

2019 DROSOPHILA BOARD OF DIRECTORS MEETING: AGENDA

Wednesday March 28, 2:00 – 5:00 PM

Location: Austin 1, Hotel 2nd Floor

Introduction (Bruce Edgar) **2:00 – 2:05**

ADRC

1. Report from the ADRC Organizing Committee (Michael Buszszak) **2:05 – 2:15**
2. Sandler Lectureship Committee (Barbara Mellone) **2:15 – 2:20**
3. Report of the GSA Senior Director (Suzy Brown) **2:20 – 2:30**
4. GSA and the Drosophila Board (Bruce Edgar for Denise Montell) **2:30 – 2:35**
5. Treasurer's Report (Michelle Arbeitman) **2:35 – 2:40**
6. Victoria Finnerty Undergraduate Award (Amanda Norvell) **2:40 – 2:45**
7. Image Award (Nasser Rusan) **2:45 – 2:50**
8. 2020 Fly Meeting @ TAGC (Helen McNeill) **2:50 – 2:55**

Discuss action items related to ADRC: 2:55 – 3:05

- a. *Focus Group formed – “Building a better Fly Meeting”, meets tomorrow.*
- b. *Discussion and vote on whether the ADRC Organizing Committee should have a mandate regarding diversity and representation of invited speakers and session co-chairs. Proposed text: “Efforts should be made each year to ensure that the organizers of the North American Drosophila Meeting and the speakers at the meeting should reflect the full diversity of the Drosophila community, along all dimensions of diversity.”*
- c. *Distribution and naming of Travel Awards from the Drosophila reserve fund.*

Community

9. Drosophila Board Elections Committee (Laura Johnston) **3:05 – 3:10**
10. Primarily Undergraduate Institutions (Amanda Norvell) **3:10 – 3:15**
11. Advocacy and Communications (Michelle Arbeitman for Andreas Prokop) **3:15 – 3:20**

Discuss action items related to community: 3:20 – 3:30

- a. *Appointment or election of another trainee representative to the Elections Committee.*
- b. *Online Forum for Drosophila researchers (Erika Geisbrecht).*
- c. *Advocacy & Communications.*

BREAK 3:30 – 3:45

Resources and Projects

12. FlyBase (Norbert Perrimon & Susan Russo Gelbart) **3:50 – 4:00**
13. Bloomington Drosophila Stock Center (Kevin Cook) **4:00 – 4:05**
14. VDRC Stock Center (Lisa Meadows) **4:05– 4:10**
15. Kyoto Stock Center (Shinya Yamamoto for Toshi Takano-Shimizu) **4:10– 4:15**
16. Species Stock Center (Patrick O'Grady) **4:15 – 4:20**
17. Drosophila Gene Disruption Project (Hugo Bellen) **4:20 – 4:25**
18. Human cDNA Project (Hugo Bellen) **4:25 – 4:30**
19. Harvard Transgenic RNA Project (Jonathan Zirin) **4:30 – 4:35**
20. Harvard Drosophila RNAi Screening Center (Stephanie Mohr) **4:35 – 4:40**
21. Berkeley Drosophila Genome Project (Bruce Edgar for Sue Celniker) **4:40 – 4:45**
22. DGRC (Andrew Zelhof) **4:45 – 4:50**
23. DIS (Jim Thompson) **4:50 – 4:55**

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

ADJOURN. Please visit the New Faculty Forum in the Press Club, here on the 2nd floor.

Drosophila Board Meeting: March 27, 2019

1. Fly Board President Bruce Edgar began with Introductions of new attendees.
2. He then gave a quick summary of some issues faced by our community. These included concerns about federal funding for our field and attendance at the Fly meeting. He announced a Focus group meeting later in the meeting which collected feedback on new ideas that might further enhance the Drosophila meeting.
3. Report from the ADRC Organizing Committee (Michael Buszszak)

Michael focused on differences from previous meetings. He discussed selection of the keynote and plenary talks. The emphasis was on great science, someone who had not presented before, with close attention paid to gender diversity. They changed abstract categories as described in Report, based on recommendations from previous organizers and survey responses (e.g combining microbiome with immunity, cell death with cell stress, and merging some categories based on abstract numbers from previous meetings). They deleted RNA Biology as it had the lowest number of abstracts, and could be accommodated in regulation of gene expression. Talk numbers were based on abstract numbers. They added a stand-alone Techniques and Technology Plenary session. They replaced one full talk in each session with several lightning talks/poster previews. The organizers were more heavily involved in fund-raising. He then opened this for discussion. Questions focused on the fact that attendance is down this year, and that this is a concern. He noted regional effects—there is not a large local population. He noted we need to think about how we can improve the meeting.

