While TAGC is designed to bring different groups together, it will also preserve important aspects of your meeting to keep your community connected. In addition to crossover sessions, approximately half of the scientific programming will be organism/community specific, and there will be designated lecture rooms for each individual group. TAGC 2020 will also feature designated locations where you can easily find others from your community to discuss science and find friends during free time.
GSA will provide events that were popular at TAGC2016, such as scholarly publications workshops, early career scientist engagement activities, policy and advocacy events, mini-sessions on career advice, and more. We'll have a full, lively exhibit hall and poster sessions, which will also provide a gathering place for attendees.
As usual, GSA will be responsible for all logistical details (registration, housing, abstract submission, program books, exhibits, insurance, promotion, A/V, etc.) and financial obligations.

What's next?
Members from each individual community will represent that community on the TAGC Program Committee. **We ask you to nominate one individual [as well as two alternates] to act as your community's representative on the TAGC 2020 Program Committee.** Your committee representative will communicate your community's perspective and will help assemble a scientific program of appropriate breadth and depth. **To ensure coordination with your group's scientific program, this person should also serve on your community's Program**

Discussion (2020 TAGC)
Debbie Andrew announced that the GSA needs a chair for the Drosophila part of the TAGC joint meeting in 2020. We need nominations/volunteers. This is a big responsibility, a chance to highlight the beauty of Drosophila as a research organism. The audience will be very large. We need 3 nominations (per organism), a primary chair and two back-ups. Nominees then volunteered: C. Berg. H. Bellen. B. Calvi. B. Oliver. They all accept. Debbie Andrew offered to follow up with these nominees and put forward the names to GSA. Other nominees are requested. We would like more minorities & women. Hugo Bellen was eventually selected by GSA as the Drosophila representative.

10. **Drosophila Elections Report (David Bilder)**
The Elections Committee consisted of David Bilder (Chair), Ela Serpe, Helen McNeill, Carl Thummel and Elizabeth Chen. Ela and Helen served last year and will rotate off next year, Carl and Elizabeth were new recruits to the committee. Next year's chair will be Laura Johnston. David will remind her to organize the committee and to select two new members to serve 2-year terms.

The Chair solicited nominations from outgoing regional representatives and from the elections committee, and the Committee then ranked the nominations. The Chair contacted the top-ranked nominees to ask them to stand for election. Some declined, but we were easily able to come up with two excellent candidates for each position. With the help of Jim Thurmond and Thom Kaufman, a ballot including two candidates for each position, along with short biographies and links to their lab websites, was disseminated to the fly community by email on Oct. 20, with a deadline for voting of Nov. 25. A reminder email was sent on November 17th.

Candidate statements are appended to the end of the Agenda.

The newly elected Fly Board members are:
President: Mark Peifer (2019)
Great Lakes: Michael Welte (through 2021)
Southeast: Laura Reed (through 2021)
Midwest: Tina Tootle (through 2021)
Heartland: Erika Geisbrecht (through 2021)
Canada: Julie Brill (through 2021)

518 votes were cast, at the historical average, although fewer than last year. The ballot included a statement that "*Voting is limited to members of the Drosophila research community",* which seemed to get the message across.

This year the Committee encouraged candidates to express within their statement any interests or goals that they would like to address during their term. The Committee also consciously considered individuals of non-Caucasian ancestry in the nomination process. We believe that these practices should be continued.

We also carried out the Board's decision to appoint a Trainee rep for a 2 year term, culled from self-nominated individuals who responded to a notice at the fly meeting. Paul Vorster, a postdoc in Joe Lipsick's lab, has agreed to be the inaugural Trainee rep.

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 2019. We are also electing representatives for the Heartland, Midwest, Great Lakes, Southeast, Midwest, and Heartland regions, and international representatives for Canada, who will serve 3-year terms starting with the fly meeting in 2018.

Please participate in this election. This is your opportunity to choose the individuals who will help set priorities and secure support for community resources.

Voting is limited to members of the Drosophila research community.

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 1, 2017.

Thank you,
Drosophila Board Election Committee
David Bilder (Chair)
Elizabeth Chen
Helen McNeill
Carl Thummel
Ela Serpe

Ballot
President-elect (Vote for ONE)

Mark Peifer
University of North Carolina at Chapel Hill
Mark Peifer grew up in Minnesota and was a first-generation college student. He spent a year after graduation working as a technician in a plant biology lab, where some terrific mentors taught him how to be a scientist. He then joined Welcome Bender's lab for his PhD. There he studied the fly homoeotic genes, participating in their cloning, identifying molecular lesions in what we now know are regulatory mutations, and developing approaches to study regulation. He then did a postdoc with Eric Wieschaus, where he continued studying Hox gene regulation and also began his life-long interest in the roles of Armadillo/beta-catenin in Wnt signaling and

cell-cell adhesion. He began his lab at UNC in 1992. They study how cell adhesion and cytoskeletal proteins allow cells to change shape and move and tissues to polarize, and also study the mechanisms regulating Wnt signaling. Both projects use Drosophila and cultured mammalian cells. Mark's involvement with the Fly Board has been thus far confined to a stint on the Nominating Committee. At the American Society for Cell Biology, he has served on Council, the International Affairs Committee, and the Education Committee. He is currently on Council for NIGMS. He is active there in promoting funding for early and mid-career researchers, and at UNC is involved in programs trying to increase STEM diversity. He also advocates for the value of model organisms in basic science.

Yukiko Yamashita
University of Michigan Medical School
Yukiko Yamashita obtained her Ph.D from Kyoto University, Japan, and completed the postdoctoral fellowship with Minx Fuller at Stanford University (2001-2006). Yukiko started her own laboratory at the University of Michigan in 2007, and is currently a professor at the University of Michigan Ann Arbor and an investigator of the Howard Hughes Medical Institute. It was during her postdoctoral training that she started using Drosophila male germline as a model system to study asymmetric stem cell divisions, with her interest shifting toward germ cell biology in recent years. Yukiko has faith in science using model systems, and is interested in advocating the importance of Drosophila in research community. She has served as a session chair at Drosophila meetings. Yukiko serves on the editorial boards of eLife, Molecular Biology of the Cell, PLoS Biology and Scientific Reports. Yamashita is a recipient of 2008 Searle Scholar Award, 2009 ASCB WICB junior award, 2011 MacArthur Fellowship, 2016 Tsuneko and Reiji Okazaki Award.

Southeast (Vote for ONE)

Wu-Min Deng
Florida State University
Wu-Min was attracted to the fly world when he began his Master's degree studies at Shanghai Institute of Cell Biology, Academia Sinica. He has continued his scientific quest with this excellent model organism ever since. After earning a Ph.D. with Mary Bownes at the University of Edinburgh and working with Hannele Ruohola-Baker as a postdoc at University of Washington, Seattle, Wu-Min set up his own lab at Florida State University in 2003 and is currently a professor in the Department of Biological Science. Wu-Min's research interests range from developmental signaling and growth regulation to modeling tumorigenesis in Drosophila. Funded by NIH, NSF and AHA, the research in his lab has led to the discovery of tumor hotspots in *Drosophila* epithelial tissues, novel mechanisms of tissue homeostasis that involve cell competition and compensatory cellular hypertrophy, and new components and modes of signaling in various pathways. Wu-Min co-founded the "Flymasters" discussion group for the growing Tallahassee fly-research community, and co-initiated the Jiujiang Fly Meeting (2016). He has been regularly involved in NIH study sections, workshop organization in fly meetings, and is on the editorial boards for Journal of Genetics and Genomics, and Scientific Reports. Wu-Min has been an active member of the fly community for about two decades. He is a strong advocate for research using model organisms, and for research involving undergraduate and high-school students, particularly students from underrepresented minority groups. Wu-Min's vision as a Southeastern representative on the fly board is to bring regional fly researchers closer together and increase the visibility of fly research to a broader scientific audience and the general public.

Laura K. Reed
University of Alabama
Laura Reed developed her interest in insect evolution working with William Bradshaw and Christina Holzapfel at the University of Oregon (Biology B.S. 2000). Her Ph.D. (2006) research was on speciation and genomics in cactophilic *Drosophila* with Therese Markow, where she learned the importance of collaboration and history to the collective success of the Fly community. In her postdoc with Greg Gibson at North Carolina State University, she studied the quantitative genetics and metabolomics of diet-modulated metabolic syndrome in *D. melanogaster.* She then continued that research in her own lab at the University of Alabama in 2010 where she is now an Associate Professor. Her work focuses on understanding the genetic architecture and evolution of genotype-by-environment interactions affecting metabolic phenotypes in natural populations, as readily modeled by flies. She is a leader in the field of metabolomics in *Drosophila* and she is also committed to strengthening science education. She runs an intensive *Drosophila*-based middle school outreach project and she is the incoming program director of the Genome Education Partnership founded by Sarah C.R. Elgin. On the Fly Board, Laura will continue to advocate for new community resources to facilitate fly research, and campaign for broader public understanding of the unique power of model organisms to promote fundamental advancements in biology.

Great Lakes (vote for ONE)

Cheng-Yu Lee
University of Michigan Medical School
Cheng-Yu Lee experienced the first taste of the power of fly genetics in investigating the role of hedgehog signaling during eye morphogenesis when he was conducting his undergraduate honors thesis project mentored by Dr. Soichi Tanda at the University of Maryland, College Park. After this initial encounter, he could not think of any other model organism to pursue his biomedical research career. He then joined Dr. Eric Baehrecke's lab at the University of Maryland to pursue his doctoral study on steroid regulation of autophagy during salivary gland and midgut programmed cell death. After completing his Ph.D., Cheng-Yu took on a post-doctoral fellow position in the lab of Dr. Chris Doe at the University of Oregon where he focused his effort on establishing and utilizing fly larval brain neuroblasts as a genetic paradigm to investigate the regulation of stem cell maintenance and differentiation. He joined the University of Michigan Medical School in 2006 where he remains as a principle investigator. Cheng-Yu is best known for his graduate work on the role of autophagy during development and his current research interest on the regulation of self-renewal and differentiation during asymmetric neuroblast division. Cheng-Yu has been an active member of the Drosophila community for more than two decades, and is a strong advocate of Drosophila research.

Michael Welte
University of Rochester
Michael Welte is a cell and developmental biologist studying organelle, RNA, and protein trafficking during Drosophila embryogenesis and oogenesis. After undergraduate studies in biology and mathematics in Tübingen, Germany, he fell under the spell of Drosophila as Ph.D. student at the University of Chicago, training with Susan Lindquist. As postdoc with Eric Wieschaus at Princeton University, he employed lipid droplets in embryos to investigate microtubule motor-based transport *in vivo.* After his first independent position at Brandeis University, he joined the University of Rochester in 2007, where he is now Professor and Chair of Biology and part of a strong local Drosophila group. His major focus is the cell biology of lipid

droplets, in particular their role in protein homeostasis and immunity. Michael has been an active member of the fly community for over 25 years, is committed to training the new generation of Drosophilists by mentoring graduate and undergraduate students, and has been invited to present his work nationally and internationally. As on organizer of two FASEB Science Research Conferences (2014, 2016) on lipid droplets, he ensured that model organisms were well represented.

Midwest (Vote for ONE)

Arash Bashirullah
University of Wisconsin-Madison
Arash Bashirullah grew up in Venezuela, received a B.S. in chemistry from the University of Winnipeg, and a Ph.D. in biology from Caltech. It was at Caltech, as a graduate student with Howard Lipshitz, that Arash fell in love with the beauty of Drosophila genetics. During graduate school, the late Ed Lewis instilled in Arash a life-long appreciation for the history of Drosophila genetics and for the global community of Drosophilists. After a postdoc with Carl Thummel, Arash started his lab at the University of Wisconsin-Madison in 2007. His lab studies the genetic control of post-embryonic development in Drosophila, using novel lethal mutations that specifically disrupt physiological processes critical for the progression and completion of metamorphosis. Arash is an active member of the genetics community, serving as associate editor for G3, and as a faculty advisor to the Early Career Scientist Leadership Program at the Genetics Society of America. If elected to the Fly Board, Arash would strive to promote programs that help influence public perception and support for Drosophila research.

Tina L. Tootle
University of Iowa
Tina Tootle received her BS in Microbiology from the University of Maryland, College Park (1998), where she earn High Honors for her thesis studying plant-pathogen interactions in *Arabidopsis thaliana*. She then served as a research assistant in the laboratory of Soichi Tanda, where she fell in love with *Drosophila* as a model system. Tina studied Ras/MAPK signaling and the Retinal Determination Network during her graduate studies with Ilaria Rebay at the Massachusetts Institute of Technology (1999-2004). As a postdoctoral fellow with Allan Spradling at the Carnegie Institution for Science in Baltimore, she began her studies on prostaglandin signaling (2004-2009). Since starting her own lab at the University of Iowa in 2009, Tina has focused on understanding how prostaglandins regulate the actin cytoskeleton to control follicle or egg chamber morphogenesis. These studies have led her to exam the roles of actin and actin binding proteins in the nucleus. Tina serves as the Director of the Cell and Developmental Biology Graduate Program. She teaches graduate level Principles in Molecular and Cellular Biology and Critical Thinking in Biochemistry and Molecular Biology. Tina also serves as the departmental Director of Diversity and the Chair of the Basic Sciences Diversity Taskforce. She has established an undergraduate outreach program with Howard University, an HBCU, and is working to expand this to other minority serving institutions; one objective of this program is to increase appreciation for the value of using *Drosophila* for biomedical research. She is also an active participant in the fly community at the University of Iowa, will be serving as part of the organizing committee for the Midwest Drosophila Research Conference, and regularly attends both the regional and national Drosophila conferences. She has served on both NSF (MCB) and NIH study sections. Tina is dedicated to improving graduate education to better prepare students for the array of career options, increasing the diversity of students

pursuing graduate degrees and careers in biological sciences, and being an advocate for model organism research.

Heartland (Vote for ONE)

Michael Buszczak
University of Texas Southwestern Medical Center
Michael Buszczak received his B.S. in Biology from Tufts University and then worked as a technician in Doug Melton's lab at Harvard University for two years. He began his fly career as a graduate student in Lynn Cooley's lab at Yale University, studying ecdysone signaling in Drosophila ovary. He then trained as a postdoctoral fellow in Allan Spradling's lab at the Carnegie Institution for Science, where he helped to coordinate a large-scale protein trap screen. In 2007, he established his own group at UT Southwestern Medical Center, where he is currently an Associate Professor in the Department of Molecular Biology. His group continues to use Drosophila to study different aspects of germ cell biology. At UTSW, he actively participates in both graduate student education and the local fly community. In the past, Mike has served as a member of the Larry Sandler Award selection committee and co-chaired the Stem Cell Platform Session at the annual Drosophila Research Conference.

Erika Geisbrecht
Kansas State University
Erika Geisbrecht developed her passion for genetics as an undergraduate at the University of Wisconsin-Madison studying *Arabidopsis* development in the lab of Dr. Kathy Barton. She received her Ph.D. from the Johns Hopkins University School of Medicine working in the lab of Dr. Denise Montell, where her dissertation research focused on characterizing genes important for border cell migration in *Drosophila* ovary. While a postdoctoral fellow with Dr. Susan Abmayr at the Stowers Institute, Erika became interested in the increasing complexity of cells and tissues that communicate in *Drosophila* myogenesis. She started her lab nine years ago at the University of Missouri-Kansas City and moved her laboratory to Kansas State University four years ago. Erika has continued to use muscle tissue in all stages of fly development as a model to understand fundamental concepts in cell biology, including cell adhesion, cell proliferation, cytoskeletal interactions, and mitochondrial maintenance. She actively promotes science communication as an essential tool for the next generation of scientists. Graduate and undergraduate student training is largely focused on the dissemination of research results at scientific meetings, with a special emphasis on promoting community outreach involving STEM or STEAM initiatives. She has participated in multiple Kansas City area fly meetings and co-organized the Midwest *Drosophila* meeting in Allerton, IL. Erika has reviewed numerous grants proposals for NIH and NSF and is particularly interested in promoting *Drosophila* as a model organism to the vertebrate community.

Canada (Vote for ONE)

Julie Brill
The Hospital for Sick Children and University of Toronto
Julie Brill received her BA in Biology with Distinction from Swarthmore College. Her first research experience was with Susan Gottesman at NIH, where she studied bacteriophage lambda and *E. coli* and gained her love for genetics and genetic model systems. Julie did her PhD with Gerry Fink at MIT, where she worked on the yeast pheromone response pathway. She

began studying Drosophila during her postdoc with Minx Fuller at Stanford University and continued as a visiting postdoc with Barbara Wakimoto at University of Washington in Seattle. As a postdoc, Julie discovered that a class of membrane lipids, the phosphatidylinositol phosphates (PIPs), is needed for spermatocyte cytokinesis. She brought her research on PIPs and male germ cell development to the Hospital for Sick Children (SickKids) in Toronto, where she started her lab in Jan. 2001. Julie is currently a Senior Scientist in the Cell Biology Program at SickKids, Full Professor in the Department of Molecular Genetics at University of Toronto (U of T), and Director of the Collaborative Program in Developmental Biology at U of T. She has been a member of the GSA since 1988 and was Associate Editor of *G3* from 2012-2014. She was Treasurer of the Genetics Society of Canada (GSC) from 2007-2010 and co-organized the joint Canadian Fly (CanFly) and GSC meeting in 2007. She has also been active in the ASCB, where she was a member of the Women in Cell Biology Committee from 2011-2016 and serves on the Editorial Board of *MBoC*. In addition to training graduate students and postdocs, Julie has supervised more than 50 undergraduates in her lab. She received the 2017 Excellence in Undergraduate Laboratory Teaching in Life Sciences Award from the Faculty of Medicine at U of T. She was elected a 2015 Fellow of the American Association for the Advancement of Science (AAAS) for her discovery of *in vivo* roles and regulation of PIPs in cell morphogenesis during animal development. Julie is passionate about mentoring and training students, communicating science to the general public and advocating for support of fundamental discovery research.