4. Sandler Lectureship Committee (Barbara Mellone)
There were 27 nominations (an increase from 19 in 2018). The initial rankings were based on Thesis Abstract and nomination letters. 3 finalists were chosen. She discussed the possibility of structuring nomination letters, to make these more helpful to the committee. Other suggestions were in the Report.
5. Report of the GSA Senior Director (Suzy Brown and Tracey D)
Suzy shared some positive aspects of the meeting-she emphasized its importance and shared positive comments from the survey. She then discussed the new Code of Conduct and its importance. Tracey thanked the organizers, and solicited further feedback, asking people to talk to her later in the meeting. She discussed ways to increase fundraising. She then talked about GSA strategic planning—it will include an evaluation of fiscal and intellectual merits of each of the GSA meetings. She then opened the floor for questions. Celeste Berg asked about the trends of financial success of Fly Meetings. Suzy and Tracey pointed out the complex set of things that affect financial success of a meeting. Rachel Cox asked how the Fly Meeting compares to other model organism meetings in this regard. Suzy noted that Drosophila meeting registration charges are still lower than other meetings, and declining slightly, whereas some other meetings (*C. elegans*) have stable attendance. Tracey pointed out that keeping meetings vibrant and sustainable is a key issue for the GSA. She emphasized that the GSA wants suggestions for how to keep

the ADCR vibrant and attractive to young and mid-career attendees. Laura Johnston noted that grant funding is currently low and this is a factor, because PI's can't afford to bring many lab members anymore. Mark Peifer pointed out that the *C. elegans* meeting is stable in attendance and their funding challenges are similar.

6. GSA and the Drosophila Board (Bruce Edgar for Denise Montell)
Denise Montell is the incoming GSA President. She sent a letter to be shared with the Board. Bruce read Denise's letter. She pointed out challenges faced by the GSA, especially the push for open access publishing and the potential impact on other GSA meetings. Denise noted that GSA meeting attendance is either steady or trending down. Noted upcoming effort of GSA to evaluate all of its model organism meeting, and potential impact of TGCA. Noted GSA strategic plan and new fundraising efforts—with a focus on new services for young and mid-career investigators.
7. Treasurer's Report (Michelle Arbeitman)
Michelle reported that the Board's funds are invested with Vanguard. The Board needs to discuss the custodial agreement, and take action on this within the next months. She asked members to send comments to Bruce and Michelle. She will work with the Presidents to decide on how to use funds to create new travel awards and discuss naming options. The GSA stepped in to support the Finnerty awards, which had run out of money. Bruce requested volunteers for a Working Group to get this off the ground. Erika Bach volunteered—Michelle and Erika are seeking additional volunteers to join this effort.
8. Victoria Finnerty Undergraduate Award (Amanda Norvell)
Amanda briefly summarized her report. There were 29 applications—slightly up from 2018. There were 2 rounds of review—for quality of research and added value (e.g. PUI, going to grad school, diversity, overcome hardship). The total available was \$5000. 15 awards were made. Each was \$500 or less. Bruce asked how many facilitate student attendance. Amanda noted that student's had to register before Awards are made, but students can cancel without penalty if finances preclude attendance.
9. Image Award (Nasser Rusan)
David Bilder cycled off and Elizabeth Chen cycled on the Award committee. They increased presence on Twitter, and sent out the request for submissions closer to the deadline (by mistake but it may have been a good idea). David created the Image Award Poster which will be distributed as a bonus for attendees. There were 85 total submissions (a 25% increase). The Awards will be presented tomorrow.
10. 2020 Fly Meeting @ TAGC (Helen McNeill)
The organizers are trying to balance excitement of mixing communities with retaining value to Drosophila community. There will be a Drosophila mixer, and gathering sites for fly people. Abstract review will start with the organism group and then go to a pan-organism committee. There will be about 100 Drosophila talks (less than the 160 at the Fly Meeting). There will be mixed organism but topically themed poster sessions, and a common technology session. Celeste Berg asked about workshops. Suzy said they will