Kirst King-Jones
University of Alberta
Kirst King-Jones grew up in Berlin, Germany and attended the Freie University of Berlin, where he received his Diplom (similar to a Master's degree) and later his Dr. rer. nat. (the German equivalent to a PhD) in Molecular Genetics. During his time at the FU Berlin, Kirst worked in the lab of Günter Korge, where he studied the mechanisms by which the steroid hormone ecdysone controls developmental processes. He then joined Carl Thummel's lab, a HHMI investigator at the University of Utah School of Medicine, for his postdoctoral research. Here, Kirst studied the action of nuclear receptors and developed a keen interest for metabolism, and how it affects developmental programs. In 2006, Kirst moved to Canada to join the University of Alberta, where he later received both CIHR and AHFMR New Investigator Awards. He is currently an Associate Professor in the Department of Biological Sciences and he studies regulatory mechanisms that coordinate heme and iron metabolism with steroid hormone biosynthesis.

Discussion (Drosophila Board Elections)

Laura Johnston asked for nominations for new members, starting in summer 2018, and introduces the new Fly Board members for this year. Voting in the next round will be exclusively for Drosophila community members. Further discussion was devoted to how to get more diversity in Fly Board membership. Debbie Andrew introduced the discussion by stating that there is a problem with diversity on the Board. Many members contributed comments. Different strategies for voting were considered, for instance having regions manage regional representative votes, and running same-sex candidates against each year, alternating 2 men and 2 women, in order to ensure gender neutrality. It was noted that there are only about 500 voters participating in Board membership elections, fewer than the number of ADRC attendees, and that most voters may be PIs. The Board and elections committee is advised to pay attention to these issues in future ballots and votes.

11. Commercial antibody data (Bing Zhang)

Since Bing Zhang sent out the original GoogleDoc requesting information from labs on the utility of commercially available antibodies on Drosophila, only David Bilder had added his lab Ab list and outcomes. In order for this to work, we will need more people to take a few moments to enter the GoogleDoc. Bing has very recently tweeted this link to the GSA and fly colleagues but he would still like for the board to encourage each lab to pitch in. In the 24 hours post-tweet, the number of entries increased 4X. Bing hopes this trend continues, but please encourage your people to submit the information they have.

https://docs.google.com/spreadsheets/d/1bUKOmbYtXMUfp3ERdRFl3Arwj3aqrQWwH5ilt-UOWqY/edit#gid=0

Discussion

Debbie Andrew reported for Bing Zhang. Bing is collecting information on which commercial antibodies work for Drosophila. The information will be posted on a website. This project will be announced at ADRC 2018. About 100 antibodies have been collated so far. Also antibodies that don't work will be listed. T. Kaufmann said that there is a section in FlyBase on antibodies, and we would be very happy to have this information there. Debbie Andrew offered to ask Bing to forward the information he has gathered to Thom Kaufman or to find a mechanism to make his list more publicly available.

12. Primarily Undergraduate Institutions (Amanda Norvell, Primarily Undergraduate Institutions (PUI) Representative)

There are several undergraduate focused events at this year's meeting, and a few other workshops that are likely to be of interest to faculty from PUIs. The pedagogy workshop focuses on challenges associated with doing original research in undergraduate-focused institutions. The undergraduate research workshop (Spotlight on Undergraduate Research) will include talks from undergraduate students.

PUI-focused activities at this year's meeting are:

- Overcoming barriers to effectively utilize *Drosophila melanogaster* in scholarship, research, and teaching at PUIs at 7:45 pm on Thursday.
- Spotlight on Undergraduate Research at 1:45 pm on Friday.

Workshops likely to be of interest to PUI faculty

- Advocating *Drosophila* through using it as an efficient teaching tool at 7:45 on Thursday.
- Publishing genetics classroom activities in CourseSource at 7:45 on Thursday.

PUI faculty have expressed some concern regarding the increased cost for attendance for undergraduate students at the meeting. In addition to the inclusion of an abstract fee, undergraduate registration (for GSA members), doubled from $50 last year to $100 this year. Because student travel requests are often due as much as a year in advance, these increases can be difficult to accommodate. While there is a one-day student/post-doc option, a reduced rate for undergraduate students was not available, making this potentially budget-friendly opportunity not feasible. Finally, in recent years, there was also more GSA sponsored undergraduate programming at the meeting, including an undergraduate mixer or plenary talks focused on an undergraduate audience. PUI faculty have expressed interest in either seeing these events return, or in exploring a more reduced one-day pass option for undergraduate students.

Discussion

Amanda Nonell reported on Primarily Undergraduate Institutions (PUI). There are several PUI-relevant workshops and events at ADRC 2018. Areas of concern by PUI faculty were voiced this year: 1. The ADRC cost for undergrads has gone up and is too high. Day passes are too expensive ($200 each). Program content relevant to undergrads is less in 2018 than previously. We would like to bring attention to undergrad-relevant program content. In the past there were mixers and sessions for undergrads. It seems like the opportunities for undergrads at ADRC are diminishing, and we would like the GSA and the ADRC organizing committee to take note of this. There are 235 undergrads at ADCR for 2018. Almost as many as postdocs. This may be due to geography. The Finnerty award winners are undergrads. Moderately priced 1- or 2-day passes to ADRC would aid undergrads a great deal.

13. Advocacy and Communications (Andreas Prokop)

A. Overview of new developments in 2018

(1) Community website (https://drosophilaresearch.org/; S. Mohr): Google Analytics tracks use at a fairly steady 400/month over the past year. 20% returning users, 80% new users in 2017. 25% returning users, 75% new users over the last six months. The "events" page is by far the most common first page folks land on—almost certainly coming from the "meetings courses" icon on FlyBase home. Majority of users are US-based. We have received through the online form requests for posting of 2 events and 1 news item (from 3 different people), plus a ~2 requests came to me by email (from 1 person). Most of the events and news posted come from things I first saw on Twitter. Adding content is quick and easy, justifying the effort despite modest traffic. Conclusion: Now that the site is one year old, it would be valuable to discuss with the Board what the long-term goals are and how to achieve them.

(2) Publications:

- First in Fly (S. Mohr) came out March 1st. This has led to interviews e.g. with radio stations and with Science magazine's podcast. An upcoming Connecticut radio interview will include a fly researcher based in that state. Also led to being approached to do an essay for Zocalo Public Square http://www.zocalopublicsquare.org/ that was published recently. Zocalo publishes online at their site and makes the content available to a large network of print media outlets (e.g. local US newspapers). I expect that other fly folks could work with Zocalo on essays in future. Happy to make introductions to my editor at Zocalo if someone's interested.
- "Deep Homology? Uncanny Similarities of Humans and Flies Uncovered by Evo-Devo" by Lewis Held was published already February 2017 but should perhaps be mentioned here since it has not had the impact it deserves.
- "Fly book" series published in Genetics, and its associated article: Bilder, D., Irvine, K. D. (2017). Taking stock of the *Drosophila* research ecosystem. *Genetics* **206,** 1227-36 – [LINK]
- Special issue: Illingworth, S., Prokop, A. (2017). Science communication in the field of fundamental biomedical research (editorial). *Sem Cell Dev Biol* **70,** 1-9 [LINK]; contains a number of *Drosophila* articles:
  - article by H. Bellen and his team about strategies to collaborate with clinicians
  - article by I. Palacios et al. about the excellent work by DrosAfrica
  - article by S. Patel and A. Prokop about the concepts and strategies of the Manchester Fly Facility
  - article by S. Patel and A. Prokop about the droso4schools project
- Vicente-Crespo, M., Muñoz-Descalzo, S., Weil, T., Martín-Bermudo, M. D., Palacios, I. (2016). Workshop-based training for capacity building: using *Drosophila* to bring research skills to Africa. *The FASEB Journal* **30,** 663.2 – [LINK]
- Adedeji, A., Vicente-Crespo, M. (2017). Rejuvenating research and training in biomedical sciences in Nigeria: *Drosophila melanogaster* as a versatile alternative model. *Arch Basic Appl Med* **5,** 1-10 – [LINK]
- numerous smaller articles in different outlets

Conclusion: There is no shortage in fly advocacy publications, but their impact spreads thin because we have no infrastructure to collate all these efforts into one powerful resource. The Manchester Fly Facility aims to fulfil this task, but should only be seen as an interim solution because the user metrics are not convincing enough: although their site is the key advocacy resource linked out from FlyBase the average number of views is only ~10K p.a. New structures are required (see part B).

(3) Manchester Fly Facility: Resources and information provided by the Manchester Fly Facility on their various web sites and online repositories are being used worldwide as is clearly demonstrated by metrics and written comments collated in a 50 page document [LINK]. Some highlights are:

- Spanish translations of teaching resources
- Translations of the first "Small Fly BIG impact" film into Spanish and Indonesion (an Arabic translation is underway)
- the co-founding of "Fly Indonesia" [LINK] providing resources in Indonesian language (mainly translations of ManFlyFacility materials)
- The publication of two articles (see above)
- The use as resource for two newspaper articles following the Nobel: one mediated by David Bilder in NY Times [LINK], one in the Observer mediated by A. Prokop [LINK].

Conclusion: there is a clear appreciation of the work of ManFlyFacility, and the example of the NYT and Observer articles illustrate how effective the generation of a central advocacy resource is. However, sustainability will be an issue: currently all the resource and strategy development as well as implementation of activities is carries by two people, S. Patel and A. Prokop, and this is unlikely to continue for long unless the community starts contributing. This will require new structures (see part B).

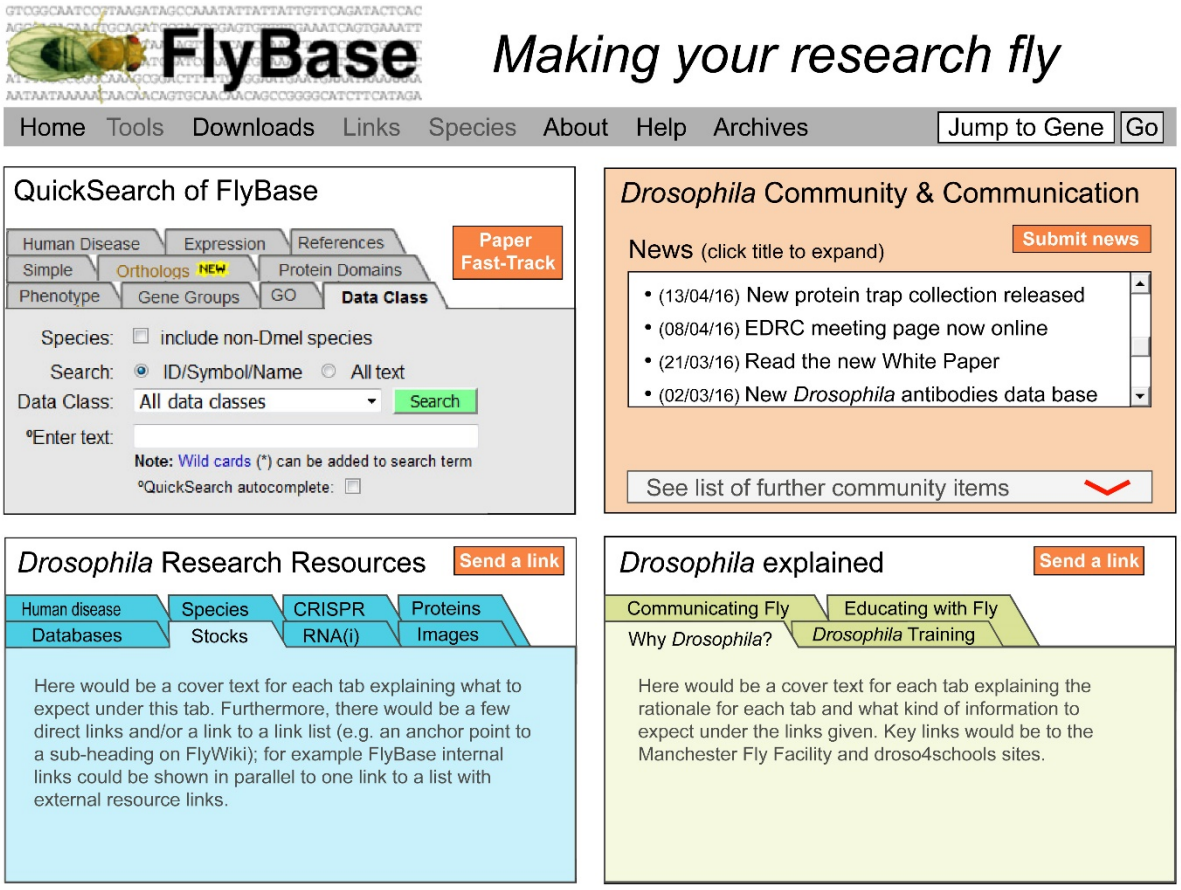
(4) International programs: "DrosAfrica" [LINK] and "TReND in Africa" (partly *Drosophila*) [LINK] are going strong and "Fly Indonesia" [LINK] is likely to aim for its first training course in collaboration with TReND. The key idea behind these initiatives is to use model organisms as a cost-effective way to carry out cutting edge research in underdeveloped countries to improve science education and free resources for infrastructure. Conclusion: Fly is becoming a strong driver of science development; Latin America is another obvious area for such engagement, but no concrete initiatives seem to have developed so far.

(5) Promoting sci comm and advocacy on fly meetings: A key goal should be to develop fly advocacy into a community effort (for explanations see LINK). One major problem is lack of horizontal communication in our community as explained in the Manchester Fly Facility article [LINK] and analogously for the field of Dev Biol in a recent newsletter editorial [LINK]. To raise awareness of the need of, resources and strategies for fly advocacy, various meetings were targeted: the Canadian Dev Biol meeting (presentation by E. Verheyen), the Yedi meeting (presentation by T. Vaccari), the CSHL Drosophila neurobiology meeting (advocacy slides put up, mediated last minute by P.Tomancak), the ADRC 2018 (workshop by A. Prokop), the Neurofly 2018 responded positively (potentially a plenary by A. Prokop).
Conclusion: Advocacy needs to become a part of all fly meetings; however, not all conference organisers are responsive. Therefore, clear procedures and new supported structures are needed (see part B).

B. Concrete suggestions to be discussed at the Fly Board meeting

(1) Improving the status of the sci comm committee: membership of the current sci comm committee is not transparent, and I would like to renew my request to list the committee members together with other officers on FlyBase [LINK]. This measure would emphasise the importance that is given to advocacy, provide clarity as to who serves on the committee, equip members with the necessary authority when speaking up for advocacy and the deserved recognition to justify the time invested. In this way it would be far easier to distribute tasks and structure the committee's activities. Also, it needs to be discussed whether serving on the committee should be longer-term, say 3 years (extendable). This would help to maintain expertise within the grouping.

(2) Horizontal communication / FlyBase front page: I have argued repeatedly that we are wasting a unique opportunity by not capitalising on the power of FlyBase in order to weave a communication network and strengthen our community. The current buttons on the left side are not very effective: 400 views of the community website and double as much for the Man Fly Facility website (see above) means that only a minor fraction of far below 3% of visitors on FlyBase are tempted to click these buttons. We need to explore new ways, and I made concrete suggestions of a portal that would present FlyBase as one tile, whilst providing one tile for other community research resources, one tile for advocacy/training/sci comm and one tile for news/communication. This tile was received with great enthusiasm by members of the sci comm committee and sparked immediate ideas of how to make use of it. This is the spirit that we require if we want to instill a culture of advocacy.



It needs to be emphasized that this portal page would in no way affect FlyBase but rather embed it in a wider community concept. In this way, resources from within our community would get a unique platform to shine and receive the necessary reward and recognition that can help to sustain them. Furthermore, we would have unprecedented opportunities to (re-) fuel our horizontal communication about relevant scientific and para-scientific topics – so to say revive the D.I.S. idea. Implementation of this portal would require (a) initial external funding to program it and (b) dedicated ownership by members of our community to maintain content of the three tiles. As key prerequisite for taking any action in this direction, FlyBase would have to agree that they will go along with this idea if satisfactory solutions are proposed. Given the fact that FlyBase asks the community for financial contributions, this might be the right time to demonstrate innovation and a new community spirit.