be selected from community submissions. All will be in a single 2 hour session. There likely will be preference for cross-community workshops. There were too many in 2016—thus there is a need to be more selective. Bruce asked more about the details of sessions. Hugo Bellen addressed this. One major difference is that the quantitative and population and evolution group is its own community, for purposes of the meeting. There will only be a single Fly specific Plenary Session and it will only have three slots. Suzy noted there will be many more joint (mixed organism) plenary sessions. Lynn Cooley noted it will be about 50/50 pan-organism to community specific sessions, with the mixed organism session grouped topically. Drosophila will be the only organism community with concurrent organism specific sessions. Overall the new TAGC program should help integrate the different organism-specific communities better than the last TAGC.

11. Board Action items

- a. Bruce noted that a Focus Group of about 15 people at all career stages had been formed – “Building a better Fly Meeting”, and would meet on Thursday. Others can attend if they wish.
- b. Next, there was a discussion and vote on whether the ADRC Organizing Committee should have a mandate regarding diversity and representation of invited speakers and session co-chairs. Proposed text: "Efforts should be made each year to ensure that the organizers of the North American Drosophila Meeting and the speakers at the meeting should reflect the full diversity of the Drosophila community, along all dimensions of diversity."

After discussion, the measure passed by a strong majority. Subsequent to the meeting, the outgoing representative from Latin America, Juan Riesgo-Escover, wrote to the Board discussing his reasons for opposing this measure. He expressed a view shared by he and some of his Latin American colleagues, stating that they “strongly feel that whenever someone is asked to participate in the meeting in any guise it should be primarily because the underlying science and research is sound and of interest; in other words, we feel that privileging the science should be the first concern”. He shared the thought that “asking people because of who they are or represent, and not necessarily paying the highest attention to the quality of their research, we feel, is demeaning and patronizing. This is an important perspective that needs to be considered as we try to ensure that the speakers and session chairs reflect the diversity of our community while also ensuring strong scientific content.

- c. Mark Peifer noted that some members of the community have pointed out the lack of diversity on the Fly Board. Tracey noted that the GSA is creating a Diversity and Inclusion Committee. Debbie Andrew has incorporated volunteers into the Nominating Committee to try to diversify the next slate of nominees. The Committee includes Debbie, Iswar Hariharan, Tin Tin Su, Laura Reed, Patrick O’Grady and Noah Whiteman, Debbie has also initiated an effort to seek nominations from the

broader community, and an announcement of this effort will be circulated by Fly Base and in the GSA e-news.

- d. Distribution and naming of Travel Awards from the Drosophila reserve fund was dealt with earlier.
12. Drosophila Board Elections Committee (Laura Johnston)
Tin Tin Su and Noah Whiteman were added to the committee. Laura discussed their efforts to increase diversity. One mechanism to address this was creating contests between two candidates of the same gender. Marianna Wolfner will be President Elect—others are named in the report. There was a minor glitch in the balloting—President Elect was left off first ballot. Despite this number of votes was among the highest ever. Bruce noted that 702 votes is still a pretty low number. We should try to publicize this election more broadly.
13. Primarily Undergraduate Institutions (Amanda Norvell)
There are several workshops and activities targeted to this community in the meeting, including the focus on undergraduate researchers. She pointed out the workshop on inclusive teaching and research Thursday evening. They have added ribbons to identify undergraduate students on badges.
14. Advocacy and Communications (Michelle Arbeitman for Andreas Prokop)
Michelle directed us to Andreas' Report, which includes materials he is using in Manchester. His stats suggest this outreach effort is working. It is working well in Manchester but he is worried he is preaching to the choir. He is trying to get word out more broadly. We discussed ways it could be better publicized on Fly specific websites. Rachel Cox asked about whether there will be a Hill Day at TAGC. Hill Day would provide a structured opportunity for attendees to meet with their Congressional Representatives. Tracey noted that such an even will occur, and is tentatively scheduled for the Tuesday before the TAGC. Bruce noted that there is more room for work in this area.