Discussion (Advocacy and Communications)

Andreas Prokop reported on Advocacy and Communcations. Andreas said that the fly community needs resource for sharing science communication materials. He runs the center in Manchester with a staff of only 2 people. Webpages have only 800 views/month. Drosafrica is growing the African fly research community, but needs more press. Overall the output is quite good, but this outreach effort needs better infrastructure. We are promoting science education advocacy in our own community. The DIS times are over and Flybase does not fully fulfill community needs. Andreas Prokop proposed that an advocacy session be held in each ADRC meeting, and he would like authority to do this. The science communication committee structure is "too vague", and needs more commitment from some people. Do we need a science communication board? Andreas requested that a science communication committee be set up. Andreas also proposed that we change the front page of FlyBase to more of a community face/portal, and would like more science communication and science advocacy on the FlyBase homepage. FlyBase gets 300,000 views/month. If all these people were looking at Advocacy & Communications this would help.

D. Andrew to A. Prokop comments: Can you please clarify what your goals are? A. Prokop: we need more exposure on the internet. FlyBase does not represent "all" of the community. Flybase could be used as a social networking platform for scientific advocacy to the outside and also for intra-community interactions. Norbert Perrimon: FlyBase does already have community info on it. There is only so much that can be done through Flybase, and we need to supply what people in the community want to see. What else is needed? Andreas Prokop's project does have a FlyBase button, but it is not hit much. D. Andrew: maybe working with GSA is the way to get community info out, perhaps using the fly community email list from FlyBase/Perrimon is a useful approach. A. Prokop: we are already working with GSA. S. Bray: The Drosophila community needs to reach out to other communities (e.g. medicine, the press), not so much to the Fly community. Sarah Bray suggests that other ways of communication between the fly community and other communities should be explored.

14. FLYBASE (Norbert Perrimon)

FlyBase Report to the Drosophila Board
(Norbert Perrimon, Thom Kaufman, Susan Russo Gelbart)

For the past twenty-five years, FlyBase has provided a centralized resource for Drosophila genetic and genomic data to enable researchers to further their research. FlyBase has three main goals:

1. To continue curation of literature and reagents relevant to Drosophila research, so that researchers can continue to rely on FlyBase to find the latest innovations in the field by prioritizing curation of data sets relevant to gene expression, cellular functions, signaling pathways, and human diseases, and displaying the information in an intuitive, integrated, readily searchable format.

2. To improve FlyBase's utility to the human genetics and population genetics communities, by curating and integrating relevant data sets, and developing tools that enable better access to this wealth of data.

3. To facilitate more integrative analyses and approaches, by continuing to expand its utility as a platform for integrating and displaying large-scale studies, transcriptomics and proteomics data sets. In addition, FlyBase improves access and display of tools available within the community, and incorporate the most useful data sets and tools for visualizing complex data sets to enable more researchers to take a more global approach to their genetic research.

FlyBase is a committed member of the Alliance for Genomic Research (AGR), working with other Model Organism Databases (MODs) to integrate data sets and develop tools to enable cross-species analyses.

April 1, 2018 begins the 1st year of our 5-year well-reviewed renewal. The NHGRI has advised us that while Year 01 of the renewal project would remain flat, we are to anticipate continued cuts over the 5-year period of up to ~20% (which normalize to 30%). This necessitated exploring alternative methods to supplement FlyBase funding, including a user-fee (explained in greater detail in this report), and will provide more information once sorted with Harvard and NHGRI administrators.

We welcome Brian Calvi as a new co-PI at the Indiana site. Brian is a Professor of Biology at Indiana University who studies mobile elements, DNA replication, cell division stress response and cancer. Brian is now regularly involved with the FlyBase-Indiana group.

Below are some high points of our activities since the last ADRC meeting, future plans, and updates, additions and changes made to FlyBase in 2016-2017, and website usage statistics

Respectfully submitted on behalf of PIs by
Norbert Perrimon
Thom Kaufman
Susan Russo Gelbart

Newer, better in FlyBase (2.0)
https://www.youtube.com/watch?v=DGUjKmeTIKE#action=share

FlyBase 2.0 was released in December 2017. It has been a multi-year effort to overhaul the current web infrastructure of FlyBase. The overall goal was to enhance site functionality using modern web technologies, improve reliability, enhance cloud compatibility, and reduce the amount of disruption for future upgrades. Those of you familiar with the efforts at AGR will recognize some of what we have done as being similar if not identical to what has been adopted there. This was not the result of copying (or theft) but rather a case of convergent evolution. Related to our ongoing involvement in AGR we have developed a RESTful API for various aspects of FlyBase data in JSON and other formats. This API provides programmatic endpoints that power users and 3rd party sites can use to integrate data into their own services.

We redesigned the website infrastructure from the ground up. Virtualized development environments using VirtualBox, Docker containers, and other technologies have been used to reduce problems arising from shared development servers, dependency conflicts. This will make transitions between development and production less problematic. The code base was shifted to a modern object-oriented system that improves code reuse and reliability *via* automated unit testing. The public facing portion of the site has been rewritten to take advantage of current modern web toolkits such as Bootstrap and React. Additionally, separation of concern approaches were used to keep view layers, search/analysis tool logic, and backend data sources relatively decoupled. This will allow swapping of individual elements of the website for future changes without greatly impacting other aspects of the website.

The home page and report pages have been configured so that they will scale to the user hardware being used. We have also initiated the use of icon links to a variety of community resources, which have been reconfigured to make updating easier and to provide a more transparent view of where the links will take the user. We have also provided direct links to Gene2Function, MIST, MARRVEL and AGR. In order to increase our contacts with the user community we have provided a link to the FlyBase twitter feed. In addition to the home page links to community resources we have added significantly to our resources fields in our cloud based FlyBase wiki. For example, we have created new LinkOuts for reagents from the wiki and FlyBase gene report pages to relevant antibody products at the Developmental Studies Hybridoma Bank and other commercial sources of fly antibodies as well as clones from the DGRC.

Highlights of major features in 2.0 that have been developed in the last year include: updated data class report pages, a new search result display tool (HitList) with more data and functionality, an improved references section on all reports replacing the reference section with an interactive widget that allows viewing, filtering, sorting, and exporting, a tool, based on the BioJS sequence-viewer, for viewing and downloading FASTA sequence (Sequence Downloader) which allows viewing, searching, and downloading FASTA sequence data, and interactive displays of protein domains in reports and genome viewers by adding interactive protein domain graphics to Gene and Polypeptide reports using tools from Pfam. We have also added SMART protein domains to GBrowse, JBrowse, and our protein domain glyph to supplement the existing Pfam domains.

Perhaps most notable amongst these is the complete rewrite of the search result list machinery (HitList) to address usability and improvements that have been gathered from our user community. These are now more comprehensive and can be managed by the user in several ways including faceting and selecting output in either a list or table format. Use statistics indicate that our Simple Search is the most commonly used tool in the FlyBase repertoire. The new HitList format now makes that general search much more powerful and inclusive and allows the user to more readily see the multiplicity of data types and formats available.

As noted above several aspects of individual gene reports (*e.g.,* the references section) have been improved. In order to provide GO annotation information more graphically we now also include the use of GO Ribbons, which use improved rendering code and updated slims. We have also expanded and consolidated the Summaries section of the gene report. There are now potentially five summary statements including: the gene snapshot, an automatically computationally generated summary, uniprot functional data, the RedBook entry and the Interactive Fly text. These are presented when available with the computed summary, the only one universally presented.

As noted in our last report we proposed to move to a JBrowse genome browser and we have now done that as an initial step in transitioning away from GBrowse, which is no longer supported. We are currently developing scripts that will allow the display of tracks showing our TopoView RNA-Seq expression data. We now have a method to do this but need to develop methods that allow user configuration of the output. We will also adopt the methods used by AGR and developed by HymneopteraBase to extract images from JBrowse genome segments for insertion into other reports in FlyBase.

Each gene report we have links to our GBrowse and JBrowse views of the gene. We also provide LinkOuts to the NCBI, ENSEMBL and UCSC genome views. In order to provide a comparative population sequence variation view we have added a LinkOut to the PopFly genome browser. PopFly includes sequence variation information of more than 960 worldwide *D. melanogaster* genomes derived from 30 populations from 18 countries on 5 continents. Their JBrowse view allows the display and retrieval of functional annotations, estimates of nucleotide diversity metrics, linkage disequilibrium statistics, recombination rates, a set of neutrality tests, and population differentiation parameters of the euchromatic chromosomes (Hervas et al. 2017 Bioinformatics.. doi: 10.1093/bioinformatics/btx301).

Finally, in a response to user requests we have developed a new tool that allows the user to search for GAL4 drivers based on their reported patterns of expression. This tool is accessed from a dedicated tab on the home page and has already seen significant use. The tab is present on both the FB 2.0 and current production servers.

Human diseases and links to relevant external resources

We have continued our human disease model reports (see the attached individual site reports). As noted, we have added icons on the FlyBase front page that provide direct links to three resources, Gene2Function, MIST, and MARRVEL, that are useful to mine information across model organisms and humans.

Gene2Function (G2F), developed by the DRSC and FlyBase, is an online resource that maps orthologs among human genes and common genetic model species supported by MODs, and displays summary information for each ortholog (Hu et al., G3. 2017). G2F makes it easy to survey the wealth of information available for orthologs and navigate from one species to another, and connects users to detailed reports and information at individual MODs and other sources. Overall, G2F addresses a broad need by integrating information about conserved genes in a single online resource.

MARRVEL (model organism aggregated resources for rare variant exploration), developed by Bellen lab with help from the DRSC, is similar to G2F but specifically designed to support searches starting with human genes and variants (Wang et al., Am J Hum Genet. 2017). MARRVEL facilitates comparison with human disease genes and variants (from OMIM, ExAC, ClinVar, Geno2MP, DGV, and DECIPHER), and maps human genes to model organism organisms and information.

MIST (Molecular Interaction Search Tool), developed by the DRSC, is a searchable database of protein-protein and genetic interactions integrated from both large-scale and smaller curated resources (Hu et al., submitted). Like DIOPT and G2F, MIST covers common

model organisms. Integration of data at MIST increases coverage and facilitates the development of new hypotheses based on interactions among orthologous proteins or genes.

Author reagent table

FlyBase formulated a prototype "author reagent table" (ART) initiative last year, in consultation with other model organism databases. The goal of this proposal is to facilitate handling of reagent source and identifier information at multiple steps -- benefiting researchers, journals, and post-publication users, such as biological databases. Provision of reagent identifiers is one of the key requirements of the system, encouraging the use of database and stock center identifiers, RRIDs, and catalog numbers for commercial providers. An important aspect of the proposed table is that it is in the format of a spreadsheet that is designed to persist through the whole process: compilation of the reagent information, submission to the journal, and facilitate downloads of data post-publication.

All journals contacted (Genetics, eLife, Development, Genes & Dev, PLOS, J. Cell Biol., EMBO/EMBOR, Mol. Cell. Biol., Dev. Biol., Mech. Dev., Curr. Biol., J. Neurosci., Mol. Syst. Biol., and Genome Biology) have expressed support for a tabulated format for presentation of reagent source information and for required use of IDs. A reagent table of some sort is becoming standard, and for some journals, mandatory. In response to journal input, we have developed a more compact version of the Author Reagent Table. However, virtually all the journals that have implemented a reagent table are using a document-table format (Word.doc table or similar). The next step is to convince journals that use of a spreadsheet and more standardized formatting would make such a significant contribution to accuracy and efficiency, in terms of input from contributors and output for post-publication users, that it is in their interest to adopt this type of format.

The FlyBase Author Reagent Table (ART) is available HERE.

Community

Surveys are regularly sent to the FlyBase Community Advisory Group (FCAG), which currently comprises >540 members representing Drosophila labs from 41 countries. We carry out at least four surveys each year on topics ranging from a general survey on the importance of FlyBase on fly research, to more targeted surveys on the expression searching tools and the annotation of non-genetically induced phenotypes. The average response rate is ~45%. Changes made as a direct result of FCAG responses include the new tool for searching by expression pattern for GAL4 drivers and reporters as well as the introduction of new GO summary ribbon displays in the gene reports.

We promote FlyBase using social media, particularly Twitter. With nearly 2,000 followers, FlyBase tweets are used to draw attention to new or little-known features, *e.g.,* Network Resources page tweets resulted in the addition of over 20 new network resources to the page based on user response, and the Gal4 search tab announcement tweet garnered nearly 50 shared tweets, including among other MODs.

We have added an icon “Community News” on the FlyBase front page that provides a link to Stephanie Mohr’s web site that provides up-to-date information on the latest news in Drosophila research and relevant community resources.

User Fees

We have recently decided to implement a fee for usage for FlyBase. This decision was taken after more than a year of evaluation of alternative strategies. Although this is not our preferred choice we see no other solution in order to maintain the robust quality of the database. Below are some of the facts behind our decision, which have been discussed at length with the FlyBase SAB and the FlyBoard, who support our decision.

Current funding situation: FlyBase is currently supported by grants from the NHGRI (90%) and the British Medical Research Council (10%). We submitted a competing renewal at the beginning of 2017 to renew the NIH grant that has supported FlyBase for the past 25 years. The FlyBase grant received a perfect score (Impact Score: 10) emphasizing the continued relevance of FlyBase to our community and beyond – thus we expect to have secured funding until March 31, 2123. The review panel stated: *"The Special Emphasis Panel (SEP) expressed uniform outstanding enthusiasm for this exceptional U41 application. The SEP cited many strengths and few weaknesses. The application was well written with the elements and components of the application well described. The PI and collaborators are exceptional and the environments outstanding. SEP members described FlyBase as essential to nearly all Drosophila research. Ninety percent of fly labs consult FlyBase on a daily basis and ninety eight percent consult FlyBase before beginning any new research. FlyBase is increasingly used by the human genetics community as an important resource. A national research board recently cited FlyBase as the number one resource model for the NIH and biomedical research."*

The problem: Despite the successful review, we have been told that NHGRI will significantly reduce the funding of FlyBase as part of a general trend towards reducing the amount of money that NHGRI is able to invest in model organism databases. Our budget cuts are estimated to be normalized to 20% next year and 30% onward. With these cuts, FlyBase will not be able to deliver high quality, essential curation and tools - at a time when the rate of accumulation of new information is increasing, and the relevance of FlyBase to the broader biomedical community expands. We have approached other NIH institutes, and global groups for supplementary funding without success.

The solution: Cuts of 30% for FlyBase will be a fatal blow and we simply will not be able to function as a useful resource. We have explored the possibility of reducing/eliminating areas of curation and tools that FlyBase provides the community but as usage is high for most categories it will not resolve the issue. Altogether, it is clear that we need to find a way to raise funds to cover the cuts if we want to sustain the database, and grow in the way that our integral, central role in the biomedical community will require.

Having exhausted the option of directly raising money from funding agencies, and with suggestions from several scientists, we decided to explore the possibility of Harvard directly invoicing individual labs for a user fee (the FlyBase grant is administered through Harvard). NHGRI confirmed that Harvard is authorized to charge user fees, while being in compliance with the terms and conditions of the award. Importantly, Harvard, which will handle the invoicing, accounting, and will not charge overhead.

We have provided a link to a form on the FlyBase web site to collect information and issue an invoice, payable via PO, credit card, check or bank transfer. Given that the NIH-supported community represents about 40% of usage, and that NHGRI is contributing 90%, and the British community about 10% of FlyBase budget, we are calling on you to help sustain FlyBase by implementing a scaled **user fee per person/per year:**

U.S. and U. K. users	**$150.00**
Non-U.S. and U. K. users	**$300.00**
For-profit users	**$750.00**

Lab heads will determine the number of users in their groups; it is at their discretion to determine yearly users. Throughout, we will continue to explore additional avenues to support this vital resource.

FlyBase also provides an option to a tax-deductible contribution.

The Diversity Action Program (DAP)

DAP continues to thrive. Since April 2014, our training plan has placed 11 post-baccalaureate Scholars (79%) in PhD programs across the country, and our earliest trainees from prior periods of support have approached graduation. In addition, we have provided access and information to genomics research through our Frontiers in Genomics class for over 40 students, many of whom have gone on to summer programs or graduate schools. Presenters during 2017 were Drs. Norbert Perrimon (Harvard Medical School), Bruce Birren (Broad Institute), Angela Brooks (UC Santa Cruz), Katrina Claw (U. Washington), Keolu Fox (UCSD), Manny Rivas (Stanford) and Thom Kaufman (Indiana University).

Alliance for Genomic Research

FlyBase is an active member of the Alliance for Genomic Resources (AGR) -- working with other Model Organism Databases (MODs) to integrate data sets and develop tools to enable cross-species analyses. We receive ~1.8 FTE support from a supplemental NHGRI AGR grant, and have FlyBase members and PIs in the AGR Leadership Team, and who participate in several working groups: Orthology; Phenotype and Disease; Search Optimization; Data Quartermasters; Architecture; User Interfaces, Gene Expression; Interatactions; and Variants.

Future plans

In addition to our ongoing projects, we have begun to initiate curation and display of information in four specific areas:

- Metabolomics. We propose to provide vitally needed database infrastructure to support the rapidly expanding field of metabolic research in *Drosophila*. This is important because the birth of metabolomics is providing unparalleled insight into how genetics, diet and environment impact on physiology and health. We will build new and improved metabolic resources within FlyBase, so that researchers benefit from their integration with the host of additional information and tools in FlyBase. Specifically, we will enhance the information relevant to Drosophila metabolic research in several ways. New Metabolic Pathway reports will synthesize the disparate computed data available from existing pathway databases, and indicate the steps that have been experimentally validated in *Drosophila*. This effort will benefit from a complementary approach to improve the nomenclature and descriptions of Drosophila metabolic enzymes and cofactors, half of which are currently unnamed and/or lack appropriate functional annotations, despite their high degree of evolutionary conservation. We will also add Metabolite reports to FlyBase, analogous to the current Gene reports, where data will be collated on Drosophila metabolite levels under a variety of conditions by incorporating key metabolomics datasets. This will enable searching for metabolites with similar abundance profiles, and comparison of metabolite abundance profiles with the existing mRNA profiles of the enzymes that produce or alter them. Finally, we will highlight the many Drosophila genes that, owing to their orthology with human disease genes, have the potential to be manipulated to create metabolic disease 'models' – i.e. Drosophila strains that recapitulate features of human disease pathology resulting from changes in orthologous genes. Such models can be used for first round drug screening, with ultimate benefits to biomedicine and healthcare.

- Proteomics. To offer a more complete picture of gene expression, FlyBase is evaluating published proteomic data for incorporation alongside the transcriptomic data that we already display. Of primary interest is a new quantitative proteomic study that measures levels for almost 8,000 proteins throughout the *D. melanogaster* life cycle (Casas-Vila et al., 2017 Genome Research). We are evaluating how to best display direct comparison of trends in RNA and protein levels to shed light on post-transcriptional regulation. Additional proteomic studies will be compiled to obtain a large library of small peptides identified by mass spectrometry with the aim of informing gene model annotation, and possibly isoform/exon-specific expression.

-Transcriptomics. To improve access to Sequence Read Access (SRA) data, and mine it for transcriptomic insight, the Oliver lab has been remapping thousands of Drosophila RNA-Seq submissions. This work, in progress, is in coordination with FlyBase to ensure efficient incorporation, and maximize usefulness to researchers and curators. During this effort, inconsistency of dataset descriptions has been an obstacle. In response, Justin Fear (Oliver Lab) and FlyBase have developed a "Drosophila" template for NCBI BioSample submission, encouraging best practices in transparency and clarity, to improve data searchability and processing. The template is under review by Tanya Barrett (NCBI GEO). Preliminary plans are to provide the community with a distilled view of the meta-transcriptomes generated (in gene reports and in G/JBrowse), and to incorporate novel protein coding exons and non-coding transcripts revealed by the data into the FlyBase D. melanogaster gene model annotation set.

- Single cell RNAseq. Data from single cell sequencing in flies have started to emerge and are anticipated to grow exponentially in upcoming years. In addition to providing insights on cell type diversity, cell lineage, gene function discoveries and analyses of mutant phenotypes, cross-model comparisons may help interpret genetic disease models. We plan to initiate the integration of single cell RNAseq into FlyBase and have begun to collaborate with several cell atlas projects.

- ***Population genetics.*** Sequence data for >1,000 genomes of *D. melanogaster* isofemales, found from adults in different geographical locations, are available, however the data are not integrated in a single access portal to enable easy comparison with the D. melanogaster reference genome and annotations. We are exploring how best to incorporate these natural variation data into FlyBase into graphics to indicate nucleotide positions where sequence variations exist, frequency of these variants in the studied populations, and whether or not alternative alleles to the *D. melanogaster* reference allele sequence, have fixed in any given lineage. Users will be able to easily expand their scope of investigation to consider whether mutant alleles occur as standing variation alleles in natural populations.

FlyBase updates, additions, changes

Here follows a time line listing most recent to oldest updates, additions and changes made to FlyBase in 2017 to present.

March, 2018

- **DIS Vol. 100 in FlyBase**
  Articles published in Drosophila Information Service (DIS) Volume 100 (2017) have been incorporated into FlyBase. They can be viewed in FlyBase here. Authors are encouraged to use our Fast-Track Your Paper tool for these articles in order to prioritize them for further data curation and to make associations with the key genes described therein.
- **New Gene Group: Glycosyltransferases**
  Glycosyltransferases catalyze the transfer of a sugar moiety from glycoside onto acceptor substrates such as proteins, lipids, DNA or the sugar moieties of glycoproteins or glycolipids. The new GLYCOSYLTRANSFERASES Gene Group comprises 21 subgroups and 142 *D. melanogaster* genes.

December, 2017

- **FlyBase 2.0 goes live**
  With the final release of 2017, "FlyBase 2.0" becomes the main FlyBase website. This major rework of the FlyBase website comes with new features, new tools, and improved mobile device browsing and stability. The look and feel of the site has also been

updated, but should still look familiar to long-time users.
Here's a video teaser, showing some of the new features.

- **Powerful new hitlist management**
  General searches now go to mixed data-class hitlists with lots of information and links in each hit item; lists can be filtered by data class and species. Hitlists with a single data class also have a compact tabular view. Analysis tools and list export for download, *etc.* are all there too.
  The main search is also now available in every FlyBase page, as a second option of the familiar "Jump to Gene" search bar in the page header.
- **Enhanced Report pages**
  FlyBase 2.0 report pages look more modern, with a fluid layout and new features like the navigation panel. Look for improvements to many report types, including greatly expanded Dataset Reports. The redesigned references section is an embedded hitlist management tool in itself, with options for filtering, sorting, and exporting reference lists. The Gene Report has many specific enhancements, with new summaries including GO summary ribbons and protein domain graphics.
- **New tools and features**
  Try the new Sequence Downloader, and take a look at JBrowse if you haven't seen it yet. Other tools will be augmented in the coming months as well.
- **Better under the hood, too**
  The FlyBase 2.0 website includes a modern Application Program Interface (API) for better programmatic access to data.

October, 2017

- **External Links to the Alliance of Genome Resources Web Portal**
  External links to the Alliance of Genome Resources web portal have been added to Gene Reports and Disease Ontology Term Reports. The Alliance brings together the efforts of the major National Institutes of Health NHGRI-funded Model Organism Database (MOD) groups, and the Gene Ontology Consortium, in a synergistic integration of expertly-curated information about the functioning of cellular systems. Their focus is to facilitate the use of these data towards better understanding of human biology and disease.
- **PopFly links from Gene Reports**
  With release FB2017_05, FlyBase introduces links from FlyBase Gene Reports to the PopFly Drosophila Population Genomics Browser, produced by colleagues in the Bioinformatics of Genome Diversity group from the Universitat Autònoma de Barcelona (UAB) and the Institut de Biotecnologia i Biomedicina (IBB).
  The PopFly browser provides sophisticated visualization and download of nucleotide diversity metrics, linkage disequilibrium statistics, recombination rates, neutrality tests, and population differentiation parameters at non-overlapping windows of varying size from the over 1100 *Drosophila melanogaster*genome sequences compiled in the Drosophila Genome Nexus data-set.
- **New TRANSCRIPTION FACTORS Gene Group**
  The major addition in this release is the TRANSCRIPTION FACTORS group, comprising over 500 genes. These have been organized into subgroups based on their sequence-specific DNA-binding domain and include the BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTORS, BASIC LEUCINE ZIPPER TRANSCRIPTION

FACTORS, ZINC FINGER TRANSCRIPTION FACTORS and HELIX-TURN-HELIX TRANSCRIPTION FACTORS.

August, 2017

- **New GAL4 and other drivers/reporters search tab**
  Searching for GAL4 and other drivers and reporters using expression patterns just got a lot easier on FlyBase. There is a new 'GAL4 *etc'* tab in the QuickSearch tool where you can search by developmental stage, anatomy or cell type, or cellular component. The 'integrated table' output groups related alleles, constructs and insertions with available stocks.
  The tool is brand-new and may undergo further revision.
- **Gene Groups update**
  New groups in this release include the P-TYPE ATPASES, IMPORTINS and several small groups relating to axon guidance (*e.g.* SEMAPHORINS, PLEXINS and NETRINS).
- **ncRNA resources updated**
  External databases and tools pertaining to Drosophila non-coding RNAs (ncRNAs) have been updated and reorganized. These can be accessed within our 'Drosophila Network Resources' page.

July, 2017

- **New FlyBase video tutorial**
  A new video has been added to our FlyBase TV YouTube channel: Finding genes with similar phenotypes.

June, 2017

- **New *D. melanogaster*-to-human ortholog file, with OMIM disease links**
  Starting with the FB2017_03 release, we are providing a downloadable file listing orthologs between *D.melanogaster* and human genes, as determined by DIOPT. (Note that ortholog calls supported by only 1 or 2 algorithms (*i.e.* DIOPT score <3) are excluded from this file.) Human diseases associated with those genes, as reported in the OMIM database, are also listed.
  In the current release, 17,446 unique fly-to-human orthology relationships are reported, of which 4,055 have an OMIM association. 8,265 *D. melanogaster* protein-coding genes (59%) have human orthologs, and 10,643 human genes have orthologs in *D. melanogaster*, by the criteria being used here. A total of 3,326 unique human diseases (OMIM phenotypes) are reported in this file, reflecting the scope for modelling diseases in flies.
  This file can be found in the Orthologs and Human Disease sections of our Downloads page or ftp site.
- **New Gene Group: Solute Carrier Family**
  Solute Carriers are membrane proteins that facilitate the transport of a wide array of substrates across membranes. The new Gene Group for this family comprises 39 subgroups and 280 *D. melanogaster* genes.
- **GAL4 stocks now in gene reports**
  GAL4 stocks are now included in the Stocks section of gene reports.

May, **2017**

- **New FlyBase video tutorial**
  A new video has been added to our FlyBase TV YouTube channel: Gene Snapshots in FlyBase.

- **FlyBase ncRNAs in RNAcentral**
  FlyBase has contributed over 13,000 non-coding RNA (ncRNA) sequences from 12 *Drosophila* species to the RNAcentral database. RNAcentral imports ncRNAs from multiple databases, assigns unique identifiers to distinct sequences, and enables integrated searching and browsing of ncRNAs across species.
  You can view the FlyBase summary page, browse all FlyBase sequences, or browse the integrated set of *D. melanogaster* sequences.

April, **2017**

- **GenBank and FlyBase releases matched**
  The FlyBase Archived Data page top section has been updated to show the correlations between archived FlyBase releases and GenBank releases. Links to NCBI assemblies have been added where appropriate.
- **SMART protein domains**
  We have added protein domain data from SMART. This domain data supplements the protein domain data already available via Pfam. These data can be seen as new tracks in both JBrowse and GBrowse, on the main FlyBase site and the new "FlyBase 2.0" beta site. On FlyBase 2, these domains also appear as graphics in several types of reports (gene, polypeptide, etc).
- **Gene Groups update**
  New Gene Groups in this release include: N-terminal acetyltransferases, phosphatidylinositol glycan anchor biosynthesis genes and water channel proteins.
- **New sources of Gene Ontology (GO) annotations**
  FlyBase has incorporated GO annotations for *D. melanogaster* genes from four new external sources: GO Central, ParkinsonsUK-UCL, BHF-UCL (Cardiovascular Gene Annotation) and CACAO (Community Assessment of Community Annotation with Ontologies). GO Central is now the largest external provider of GO annotations to FlyBase, adding over 11,000 new annotations to our set. GO Central assigns GO terms based on phylogenetic ancestry using their Phylogenetic Annotation INference Tool (PAINT) to semi-automate the transfer of annotations between species. We have also updated the set of GO annotations provided by UniProt Gene Ontology Annotation curators.
- **OrthoDB9.1**
  FlyBase has updated its OrthoDB orthology data from OrthoDB7 to OrthoDB9.1. OrthoDB provides orthology relationships for a broad scope of species and is particularly useful for assessing orthology within arthropods. These data are displayed in the Orthologs → Orthologs (via OrthoDB9.1) section of gene reports.
- **DGRC clone resource links**
  Links to the DGRC clone resource page have been added to relevant gene reports underStocks and Reagents → cDNA Clones → DGRC cDNA clones.
- ***D. grimshawi* annotation update (R1.05)**
  In the previous FlyBase update (FB2017_01), the new NCBI Gnomon annotations for *D. grimshawi* (R1.04) were released. However, previously existing transcripts and polypeptides that persisted from R1.3 (pre-Gnomon) to R1.04 (Gnomon) were incorrectly given new names and "FBtr" identifiers. This issue is corrected in this release with an updated *D. grimshawi* annotation set (R1.05), such that transcripts that existed before the Gnomon update retain their original name and "FBtr" identifier. A mapping file for genes affected by this change is available here.

- **FlyBase ADRC materials**
  All the FlyBase talks, posters and pamphlets from the recent ADRC meeting in San Diego have been uploaded to our FlyBase guides page.

March, 2017

- **Gene Snapshots acknowledgements on wiki**
  FlyBase has created an acknowledgements page listing contributors who have written gene snapshots for us. This list can be found by following the link at the bottom of the FlyBase "Gene Snapshots" wiki page; you can get there from any FlyBase page through the navbar menu at Community → Gene Snapshots.

February, 2017

- **FlyBase 2.0 is here!**
  The next-generation FlyBase website is now in beta release. Expect an improved browsing experience on mobile devices, and also try out the new search hit-lists through QuickSearch, preview additions to the gene, *etc.* reports such as GO ribbons and graphical protein domain displays, and more. Visit the new site at beta.flybase.org.
  N.B. The beta site is still in development! Reports are not yet complete, and other features will change and improve as we work towards transition to the new site.
  A survey asking FlyBase users for comments/opinions on these new features will be coming soon. In the meantime, please report any bugs you notice via the contact FlyBase form.
- **Huge collection of polytene chromosome maps**
  FlyBase has curated a large collection of polytene map images, now available in the Maps section of the FlyBase Resources page.* This collection includes original illustrations of *D. melanogaster* polytene chromosomes by Bridges (published in 1935-1942) and Slizynski (published in 1944), as well as micrographs by Lefevre (published in 1976). FlyBase has also assembled annotated images that combine the original illustrations and/or electron micrographs of polytene or mitotic chromosomes with known sequence, cytology and recombination map data for select genes.** These images have been compiled for the Muller Elements of all 12 originally sequenced *Drosophila* species, using species-specific polytene images where available, but otherwise showing the *D. melanogaster* polytene chromosome image as a reference. These annotated maps are also available on the FlyBase Chromosome Maps browser. Images also available for *D. melanogaster* Y and mitochondrial chromosomes.
- *Polytene images were first made available in October 2016.
  **A full map correspondence table of recombination, cytology and sequence map values for *D. melanogaster* genes on the reference genome assembly is available in the Maps section of the FlyBase Resources page.
- **Improved recombination map data**
  FlyBase has incorporated two datasets that provide genome-wide recombination map values to *D. melanogaster* genes on the reference genome assembly.* The first dataset is a FlyBase analysis that computes the recombination map position of genes from the known cytological location of over 1200 neighboring P-element insertions and estimates of polytene band size (kb) from Sorsa and colleagues. The second dataset is based on the work of Comeron et al., 2012, who mapped over 100 million SNPs in 5,860 female meiosis events to calculate cross-over frequencies for 100 kbp intervals along chromosomes X, 2 and 3. Cumulative cross-over frequencies along the genome assembly were used to calculate the recombination map position of genes based on their sequence location, as described here. The correspondence of these two datasets is

quite good, though estimates for genes in the middle of chromosomal arms can differ by several centiMorgans (cM). For quick access, the FlyBase-calculated recombination map value is shown in a new "Recombination Map" field near the top of the gene report next to other location data.** All data are reported in full in the "Genomic Location and Detailed Mapping Data" section of the gene report. A full map correspondence table of recombination, cytology and sequence map values for *D. melanogaster* genes on the reference genome assembly is available in the Maps section of the FlyBase Resources page. **Recombination map data were first made available in FB2016_05 (September 2016).*
***The new "Recombination map" section was first released in FB2017_01 (February 2017).*

- **New iBeetleBase, Fly-FISH linkouts**
  FlyBase has added linkouts to iBeetleBase, and updated our Fly-FISH linkouts.

2017 FlyBase Web Usage

The following are web statistics from the FlyBase website as captured by Google Analytics. In summary, the statistics, when compared to the previous year period, indicate that our overall usage, user activity, and number of users have decreased slightly. In addition, data class report and tool usage has not changed from previously observed and well-established patterns.

Figure 1 shows FlyBase pageviews for 2016-2017. A pageview is defined as a hit to an HTML page, script output or other content that does not include non-document files (CSS, images, JavaScript, etc.). The average number of pageviews during the most recent period was 990k, with a high of 1.1 million and a low of 803k. The periodic dips all correlate with expected holiday patterns. Compared to 2016, pageviews are down 8% overall.