Action items related to community:

- a. Appointment or election of another trainee representative to the Fly Board (Laura Johnston)
It's been viewed as a good change—should we expand it to two, and should it be an elected or appointed position. Lynn Cooley noted the positive aspects of this based on the GSA experience—they have one postdoc and one grad student, and also added an early and a mid-career scientist, who are elected. Tracey discussed this. David Bilder discussed the logistics, and importance of selecting the right person—probably not via election. Bruce brought it to a vote—add a grad student and a postdoc representative, each for a two year term. We will solicit self-nominations and the election committee will select. This passed unanimously. Laura Johnson asked if we would help support costs of attendance of the student reps—this will need to be discussed. There is a possibility of using travel fellowships for this.

- b. Online Forum for Drosophila researchers (Erika Geisbrecht).
Erika suggested the creation of an interactive forum like Slack for the Drosophila community, and solicited feedback on the idea. Brian Oliver pointed out the successful New PI Slack. Laura Reed noted Slack is not good for archiving. Kevin Cook discussed the history of this—old versions were not very well used, but the formats of these were not generally popular and are now outdated. There was general enthusiasm for this idea, and FlyBase (Norbert Perrimon) offered to help publicize it. Erika solicited feedback from the Board, and has begun to create a Working Group to spearhead this effort.

Resources and Projects

15. FlyBase (Norbert Perrimon & Susan Russo Gelbart)

FlyBase is doing well—this includes doing more of the same, along with several new innovations. He discussed Micropublications (<https://www.micropublication.org>). It reports results of single experiments or datasets, and will be directly incorporated into the Model Organism Databases. Flybase is part of The Alliance for Genomic Research (AGR). FlyBase will work closely with other Model Organism Databases (MODs) to integrate data sets and develop tools to enable cross-species analyses. This effort will have a major impact on the fly community, accelerating the development of models of human diseases. This going well. They are discussing how to add single cell RNA seq data and other large datasets, and trying to make these accessible. We're behind the human genome community in this regard. They are working with experts in these efforts, and will be part of a meeting at Janelia Research Campus about this. He next discussed curation, requesting help from the community, e.g, for gene summaries. He discussed funding, and the different agencies that contribute. They have had a reasonable response from request from labs to contribute, via the new user fee mechanism. 300 labs have contributed, \$196K was pledged, \$143K is in hand. However this will support only one or two salaries and is a small fraction of the total FlyBase budget. There were questions about mechanisms to contribute. This was clarified—e.g., NIH is now OK with a FlyBase user fee being included on your budget. There was a question about the disparity in costs between US/UK versus Europe, Canada, and other regions—he noted the reasoning behind it and discussed whether evening out costs might bring in more money, since at the moment very little comes in from Europe. Hugo noted that efforts to have European funding agencies contribute have failed. They mentioned that funding from The Alliance for Genomic Research (AGR) came in higher than expected, meaning that the amount needed from “lab fees” was reduced. Overall, Norbert concluded that the funding for FlyBase is stable for the current grant cycle, but not necessarily into the future beyond that. Hugo and Norbert reported that NIH has recognized (with community feedback) that we need individual Model Organism Databases, and so it is accepted that we will not totally replace FlyBase with with a unified AGR model in the near future.

16. Bloomington Drosophila Stock Center (Kevin Cook)

BDSC is currently splitting operations into two buildings, with backup stocks separate from main stocks. They are in the last year of a five year grant. They requested a 5% increase. They received good reviews but the funding level is not yet clear. A competing revision was submitted to support the Janelia split-GAL4 stocks, which are important but

low use. Overall use numbers are in the Report. They have doubled the number of stocks since 2010, though stock use is flat. They are now at the limit of the number of stocks that can be supported and will need to raise fees in 2020. The increase will be roughly 14-19%. Hugo asked about the very high inspection fees for stock shipment to Europe—can be 150-400 Euros per shipment. Kevin reported that a solution may be in the works, and noted that part of the problem is that many institutions don't do the paperwork correctly. Australia solved this with a centralized distribution center. David Bilder asked about how the changes in Janelia leadership may affect stock generation and maintenance. Hugo said this will not likely change things much.

17. VDRC Stock Center (Lisa Meadows)

Lisa reported finances are a bit low, and support from current sources will be cut in the coming year, and they need to find new ways to fund costs.

18. Kyoto Stock Center (Shinya Yamamoto for Toshi Takano-Shimizu)

He described an ongoing fly preservation project. They have established a protocol to remove germ cells, freeze the needle, and then transplant PGCs. It doesn't reduce costs. The current capacity is 400-800 stocks. They currently have verified at least a one-year success rate. They would like suggestions from the Board and the Community as to which stocks are most important for cryo-preservation.