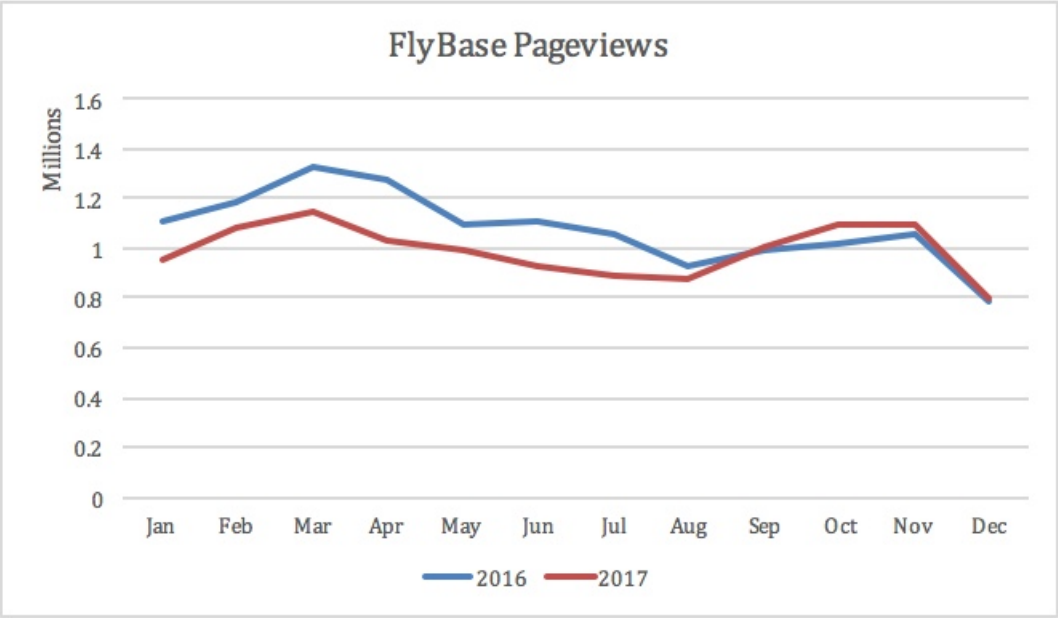


Figure 1 – FlyBase Pageviews

Figure 2 shows FlyBase sessions (visits) for 2016-2017. A session is defined as a period of activity by a unique web user. If no activity is recorded for 30 minutes, any subsequent activity is counted as a new session. The average number of sessions during the most recent period was 143k, with a high of 169k and a low of 118k. Compared to 2016, sessions are down 2%.

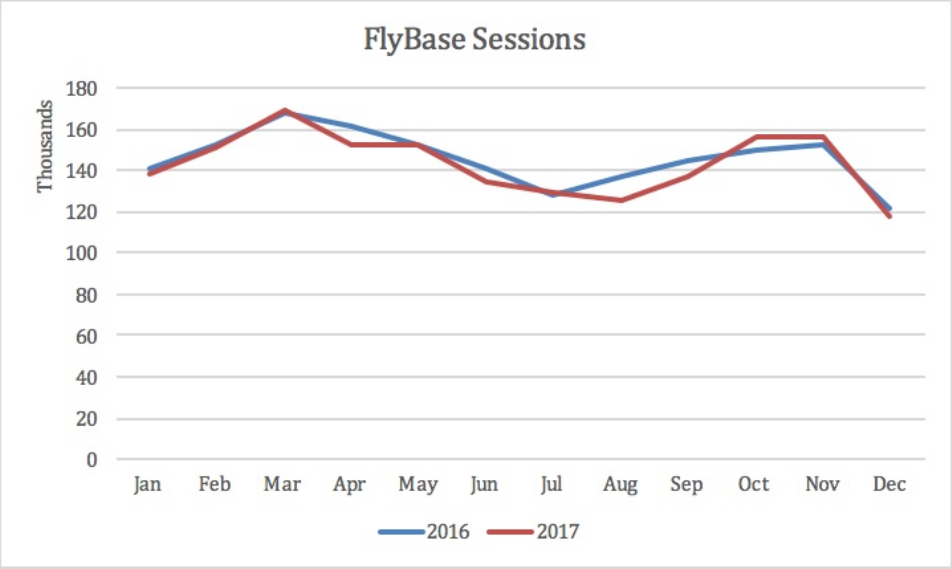


Figure 2 – FlyBase sessions.

Figure 3 shows FlyBase users for 2016-2017. A user is defined as a unique session ID that Google analytics generates. This value does not take into account a single user using multiple computers and/or browsers. The average number of users during this period was 48k/month, with a high of 59k and a low of 40k. Compared to 2016, the number of FlyBase users is down 2%.

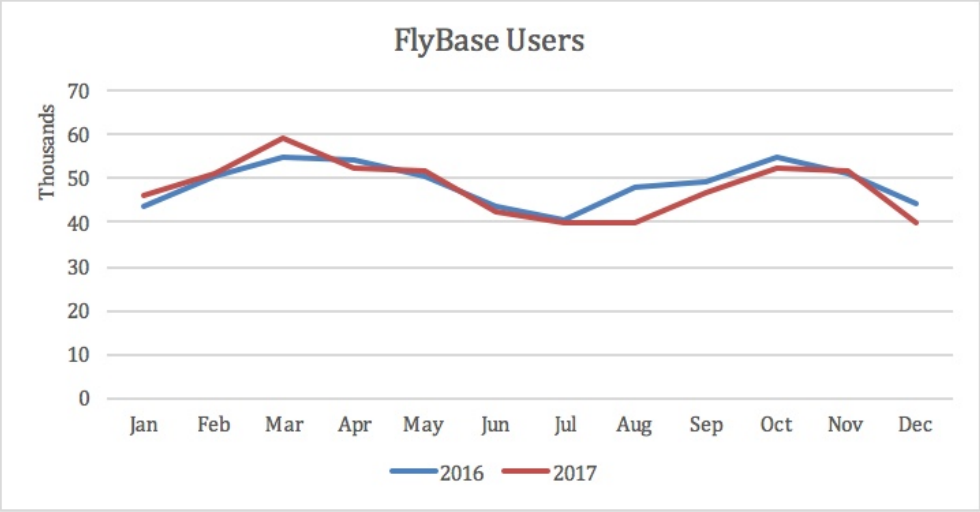


Figure 3 – FlyBase users

Figure 4, "Data Class Usage", shows the top pageviews for FlyBase data class reports. This data class usage pattern has held for 10+ years with Genes, Stocks, References and Insertions topping the list.

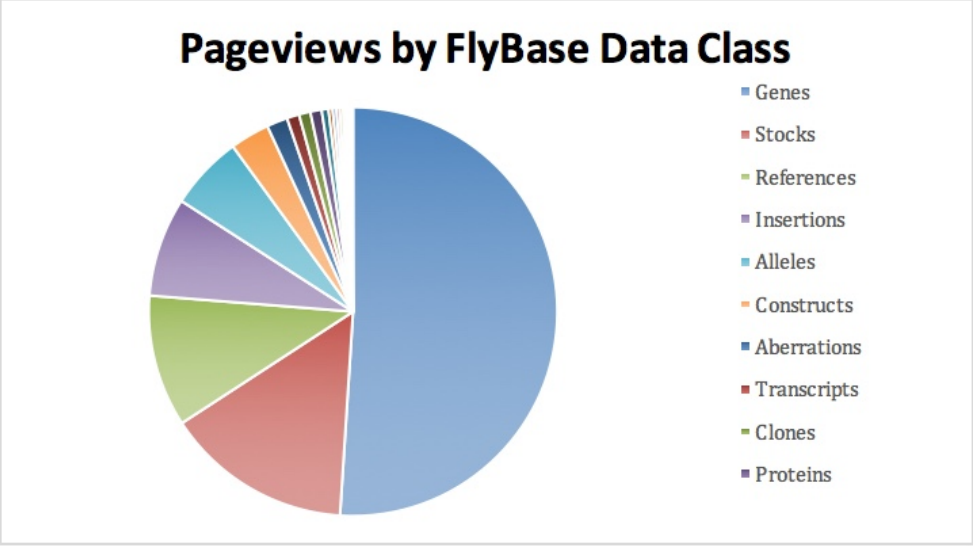


Figure 4 – Pageviews by FlyBase Data Class.
* Data class list truncated

Figure 5, "FlyBase Tool Usage", shows that our top 5 tools are Simple Search, BLAST, GBrowse, Jump to Gene, and Vocabulary reports. As with data class report usage, this pattern has remained unchanged for many years.

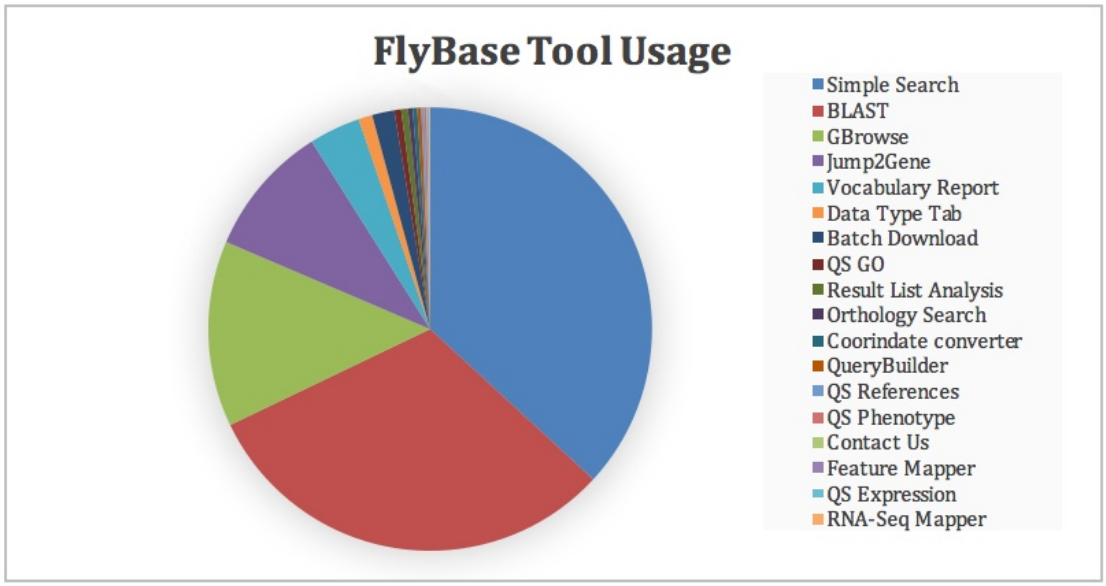


Figure 5 – FlyBase Tool Usage.

Discussion (FlyBase)

FlyBase report: Norbert Perrimon & Sue Gelbart
Norbert Perrimon: Flybase is doing well. Links have been added for the community (advocacy, outreach, etc). We will add metabolomics & single cell RNAseq data bases. Links to DGR have been added. It is important to maintain FlyBase. We have lost full support from NIGRI so, after discussions amongst the Fly Board during the year, user fees have been instituted. This is working well so far, but we just opened the fee structure 2 weeks ago. This is an experiment. NIGRI cut support to FlyBase by 30% for the coming year. We'd like to have more support for FlyBase from the Europeans and others who have not contributed in the past.
Comment (unidentified Board member): Since fees are voluntary, some institutions and granting agencies may not allow users to pay. Since it's not necessary to pay for something that is free, international laws against "money laundering" may be invoked. Could the FlyBase fee be classified as a donation? Or could there be a special service returned to those who pay (*e.g.* classify it a fee for "premium service"). This might make it easier for a lot of people outside the US to contribute. This is also an issue in Japan.
Sue Gelbart: Flybase did carefully consider fee structure and labels. This fee cannot technically be a "user fee" since it's voluntary. We were very careful in defining it, and received a good deal of input from community members.
Laura Johnston: Is there a way to incorporate the fact that FlyBase is not actually free, but is funded by the US government for US taxpayers? This might help justify the fee for non-US users.
Comment: Could it be a donation, from PI salaries perhaps?
Debbie Andrew: Please work with Norbert or Susan as these problems arise. The fee definition and structure can be modified if it proves to be problematic.
Thom Kaufmann: To end this on a high note, the FlyBase grant was funded for 5yrs with a "10" priority score from NIH, which is a perfect score. But it was still cut 30%!
Mark Peifer: Noted that NIGMS is "our advocate" at NIH, and people there are who we need to contact, directly. We need to be directly engaged with Jon Lorsch (NIGMS Director). We have many allies there. Lorsch can talk with NIGRI. His is our ally. He really is. Have a conversation with him. Set up a meeting with him. You're not going get a better advocate for model organisms than the director of NIGMS.
Debbie Andrew: However, my letter to Jon Lorsch about FlyBase was not so positively received. We will need to revisit this and determine the best way to advocate with NIH for continued FlyBase funding.

15. Blooming Stock Center Report (Kevin Cook)

New website After several years of effort, our new website (https://bdsc.indiana.edu/) was released in December.

Stock Holdings as of March 7, 2018

- 68,419 stocks with 71,428 unique genetic components
- 17,454 annotated *D. melanogaster* genes are associated with alleles or constructs in the collection

2017 Use Statistics

- 218,429 samples shipped in 13,672 shipments
- 3.3 orders per stock on average with a range of 0 to 157; 67% of stocks ordered at least once, 19% ordered 6 or more times, 9 stocks ordered >100 times, the most popular stock was elav-GAL4 (#8760), which expresses GAL4 in the nervous system.
- 3,488 registered user groups, 2,018 of which ordered stocks in 2017
- 7,075 registered users, 2,899 of whom ordered stocks under their own name in 2017

Growth 9,971 stocks were accessioned in 2017:

- 7,447 split-GAL4 drivers from Janelia Research Campus
- 577 TRiP UAS-RNAi stocks
- 413 guide RNA stocks for gene knockout from TRiP
- 365 GAL4 swap-ins into *Mi{MIC}* insertions from Hugo Bellen and colleagues
- 249 stocks for gene overexpression using a Cas9 activator from TRiP
- 129 UAS-human-cDNA insertions from Hugo Bellen, Sue Celniker and colleagues
- 81 GFP-tagged transcription factors from the modERN Project
- 58 Huntington Disease stocks from Larry Marsh
- 49 Cas9 nuclease and Cas9 activator stocks from TRiP
- 39 Sleep Inbred Panel stocks from Susan Harbison
- 25 second-generation chemical tag stocks from Greg Jefferis and colleagues
- 539 stocks from other donors

Staff 52 stock-keepers (23.5 full-time equivalents) and 9 managers/scientists.

Grant Funding We are in year 4 of a 5-year grant from NIH with $427,210 direct costs. We received $62,074 in supplemental funding to acquire the split-GAL4 stocks from Janelia Research Campus and place them in distribution for a limited time.

New Stocks We expect to add ~5,100 new stocks in 2018:

- 2,400 TRiP guide RNA and RNAi stocks
- 1,000 CRIMIC insertions from the Norbert Perrimon, Hugo Bellen and colleagues
- 1,000 UAS-human-cDNA stocks from Hugo Bellen, Sue Celniker and colleagues
- 200 InSITE Project stocks
- 100 GAL4 driver lines from Sue Celniker and colleagues
- 500 assorted stocks from the community at large

Pruning In 2017, we discarded 1,395 redundant transposon insertion and assorted low-use stocks.

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

Discussion (BDSC)
Kevin Cook reported on BDSC. One thing to add to the written report is that today, we distributed our 3.5Mth stock. Financially BDSC is doing well, and also operationally (see appendix). However, we were stunned to have lost Kathy Matthews this year. This has been difficult, but we have a good management team and we'll get on without her. Therefore it will be a year of adjustment for the stock center.

16. Vienna Drosophila Resource Center (VDRC), Vienna, Austria (Lisa Meadows)

The VDRC (**www.vdrc.at)** is a **non-profit** research infrastructure. Its mandate is to maintain and distribute transgenic RNAi lines and other resources to Drosophila researchers, both locally and worldwide, and to further develop and expand VDRC resources according to the emerging new technologies and community needs.
Core funding from the 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. Current funding will continue until June 2020.

Key changes during 2017
1. More shRNA lines added.
2. Large cull of Vienna Tiles (VT) Gal4 lines: 7,500 discarded and 964 maintained further.
3. 10 year anniversary celebrated!

Usage Statistics 2017
- Registered users worldwide: **2,669**
- Stocks delivered externally in 2017: **42,440** in **1,642** separate orders
- Total stocks delivered to Drosophila community since 2007: >**1,300,000**

Resources as of Mar 2018
Total stocks currently available to the community: **29,337**
- 27,127 RNAi lines (16,763 in GD, 9,822 in KK and 542 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.

- 964 enhancer-GAL4 lines (VTs, Vienna Tiles). Expression patterns annotated in adult brain and embryo. Searchable databases available.
- 903 Tagged FlyFos TransgeneOme (fTRG) lines.
- A small, but growing 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.
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.

Discussion (VDRC)

Lisa Meadows reported on the VDRC (Vienna Drosophila Resource Center): The order base for RNAi transgenic is still stable, but not growing. We have culled many Gal4 lines because they were not being ordered, but BDSC has many similar ones. This year was our 10yr anniversary. We have funding until June 2020, and are already applying for future funding past that date. VDRC started at 50% cost recovery and is now running at 70% cost recovery. We are being pushed to get to 100% cost recovery, but we are resisting this as we don't think it's realistic; we'd have to raise stock prices, which are already high enough. So instead we're pushing for more funding.

17. Kyoto Stock Center Report (Toshiyuki Takano-Shimizu)

Although it is not secured yet, we expect that the upcoming funding for Kyoto stock Center from government and Kyoto Institute of Technology will be maintained at the same level in fiscal year 2018.

Results from our attempts to cryopreserve primordial germ cells are promising; we would appreciate any suggestions and comments on what stocks should be prioritized for cryopreservation (via web mail at https://kyotofly.kit.jp/cgi-bin/stocks/webmail_usr.cgi).

We joined the human ORF project led by Drs. Hugo Bellen and Shinya Yamamoto at Baylor College of Medicine and Dr. Susan Celniker at Lawrence Berkeley National Laboratory.

Since Dr. Masayoshi Watada, director at Ehime Species Stock Center, is retiring in March, 2019, copies of the Ehime stocks have been transferred or are under relocation to Kyorin University and Kyoto Stock Center. They will be distributed from these two sites in 2019.

Discussion (Kyoto Stock Center)

Deborah Andrew presented in place of Toshiyuki for the Kyoto Stock Center: This stock center didn't have a lot to report. They are funded through 2018 by the Japanese government. They have had some success with germ cell cryopreservation. This group is also contributing to the human ORF project, to clone all the human ORFs into UAS vectors with an HA tag.
The director of the Kyoto Species Stock Center is retiring and that stock center is shutting down, but all the stocks will be transferred to either the Kyoto or Kirin stock centers and maintained there.

18. Species Stock Center (Patrick O'Grady)

Background
The *Drosophila* Species Stock Center (DSSC) maintains a diverse collection of over 1400 living stocks from approximately 250 species of *Drosophila* and related genera. The DSSC distributes *Drosophila* cultures to a broad user base from the fields of ecology and evolution, genetics and developmental biology, physiology, neurobiology, comparative genomics, and immunology. The DSSC also provides technical expertise in the areas of husbandry, natural history, systematics, evolution, and ecology of *Drosophila*. The DSSC maintains over 30 *Drosophila* species that have had their whole genomes sequenced, a number that is increasing each year. This aspect of the collection further adds to its value and utility as a resource for comparative research into the correlation between phenotypic change, genome evolution, and species divergence. The DSSC services compliment the goals of the NSF Directorate for Biological Science, which supports research aimed at studying the principles and mechanisms of life.

Report
The DSSC moved in Fall 2017 when Dr. Patrick O'Grady (Cornell University), an expert in the taxonomy, phylogenetics, and evolutionary biology of the family Drosophilidae, assumed the directorship following the retirement of Dr. Therese Markow (UCSD). The stocks and equipment transferred without incident. NSF has been processing the transfer of remaining funds from UCSD to Cornell and a RAPID grant meant to provide bridge funding since late November 2017.
Several significant changes have been made to the stock center:

(1) The fee for standard stocks has increased to $40 after the transfer to Cornell. All other prices will remain the same.
(2) Since restarting shipping in early December, we have sent out 70 shipments, totalling 426 different stocks to 66 labs.
(3) We have hired a full-time Collection Manager, Ms. Lidane Cruz Noronha. The duties of the collection manager will be to 1) oversee hiring, training, and managing the undergraduate stock keepers, 2) receive, process, and ship all orders, 3) execute all quality control protocols and maintain sick stocks, 3) manage the website/database, 4) develop materials for the online species key and species pages.
(4) We plan to develop a new website that incorporates the existing MySQL database into a new, user friendly framework to provide a searchable stock list that is integrated with our credit card and PO ordering system. A new website will not only facilitate orders, but can also provide users with essential natural history information necessary for culturing a wide array of *Drosophila* species.

Discussion (North American Species stock center)

D. Andrew presented for P. O'Grady. This stock collection moved from UCSD to Cornell in December, also due to the retirement of Teresa Markow. They have ~1400 stocks representing ~250 Drosophila species, 30 of which have been genome sequenced. The move was successful. Since the move, 400 stocks have been sent to 66 labs since December. They have new permanent staff and will have a new website soon.

19. Current Gene Disruption Project (GDP) Progress Report (May 2017-April 2018) (Bellen, Perrimon, and Spradling Laboratories)

Funding support for the GDP (NIGMS R01 GM067858) has entered year 16 (Bellen et al., 2011; Spradling et al., 2011; Venken et al., 2011; Nagarkar-Jaiswal et al., 2015a; Lee et al, 2018a). We continued to utilize the MiMIC collection as the foundation for our current project to GFP tag many genes using Recombinase-mediate cassette exchange (RMCE) to introduce Splice Acceptor-GFP-Splice Donor (SA-GFP-SD). We have now tagged about 600 genes with GFP and these are now available from the BDSC (Nagarkar-Jaiswal et al., 2015a; FlyPush Bellen lab). The GFP-tagged genes allow numerous elegant manipulations, including tissue specific, conditional and reversible removal of the tagged proteins (Neumüller et al., 2012; Nagarkar-Jaiswal et al., 2015a; Lee et al., 2018b). This project ended in the past year.

Two teams have developed a very useful and efficient strategy to insert an artificial exon that encodes GAL4 in MiMICs inserted in coding introns (Diao et al, 2015; Gnerer et al., 2015). We have expanded the GDP collection by inserting a small MiMIC-like swappable insertion cassette containing SA-T2A-GAL4-polyA into 600 genes that carry a MiMIC and 500 genes that currently have no MiMIC insertion using CRISPR (a.k.a. CRIMIC). Hence, we generated a library of ~1,100 Drosophila stocks expressing GAL4 under the control of endogenous promoters while prematurely truncating the mRNA of the target gene with a polyadenylation signal 3' of the GAL4. We showed that ~90% of insertions in introns of essential genes cause a severe loss-of-function phenotype, demonstrating that this is an effective way to mutagenize genes. Interestingly, the vast majority of chromosomes engineered through CRISPR do not carry second-site lethal mutations. Second, 26/36 (70%) of lethal insertions tested were rescued with a single UAS-cDNA construct, yet 90% of the targeted genes produce two or more protein isoforms. Third, loss-of-function phenotypes associated with many CRIMIC T2A-GAL4 insertions can be reverted by excision with UAS-flippase, as they are flanked by FRT sites. Fourth, GAL4 driven UAS-GFP/RFP reports tissue and cell type specificity of gene expression with high sensitivity revealing the expression patterns of hundreds of genes not previously reported. Finally, the cassettes containing SA-T2A-GAL4-polyA can be converted by RMCE to SA-GFP-SD (an artificial exon) to tag the gene of interest. Hence these stocks comprise a powerful resource for assessing gene function (Lee et al., 2018b; Kanca et al., 2017). Each month, we are currently cloning 60-70 constructs in the Perrimon lab and injecting them in the Bellen lab. We have a transformation success rate of about 70-75%. However, this project is very labor intensive as we need to spend a significant amount of effort on designing, cloning, sequencing, and injecting the constructs. We then have to balance the stocks and assess expression patterns. We typically inject 500-600 embryos for each construct (versus 100 for UAS-human cDNA constructs, see below). We submitted a manuscript with the first 1,000 T2A-GAL4 tagged genes to eLife (Lee et al., 2018a) and nearly a 1000 of these stocks should be in the BDSC by the end of April 2018.

Finally, we have also created highly useful new tools, including the FLIP-FLOP and double header strategies (Nagarkar-Jaiswal et al., 2017; Kanca et al., in prep.). We are currently in the process of trying to create a CRISPR mediated strategy that obviates the cloning. This strategy works in cells and *in vivo* but the efficiency needs to be optimized.

A library of 7,000 UAS-human cDNA constructs (Bellen and Celniker laboratories)

Much of our understanding of the genetic basis of development and the physiological processes in humans is derived from studies in model organisms. Studies in flies have provided critical insights into the *in vivo* molecular function of conserved genes and allow one to test the

potential pathogenicity of variants that are associated with human diseases. Such experiments are timely due to the recent advent of whole-exome sequencing (WES) and whole-genome sequencing (WGS) as clinical diagnostic tools, thereby increasing the need for functional gene studies in model organisms. Conceptually, it is possible to systematically mutate fly genes using the SA-T2A-GAL4-polyA strategy and express human homologs to assess if they function similarly in the fly. To facilitate "humanization" of flies, we try to coordinate the production of the T2A-GAL4 mutations and generation of UAS-human cDNA-HA constructs to assess rescue and probe human variants (Bellen and Yamamoto, 2015). Our success rate of rescue of fly mutations with human cDNAs is ~50-70%. To facilitate these functional studies, we obtained support from ORIP (NIH resources) to create a UAS-human cDNA library (ORIP, R24 OD022005) and are in the second year of support for this project (2016-2020). This collection will allow investigation of human gene function in flies and permit structure-function experiments. In addition, this library facilitates the use of Drosophila studies in clinical genomics interpretation, especially for variants of unknown significance (Yoon et al., 2017; Chao et al., 2017; Tan et al., 2018; Lin et al., 2018; Senturk and Bellen, 2017).

There are currently ~10,000 human genes that are annotated to be conserved in Drosophila. We are in the process of Gateway cloning ~8000 of these conserved genes into the fly transgenesis vectors pUASg-HA.attB or pGW-HA.attB using large cDNA collections at LBNL and BCM, including a library of 33,000 sequenced full length clones that was assembled by our late colleague Dr. Kenneth Scott at BCM. These collections have allowed us to generate so far over 1800 reference, or wild type, clones and around 220 clones with potentially pathogenic human variants representing a variety of diseases. These clones are currently being injected into flies and the transgenic stocks have been or will be deposited into BDSC. At present, we have generated ~1100 reference fly stocks and ~220 variant fly stocks integrated site specifically into the Drosophila genome. The grant supports the generation of 1500 reference stocks but we estimate that we will be able to generate more of these stocks.

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DISCUSSION (DROSOPHILA GENE DISRUPTION PROJECT)

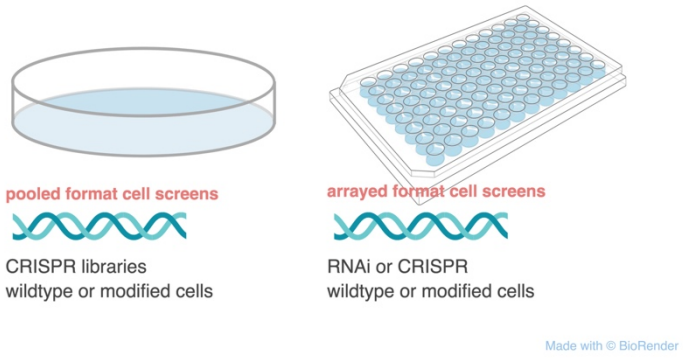
Hugo Bellen reported. DGDP has switched to making constructs with T2A-Gal4 – new paper in eLife reports the first 1000 T2A-Gal4 lines. This is a very useful vector because it creates a mutation in the target gene, flanked by FRTs for removal, but can also drive GFP or the UAS

cDNA to do rescue of gene expression. It's a very versatile tool. Data management for all the new stocks has been challenging. We are now using CRIMIC (CRISPR mimics), not MIMIC. We are working with Sue to make a collection of 1000's genes with human cDNAs under UAS control, in flies. We are sequencing all lines and putting them in the BDSC. DGDP is also applying for funds to make more lines.

20. *Drosophila* RNAi Screening Center (DRSC) at Harvard Medical School
Prepared by **Stephanie Mohr**, Director of DRSC/TRiP Functional Genomics Resources, March 2018

I. *Drosophila* cell modification at the DRSC. Cell modification can be an important pre-step for screening and opens doors to other types of studies, such as RNAseq analysis in perturbed mutant backgrounds. We are working in two areas to improve methods for making knockout and knock-in cell lines using CRISPR/Cas9.

- **CRISPR knockouts**. We are partnering with the Perrimon lab on cell knockout technologies, and now have an improved approach.
    - Deposited two CRISPR knockout cell lines to the DGRC (Indiana) and will be depositing more knockout cell lines soon
    - Have active collaborations that combine cell knockout with screening
    - Making additional knockout cell lines as per our funded R24 OD024984



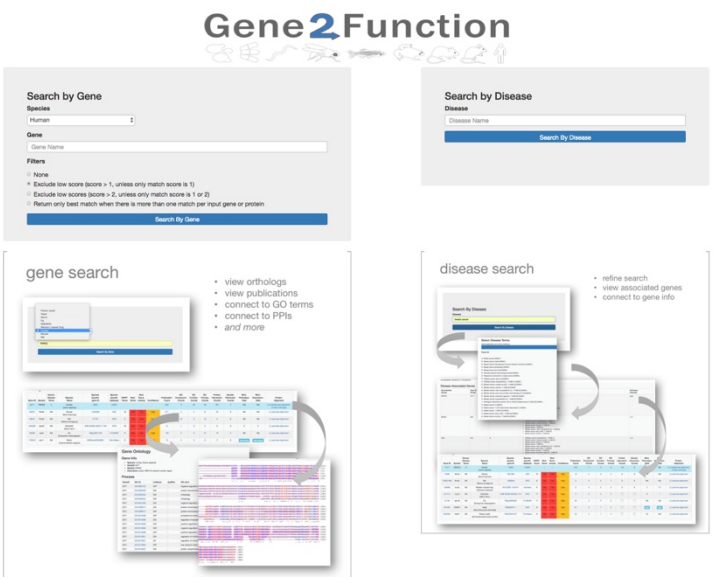
- **CRISPR knock-ins**. We are partnering with the Perrimon and Bellen labs on cell knock-in technologies. We are working towards a goal set out in our funded R24 OD024984 to build cells tagged in specific sub-cellular compartments.

II. *Drosophila* cell screening at the DRSC. High-throughput screening continues to be a key technology supported by our group. We have the following options available, in either an early technology collaboration stage or for off-site and on-site screens (RNAi).

- **CRISPR pooled screening—knockouts**. We are partnering with the Perrimon lab on pooled-format knockout CRISPR screens (Viswanatha et al. BioRxiv). We helped the lab designed and build a large-scale library. Protocols are in place for essential and synthetic lethal screens (+/- perturbagen).
    - Active collaboration in an additional topic area (FACS-based selection)
    - Seeking additional collaborations in the community
- **CRISPR pooled screening—activation**. We are partnering with the Perrimon lab on pooled-format CRISPR activation screens. A large-scale library was designed and built. Protocols for screening and analysis are being developed. We seek collaborations.
- **CRISPR arrayed format screens**. We are actively testing arrayed CRISPR approaches at moderate scale, towards the goal of supporting this at genome-wide scale. Arrayed

CRISPR screens would leverage our existing assay readout equipment and complement our mature arrayed RNAi technology.

- **RNAi screens—still going strong.** We are supporting several RNAi screen projects, both on-site and off-site at other institutions, and have written letters of support for additional projects. The current projects use dsRNA (full genome, sub-library, or custom library). We also offer support the variable dose analysis (VDA) approach using shRNAs (Housden et al. 2017 PMID: 29183982).



III. Bioinformatics at the DRSC. The DRSC continues to develop new bioinformatics tools with the overall goal of supporting search, view, and integration of large-scale data and the literature. Our popular DRSC Integrative Ortholog Prediction Tool (DIOPT) approach is used for ortholog mapping in some of our new online resources (e.g. G2F, MIST), and is used for ortholog mapping at MARRVEL, FlyBase, and the Alliance of Genome Resources. We get ~5,000 users per month of our website and tools. Recently we:

- **Updated DIOPT (version 7.0)**. More species (*Arabidopsis*), three more algorithms, updated information. As in version 6, we support ortholog and paralog searches among common model species in single gene or batch mode. By request, we recently created a YouTube tutorial. We next plan to make it possible for users to submit ortholog pairs missed by all prediction algorithms and submit comments about predicted ortholog/paralog relationships.
- **Updated Gene2Function (version 1.2)**. This tool was designed with physician-scientists and biologists in mind. We wanted to make it easier to quickly identify in which species a human gene is conserved and/or well-studied, then access information about the orthologs. Hu et al 2017 in G3. Since the initial release, we added information about PIs associated in the literature with a given gene. This should help facilitate identification of the most appropriate collaborators.
- **Launched the Molecular Interaction Search Tool (MIST)**. This tool lets users compare a list of newly identified protein or genetic interaction pairs with the literature or view interactors for a given protein/gene or list of proteins/genes. DIOPT ortholog predictions are used to define “interologs” (predicted interactions based on interactions experimentally observed among orthologs in another species). Hu et al 2018 in NAR.
- **Performed routine maintenance and updates** to existing tools for reagent design (e.g. Find CRISPRs), reagent identification (e.g. RSVP), data view tools, website, etc.
- **Made a high-content screen image dataset available online using the OMERO platform.** The dataset can be searched and viewed at http://www.flyrnai.org/tools/drsc_images/web/

IV. FlyBi project. With the BDGP/Celniker and CCSB/Vidal groups, we have an ongoing NHGRI-funded project to use yeast two-hybrid (Y2H) analysis to build an improved binary interaction map for *Drosophila*. The Gateway entry clone collection built as a pre-step to screening is available from the DGRC and other repositories. Four rounds of 10K x 10K Y2H screening are complete. Data from the first two rounds of 10K x 10K Y2H screening are public. Additional data will be made public following validation tests.

V. Outreach by the DRSC. We continue to inform the community about the three areas of focus of the DRSC/TRiP-Functional Genomics Resources: in vivo fly stock production, fly cell screening, and bioinformatics. We are using both online and in-person approaches. We also maintain broader online resources, including informational blogs and a community website built in response to a fly board request.

A. Working to increase community awareness of DRSC/TRiP resources

- **Workshop at the ADRC**: "Functional Genomics Resources from the DRSC and TRiP," on Friday, April 13 from 1:45 to 3:45 PM. We also have posters at the meeting.
- **Presentations to groups of fly labs**. We present on our resources at local fly group meetings (e.g. Boston Area Drosophila meeting, Brown University Fly Club, fly labs at U Mass Worcester). Additional on-site presentations, including beyond our region, are in the works. Let us know if you are interested to have us present about in vivo and cell resources, do a hands-on bioinformatics tutorial, etc.
- **Flyrnai.blogspot.com**. New and past content related to fly RNAi technologies, cell line production, and other related topics. ~500 views/month.
- **News and events** regularly posted on our DRSC/TRiP-Functional Genomics Resources webpage
- **Now on Twitter** @DRSC_TRiP

B. Broader community outreach

- **Drosophila protocols portal**. We maintain and update a searchable database of protocols distributed across different platforms (publications, websites, YouTube, etc.).
- **Drosophilaresearch.org**. We regularly post news and events, and occasionally post new content to other pages. The site has found a niche as a way to share news and events among fly researchers. The online submission form has been used by community members to submit news or events, which we take as evidence of value. Most hits to the site appear to come from the "Community News" and "Meetings and Courses" buttons on the FlyBase home page. ~400 users/month.
- **Flydiseasemodels.blogspot.com**. We regularly post new content related to use of Drosophila in human disease-focused studies. Collective value has grown from the keyword tagging strategy. No longer as comprehensive as it was. ~1200 views/month.

VI. Publications or preprints from our group and/or using our resources:

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Discussion (Drosophila RNAi screening center; DRSC)

Stephanie Mohr presented. DSRC is doing pooled cell-based screening for the community. The most exciting thing this year is that we are making CRISPR libraries for Drosophila cells. We are tagging organelles, and we are working with Hugo (Bellen) and Norbert (Perrimon) to improve CRISPR knock-out and knock-in efficiency in Drosophila cell lines. Many of you are aware that these are methods now commonly used on mammalian cell lines, and we are working to bring this technology to Drosophila cells too. DSRC is presenting a workshop at ADRC that will cover DSRC's new CRISPR work and new bioinformatics techniques.

21. Transgenic RNAi Project (TRiP) at Harvard Medical School

Jonathan Zirin, PhD, Assistant Director DRSC/TRiP (March, 2018)

The Transgenic RNAi Project (the TRiP) has entered its second year of its third round of funding (NIGMS R01-GM08494; N. Perrimon, PI; ends June 2020). We thank the board for their steadfast support of this project. The TRiP has transitioned from predominantly RNAi fly stock production to development of new resources based on CRISPR technology. Our goal is to generate high quality *in vivo* RNAi and CRISPR community resources with the established and proven TRiP platform.

RNAi Resources

The TRiP continues 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 Bloomington Drosophila Stock Center (BDSC). Since its establishment at Harvard Medical School (HMS) in September 2008, the TRiP has generated approximately **~14,259** Fly RNAi stocks, with **~458** in production. These completed stocks, in production and nominated represent **~10,535** unique FBgns which we calculate covers **75%** of the genes in the fly genome (**85%** of highly conserved genes).

TRiP RNAi Stocks at BDSC

Generation	Vector	Hairpin	# Stocks	Use in	Ref
1st Generation	VALIUM1	dsRNA	678	Soma	21
	VALIUM10	dsRNA	1808	Soma	20
2nd Generation	VALIUM20	shRNA	9059	soma, germline	19
	VALIUM21	shRNA	96	soma, germline	19
	VALIUM22	shRNA	1620	soma, germline	19

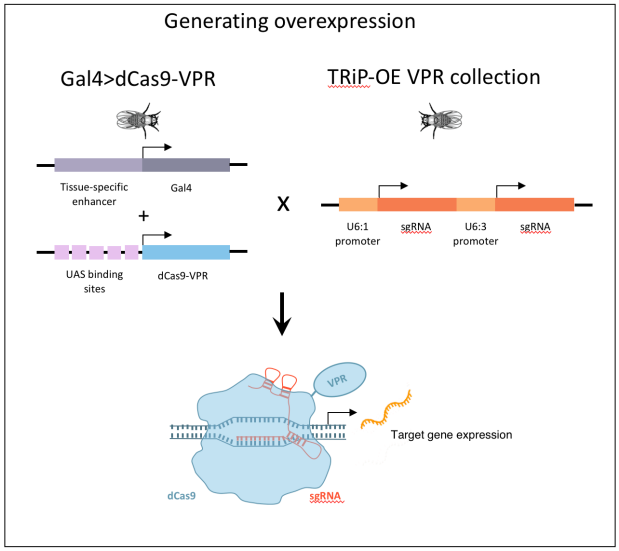
We are producing the lines with the help of two outside groups, the National Institute of Genetics (NIG) in Japan (coordinated by Drs. Shu Kondo and Ryu Ueda) and the THFC at Tsinghua University in China (coordinated by Dr. Jianquan Ni). Importantly, these outside labs use established TRiP nomenclature 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 (http://fgr.hms.harvard.edu/) and on FlyBase, and transferred as soon as possible to the BDSC for distribution to the community. Select stocks are also available from the NIG and the THFC. 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).

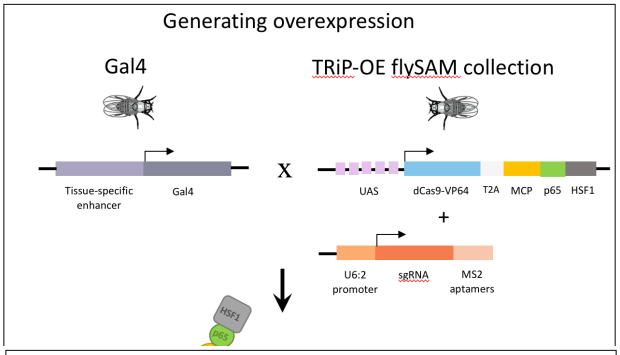
The TRiP-CRISPR Project

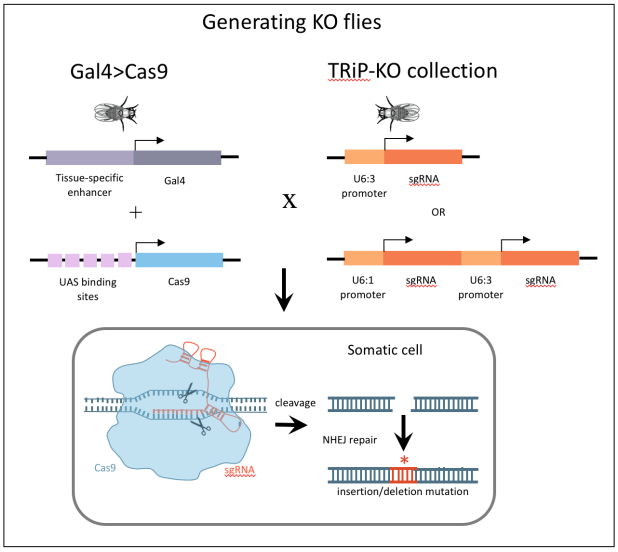
The TRiP has continued development of resources based on CRISPR technology, leveraging the existing transgenic RNAi platform to produce the stocks and making them available at the BDSC. As with TRiP-RNAi lines, we are producing TRiP-CRISPR lines with the help of the NIG in Japan and the THFC at Tsinghua University in China. All TRiP-CRISPR stocks undergo rigorous quality control at our facility at HMS, before being shipped to the BDSC for distribution. Available stocks are annotated on the DRSC/TRiP sgRNA Fly Stock Database (see below) and on Flybase. As we build the new CRISPR collections, we encourage and receive gene target nominations from the community. Detailed information about the TRiP-CRISPR project can be found on the in vivo CRISPR pages of the TRiP website (http://fgr.hms.harvard.edu/fly-in-vivo-crispr-cas). Below are summarized the TRiP-CRISPR libraries currently in production:

1) **TRiP-CRISPR Overexpression (TRiP-OE)** http://fgr.hms.harvard.edu/trip-overexpression-stocks

TRiP-OE stocks express sgRNAs targeting upstream of a gene transcription start site. Gene activation is triggered by co-expression of catalytically dead Cas9 (dCas9) fused to an activator domain, either VP64-p65-Rta (VPR) or Synergistic Activation Mediator (SAM). **The VPR method** is based on work from the Perrimon and Church labs that demonstrated that CRISPR/Cas9-based transcriptional activation is effective in vivo in Drosophila (Lin et al., 2015; Chavez et al., 2015). Here, the TRiP-OE sgRNA stocks are crossed to a stock in which Gal4 directs expression dCas9-VPR. In the resulting progeny (Gal4>dCas9-VPR; sgRNA-gene), the gene of interest is overexpressed in the Gal4 domain. **The TRiP-OE flySAM method** is based on the mammalian engineered protein complex (Konnerman et al., 2015). In our version, a collaboration between the Ni and Perrimon labs (Jia et al., 2018), a VP64 domain is fused to dCas9, and two additional activator domains, p65 and HSF1, are recruited to the complex via MS2 stem loops in the sgRNA tail. Because the stocks contain both the protein complex and the sgRNAs, gene activation is achieved by simply crossing to the Gal4 line of interest. This method gives considerably greater levels of activation compared to VPR.







2) **TRiP-CRISPR Knockout (TRiP-KO)**

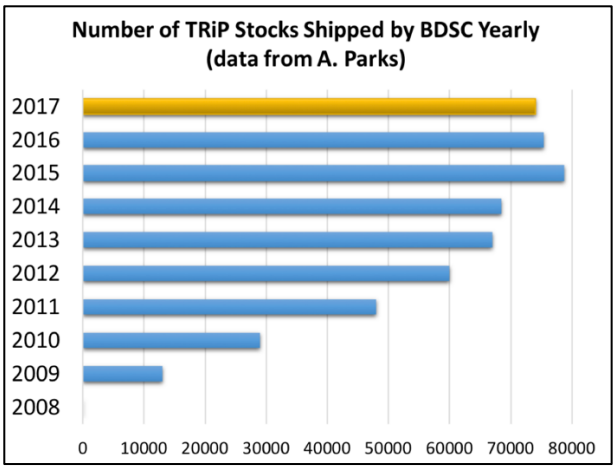
We, and others, have found that the CRISPR/Cas9 system efficiently generates double strand breaks (DSBs) in Drosophila, which can be used effectively to generate mutations or for genome engineering approaches (Ren et al., 2013). TRiP-KO flies ubiquitously express sgRNAs targeting gene coding sequence. Mutant animals or tissue-specific mosaics can be produced by simply crossing TRiP-KO flies to germline-specific-Cas9 or somatic tissue-specific-Gal4>Cas9 flies, respectively. To maximize coverage of the genome for the benefit of the research community, production of TRiP-KO stocks is coordinated with similar efforts headed by Drs. Fillip Port and Michael Boutros at the German Cancer Research Center (http://www.crisprflydesign.org/) and Drs. Shu Kondo and Ryu Ueda at The NIG, Japan (https://shigen.nig.ac.jp/fly/nigfly/cas9/).

3) TRiP-CRISPR toolbox http://fgr.hms.harvard.edu/trip-crispr-toolbox-fly-stocks
Along with the sgRNA lines targeting individual genes, we have produced a TRiP-CRISPR/CAS9 Toolbox set of Gal4/Gal80ts/UAS stocks that allow spatial and temporal expression of nuclease dead Cas9 fused to the VPR transcriptional activator (dCas9-VPR), which can be used for gene activation in conjunction with non-SAM TRiP-OE stocks. Additional wild type Cas9 toolbox stocks are also available for generating mutant mosaics in the soma, or generating small deletions and modifications in the germline. **55** TRiP CRISPR/CAS9 Toolbox lines are complete and have been shipped to BDSC for distribution.

To date the TRiP has produced **~2000** sgRNA fly stocks for either gene overexpression or gene cutting, with **~1500** more constructs in the transformation pipeline. Finished stocks are being processed by the BDSC for distribution, and available lines can be found on their guide RNAs page (https://bdsc.indiana.edu/stocks/genome_editing/sgrna.html).

TRiP sgRNA Stocks at BDSC			
Collection	**Vector**	**Use for**	**# Stocks**
TRiP-KO	pCFD3, pCFD4	Gene cutting	720
TRiP-OE	pCFD4, flySAM2.0	Gene overexpression	591

In 2017 the BDSC sent **74,050** subcultures of TRiP stocks to **1352** different user groups in **40** countries. **72,339** of these were RNAi, **1095** of these were Toolbox, **466** of these were UAS-LUC-mir stocks and **150** were from the new TRiP-CRISPR library (see below) of sgRNA stocks. As of March 1, 2018, there were **14,572** TRiP stocks in distribution at the BDSC. The TRiP expects to send **~250** new RNAi stocks and **~2150** sgRNA stocks to Bloomington in 2018.

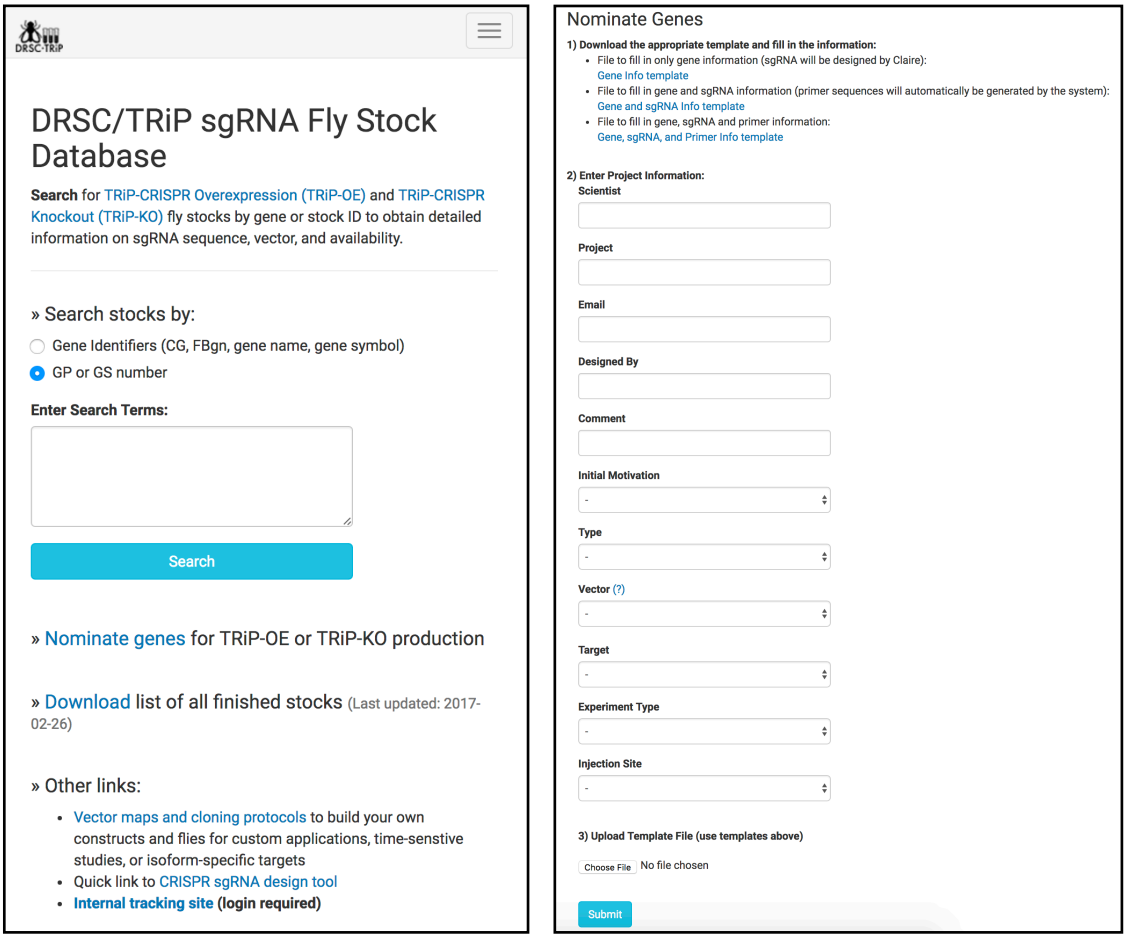


Validation of the TRiP lines

The TRiP continues its curation of reagents via the **RNAi Stock Validation and Phenotypes Project (RSVP)** (http://fgr.hms.harvard.edu/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). RSVP includes results curated by FlyBase for other major stock collections, such as phenotypes associated with VDRC fly stocks, and we hope in the future to also include CRISPR stock validation.

Currently on RSVP there are **>9,500** data entries for **about 5,500** TRiP lines representing **about 3,900** fly genes. In addition, the RSVP contains **23,451** data entries extracted from FlyBase for **17,782** RNAi lines representing **11,346** genes. In the coming year we will be adding phenotypic data from TRiP-CRISPR sgRNA lines to the database.

DRSC/TRiP sgRNA Fly Stock Database http://www.flyrnai.org/tools/grna_tracker/web/ Dr. Claire Yanhui Hu and team recently developed a database that allows users to download and search existing TRiP-OE and TRiP-KO fly stocks by gene or stock ID to obtain information on sgRNA sequence, function, vector, injection site, and availability. The database also has a nominations page that serves as the online access point for the public to nominate genes for TRiP-CRISPR production.



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Discussion (Transgenic RNAi Project (TRiP) at Harvard)

Jonathan Zirin presented. The TRiP project is still making RNAi lines, but not as rapidly as before. This last year, we shipped over 75,000 lines to 40 different countries, so RNAi remains strong. But our main efforts have been in making new libraries for CRISPR transgenic sgRNAs, which can be crossed to Cas9-transgenic flies to generate knock-outs. We are also making sgRNA lines for use in CRISPR activation, which can be crossed to Cas9 activator lines to activate transcription of a target gene. We are making many thousands of these lines. It is not yet clear how widely they be used but we'll see. The TRiP project is also giving a workshop at ADRC 2018, which is important because the reagents and technologies are always getting better and we need good advertising for them.

22. 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. We've continued to expand activities with the goals of improving the functional annotation of the genome and expanding community resources. Release 6 was made public in 2015 (GenBank and FlyBase). PacBio sequencing of *Drosophila melanogaster* was done in 2014. We sequenced the microbiome of the reference stock and published five short Genome Announcement papers of *A. tropicalis, A. pomorum, B. kochii, E. durans and L. plantarum.* We are working on papers that describe the genomes of *B. flexus*, *L. brevis, L. mesenteroides, L. plantarum and P. taichungensis*. The finished sequences can be accessed from BDGP or from GenBank. We continue to characterize the transcriptome (smORFs). We are continuing the modENCODE project rebranded as modERN to map transcription factor binding sites. 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 on 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. There is currently no budget for these studies.

C. Reference Microbiome Genome sequence

As part of an LBNL funded program we sequenced the microbiome of the reference genome strain, y;cn, br, sp. These are complete genomes sequenced using the PacBio platform and include conjugative plasmids and virions. They were automatically annotated using the RAST and GenBank annotation pipelines. We cataloged protein-coding genes, RNA genes including rRNA operons, tRNAs, pseudogenes and prophages. We determined the phenotype of *A. tropicalis* since it is very similar (97%) to *A. senegalensis*.

D. 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 submitted the sequence to GenBank as full-length cDNA clones when they are finished and as ESTs when they are incomplete. The accession

numbers for the 890 clones submitted full-insert sequenced to GenBank are KX531261-KX532150. The rest of the submission to the SRA is under SRA accession is SRP091922

The following are our summary statistics of clones submitted to GenBank - DNA sequence for 258,891 cDNA clones, of which 22,184 were fully sequenced and 18,990 fully support a FlyBase Release 6.13 protein model. The Gold Collection of cDNAs whose amino acid translation matches a FlyBase Release 6.02 protein with 100% identity, now contains 13,335 clones. From the Gold Collection, we have produced 10,389 expression-ready donor clones lacking the native stop codon (for making C-terminal fusion constructs) and 10,470 expression-ready donor clones containing the native stop codon (for making N-terminal fusion constructs). Using the donor clones, we have generated sets of expression clones in different vectors with a variety of tags (Table 1).

Table 1. Summary of Expression Clones.

Collection	Vector	Promoter	N-term Tag	C-term Tag	ORF Stop Codon?	System	Past year (2/2017-3/2018)	Total
XO	pDNR-Dual	T7	--	6xHN	No	*E. coli*	0	10,389
XS	pDNR-Dual	T7	--	--	Yes	*E. coli*	0	10,470
MXO	pMK33-CTAP-BD	Metallothionein	--	TAP	No	Cell culture	0	1960
FMO	pMK33-CFH-BD	Metallothionein	--	Flag-HA	No	Cell culture	0	10,146
UFO	pUAST-CFLAGHA-BD-PHI	UAS	--	Flag-HA	No	Gal4-UAS	0	7,110
URO	pUAST-C-mCherry-BDatt	UAS	--	mCherry	No	Gal4-UAS	0	245
UGO	pUAST-C-eGFP-BDatt	UAS	--	eGFP	No	Gal4-UAS	0	230
URS	pUAST-N-mCherry-BDatt	UAS	mCherry	--	Yes	Gal4-UAS	0	247
UGS	pUAST-N-eGFP-BDatt	UAS	eGFP	--	Yes	Gal4-UAS	0	237
MSN	pMK33-BD	Metallothionein	--	-	Yes	Cell culture	0	71
GEO	Gateway Entry	-	--	-	No	Y2H*	0	11,672
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	0	346
CRO	pCopia-C-Clover-BD	Copia	--	mRuby2	No	Cell culture	0	345
GCO	pCopia-C-EGFP-BD	Copia	--	eGFP	No	Cell culture	0	23
ECD	pECIA2	Metallothionein	--	Fc; V5; 6xHN	No	Cell culture	0	207
ECD	pECIA14	Metallothionein	--	Alkaline Phosphatase; Flag; 6xHN	No	Cell culture	0	207
hGUHO	pUASg-HA.attB	UAS	--	3xHA	No	Gal4-UAS	833	1071
hGUHO	pGW-HA.attB	UAS	--	3xHA	No	Gal4-UAS	238	238

*Not colony purified

Table 2. Summary of clones available at the DGRC:

Collection	Past year (Feb 2017 – March 2018)	Cumulative
AU (Gold)	96	11,975
XO	0	9,685
XS	0	9,600
MXO	0	1961
FMO	0	10,051
UFO	0	7,110
ECD	0	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 selected CRM-driven reporter constructs from the Rubin/Janelia collection and additional constructs generated as part of our collaboration with the Berkeley Drosophila Transcription Network Project. We have started to incorporate the CRM 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. Last year we released a new version of the gene report pages. The improved gene reports now 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 allows 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. A manuscript describing the automation software has been submitted and accepted in principle (iScience). To date annotated experiments for 8275 genes, documented with over 131,000 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 328 transgenic GFP tagged-TF fly lines for a total of 437 lines for 429 TFs. They are deposited at the Bloomington Stock Center. The White Lab has performed ChiP-Seq for 349 lines. The data is being processed through the ENCODE pipeline and is being distributed through the ENCODE DCC. In addition we produced TF knock-down RNAi followed by RNA-seq experiments for a number of TFs [~26 sequenced (276 RNA samples) – 30 more in process]. Once validated the RNA-seq files will be submitted to the ENCODE DCC and the SRA. A grant to generate the remaining GFP tagged-TF fly lines and additional RNAi TF experiments was recently renewed with Bob Waterston as PI (2022).

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. We have the Oxford Nanopore platform and software running in the lab and it was used to sequence some of the microbes from the *Drosophila* gut microbiome. We have access to the latest Illumina machines through the UCB QB3 sequencing core. Other sequencing platforms (PacBio) are commercially available at reasonable cost.

H. Funding
The BDGP is funded almost exclusively by NIH grants (NIGMS). An R01 (SEC) funds the spatiotemporal gene expression studies and was renewed in 2015. A new RO1, "Systematic, Genome-Scale Functional Characterization Of Conserved smORFs" (Celniker, PI and Perrimon co-PI) was obtained to functionally characterize genes that may or may not be coding proteins that have small open reading frames (<100 aa) and are conserved from flies to humans. We are also funded under subcontracts from Harvard University (Perrimon, PI, Celniker, co-PI) to participate in the analysis of the Y2H data, 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 from Baylor College of Medicine (Bellen, PI, Celniker, co-PI) to construct human ORF clones for expression in flies.

Discussion (Berkeley Drosophila Genome Project (BDGP))

Sue Celniker presented. We are in the process of making more transgenic lines w/ human cDNAs under Gal4/UAS control, with Hugo Bellen. We are also working with Norbert (Perrimon)

to study conserved small open reading frames in Drosophila. We got some internal funding to sequence the fly microbiome, and have a grant to continue looking at control of gene expression in the embryo. We are still collaborating with Bob Waterston to ChIP all the fly transcription factors – this is the final effort of ModENCODE, now called MODern. So far we've done ChIP for about 350 transcription factors. There was a PacBio sequence of *D. melanogaster* release. Release 7 of the Drosophila genome is being worked on now – this new reference sequence will be better, especially for heterochromatin. But this work is not covered by NIGRI. The fly genome is still not finished in heterochromatin. A Drosophila microbiome genome sequence has been added to our website and is very high quality.

23. Drosophila Genomics Resource Center (DGRC): Andrew Zelhof

Key Changes to Report:
1. Personnel
2. Status of Renewal
3. Looking for a 5th member of Advisory Board – Assistant Professor

Personnel:
Andrew Zelhof, Director
Arthur Luhur, Associate Director of Cell Resources
Kris Klueg, Associate Director of DNA Resources
TBD, Associate Director of Development
Chris Hemmerich, Database Specialist
Johnny Roberts, Project Scientist
Jessica Gonzalez, Project Scientist

Use Statistics:
The DGRC serves ~3200 registered laboratories. Each individual laboratory decides how each account is managed, thus some laboratories may have multiple users and others may have a single designated user. During 2017, demand for our "products" (cDNA clones, vectors, and cell lines) remains substantial; we shipped 3522 individual items at a value of $188,912 in 2017.

Year	Vectors/cDNAs Shipped	Cell Lines Shipped	Products Shipped[1]	Total Value Shipped[2]
2013	4372	260	4653	$179,712.00
2014	3522	202	3843	$189,026.00
2015	3144	265	3625	$194,049.00
2016	3097	217	3586	$189,773.00
2017	2965	230	3522	$188,913.00

Table 1: Summary of items shipped over the last four years of this grant. Years are represented from Jan.1st – Dec.31st. [1] Products shipped is the total number of items shipped and not limited to cell or cDNA/vector clones. [2] Total value shipped represents the charged amount for the items shipped, but does not include the shipping fee that we recover.

Pricing and Best "Business" practices:
We have initiated a collaboration with the Indiana University Kelley School of Business. This is a multiyear collaboration in which they will review our general business practices and help develop an updated model for pricing. This review will better help us calculate and manage our cost recovery program as mandated by the NIH.

New and Future Collections:
1. ~650 tagged transcription factors in BACs for phiC31 integration from Dr. Kevin White.
2. Trojan Plug and Play vectors (33) from Dr. Ben White.
3. A UAS-human ORF clone collection (several hundred) from Dr. Travis Johnson. *A larger UAS-human ORF collection is anticipated from Dr. Hugo Bellen.*
4. Flip-Flop vectors from Dr. Hugo Bellen.
5. Fly31C vectors (e.g. pUASTattB, pattB etc.) from Drs. Konrad Basler and Johannes Bischof.
6. pUASz and UASzMiR from Dr. Alan Spradling.
7. CRISPR mutant lines derived from S2R+ (*ZnT63C-KO* and *IA2-KO*) from Perrimon lab.
8. Anticipating an Ovarian Sheath Cell (OSC) cell line (mbt OSC) from Dr. Mikiko Siomi.

Grant Funding: NIH P40OD010949 – Current funding ends March 31st, 2018. Both the direct costs and program income currently support our activities.

Grant Renewal: We submitted the renewal proposal in May 25th, 2017.

1. The renewal received a perfect score of 10.
2. We would like to thank all of the labs that responded to our call for citations (Jan 2013-March 2017). We will try to do this on an annual basis (each September).
3. We also thank all the PIs who took the time to write letters of support.
4. As of March 15th we have yet to receive the notice of award or budget. We will hopefully have an update at the Drosophila Board Meeting.

Booth #20: Please come by and gives us your comments and feedback. We will have a DGRC user survey available.

Scientific Advisory Board:
We are requesting nominations for a 5th member, specifically an Assistant Professor. Please speak to or email me (azelhof@indiana.edu) if you have any suggestions.

Susan Parkhurst, Fred Hutchinson Cancer Research Center (Chair)
John Abrams, University of Texas Southwestern Medical Center, Dallas
Deborah Andrew, John Hopkins School of Medicine
Stephen Rogers, University of North Carolina, Chapel Hill

Discussion (DGRC)

Andrew Zelhof reported. DGRC has a good funding base. We got a perfect score on our NIGRI grant but are still waiting on the actual award letter so we don't know the budget amount for the next 5 years. We are actively looking for an assistant Professor level person as a new 5th member of our advisory Board. In addition, we will hire a new associate director (a PhD scientist) this year.

24. DIS Report (Jim Thompson)

This year, Drosophila Information Service published volume 100 with reports submitted in calendar year 2017. Beginning in 1934, DIS has published research, new mutant, teaching exercises, and other reports annually, with occasional special issues and additional volumes from time to time. Volume 100 is one of the largest recent issues (50 papers and reports; over 240 pages). Included among these are two long articles with valuable data for which DIS serves as a readily accessible archive. We welcome this role. DIS is freely available at www.ou.edu/journals/dis. Printed copies can be obtained from www.lulu.com.

Although we publish at the end of each calendar year, submissions are accepted at any time. The firm deadline is 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.

Discussion (DIS)

Jim Thompson did not speak but announced that he is open for questions, online or offline.

25. Larry Sandler Symposium (Celeste Berg)

The Department of Genome Sciences at the University of Washington in Seattle will host an all-day symposium in honor of Larry Sandler in the spring of 2019.
We would like to invite all of Larry's Ph.D. students, and we are assembling a contact sheet now, but if you or anyone you know is interested in attending this symposium, please contact Celeste Berg (caberg@uw.edu).

Discussion (Larry Sandler Symposium)

Celeste Berg spoke. Celeste announced a one-time symposium scheduled for May 2019 in Seattle in honor of Larry Sandler. Celeste is gathering contact information on all of Larry Sandler's trainees and collaborators. If you know of anyone, please send this info to her. Of course anyone will be welcome to attend.

26. Miscellaneous Ongoing Agenda

Discussion (Ongoing Agenda)

Debbie Andrew re-iterated that nominations for GSA for 2020 meeting organization (TAGC) are needed for GSA.
Debbie also thanked Mark Peifer for bringing up the issues with Jon Lorsch at NIGMS & funding of FlyBase via NIGRI & new fees. How will NIH fund FlyBase in the future? NIH intends to reorganize databases and has proposed to have a single database for all model organisms. Brian Calvi commented that he will see Jon Lorsch (NIGMS director) at NIH this month (April 2018), at a reverse site visit for the AGR. He noted that he will lobby for Flybase. D. Andrew and AGR already wrote him very similar letters to this effect. Mark's group will emphasize that FlyBase is at the vanguard of what they (NIH) are trying to do.
Laura Johnston proposed to post Committee Chair names (e.g. Andreas Prokop) on the FlyBoard Wikipedia page. This motion was not objected to, and so the Committee Chair names will be added to the Fly Board Wiki page, provided this is OK with the chairs. Debbie Andrew reminded the Board that the complete notes from the Fly Board meeting will be posted on the Fly Board area of the Wikipedia webpage, which is linked to FlyBase. Thom Kaufman organizes this. The materials (assembled in this document) are very complete with regard to tools development; Board members should share this info with their Drosophila colleagues.

27. Appendix 25

List of all national Drosophila meetings to date: Thom Kaufman

2018: Philadelphia, PA	1997: Chicago, IL	1977: La Jolla, CA.
2017: San Diego, CA	1996: San Diego, CA	1976: Tempe, AZ
2016: Orlando, FL	1995: Atlanta, GA	1975: Baton Rouge, LA
2015: Chicago, IL	1994: Chicago, IL	1974: Banff, Alberta
2014: San Diego, CA	1993: San Diego, CA	1973: DeKalb, IL
2013: Washington, DC	1992: Philadelphia, PA	1972: Raleigh, NC
2012: Chicago, IL	1991: Chicago, IL	1971: Ithaca, NY
2011: San Diego, CA	1990: Asilomar, CA	1970: Pasadena, CA
2010: Washington, DC	1989: New Orleans, LA	1969: Ames, IA
2009: Chicago, IL	1988: Toronto, ON	1968: New Haven, CT
2008: San Diego, CA	1987: Chicago, IL	1967: Austin, TX
2007: Philadelphia, PA	1986: Asilomar, CA	1966: Chicago, IL
2006: Houston, TX	1985: Charleston, SC	1965: Seattle, WA
2005: San Diego, CA	1984: Chicago, IL	1964: Madison, WI
2004: Washington, DC	1983: Asilomar, CA	1963: *Skipped due to change from fall to spring*
2003: Chicago, IL	1982: Storrs, CT	1962: St Louis, MO
2002: San Diego, CA	1981: Chicago, IL	1961: Oak Ridge, TN
2001: Washington, DC	1980: Salt Lake City, UT	1960: Bloomington, IN
2000: Pittsburgh, PA	(Snow Bird)	1959: Chicago, IL
1999: Bellevue, WA	1979: Bloomington, IN	1958: Madison, WI
1998: Washington, DC	1978: *Coal Strike, Cancelled*	1957: La Jolla, CA.