19. Species Stock Center (Patrick O'Grady)

They moved to Cornell in October 2017 and have been shipping stocks for about a year. It is funded by an NSF grant. The website is currently primitive, but a new one will be out later this month. Celeste Berg asked whether most lines are sequenced—answer is yes.

20. Drosophila Gene Disruption Project (Hugo Bellen)

This group has switched to a CRIMIC strategy (targeted integration of MiMIC-like cassettes through CRISPR/Cas9 mediated homologous recombination) for tagging and disrupting genes. Their grant got a 14% score, but they still have not heard about funding.

21. Human cDNA Project (Hugo Bellen)

This group is generating a library of UAS-human cDNAs, as a combined effort of three different labs. They are seeking to generate a library of 8,000 epitope tagged human cDNAs that are conserved between Drosophila and human. They are now using a robotic cloning pipeline—they have 3500 clones in hand. They recently obtained a larger commercial collection of human clones.

22. Harvard Transgenic RNA Project (Jonathan Zirin)

They are continuing to make RNAi and CRISPR reagents. He noted their collaboration with Flybase. Usage numbers of RNAi stocks rose and are now stable; this might increase with the new CRISPR stocks. There is an expanded RSVP website—he reminded us to seek feedback. There was a discussion of off-target effects or other abnormalities.

23. Harvard Drosophila RNAi Screening Center (Stephanie Mohr)

They continue to support RNAi screens and have expanded into CRISPR screening. There is more information on posters at the meeting. They are expanding resources for proteomics, other databases, and increasing outreach.

24. Berkeley Drosophila Genome Project (Bruce Edgar for Sue Celniker)
They have ongoing and new projects. They have a new focus on the microbiome, the human cDNA clone resource, and are expanding curation of gene expression patterns, with MOD-ENCODE continuing but is re-named MODERN.
25. DGRC (Andrew Zelhof)
They have expanded personnel. They are searching the community and requesting resources. Funding is in good shape (in year 2 of a 5 year grant). Their usage is consistent. He invited us to come by their booth and examine new resources.
26. DIS (Jim Thompson)
He directed us to his report.

Final thoughts

Brian Oliver noted some new efforts from his group in annotation and re-annotation. Hugo Bellen noted email from Steve DiNardo, with concerns about the new and very onerous rules at Penn, based on longstanding NIH guidelines, for the use of transgenic flies. Hugo encouraged the Board to let the Fly Board President know if this an issue any other institution. Kevin Cook discussed the BDSC view on these NIH guidelines—he noted that an inventory of transgenics is probably required but records of all crosses are probably is not. BDSC has followed the NIH guidelines for many years, and has never been audited by NIH. He suggested we need to go to NIH to get the exemptions from these guidelines, similar to those the mouse community has already obtained. These exemptions would cover the whole fly community, simplifying compliance for institutions.

The Board meeting is adjourned and Board members are encourage to attend the nearby social at the new Faculty Forum.

<u>Table of Contents for Reports and Discussion Items:</u>		<u>Page</u>
Appendix 1	Report of the ADRC Organizing Committee	3
Appendix 2	Sandler Lectureship Committee	11
Appendix 3	Report of the GSA Senior Director	15
Appendix 4	GSA & The Fly Board	28
Appendix 5	Treasurer's Report	29
Appendix 6	Victoria Finnerty Undergraduate Award	33
Appendix 7	Image Award	34
Appendix 8	2020 Drosophila Meeting at TAGC	35
Appendix 9	Drosophila Board Elections Committee	36
Appendix 10	Primarily Undergraduate Institutions	44
Appendix 11	Advocacy and Communication	45
Appendix 12	FlyBase	50
Appendix 13	Bloomington Stock Center	65
Appendix 14	VDRC Stock Center	67
Appendix 15	Kyoto Stock Center	68
Appendix 16	Species Stock Center	69
Appendix 17	Drosophila Gene Disruption Project	70
Appendix 18	Human cDNA constructs	73
Appendix 19	Harvard Transgenic RNA Project	74
Appendix 20	Harvard Drosophila RNAi Screening Center	81
Appendix 21	Berkeley Drosophila Genome Project	84
Appendix 22	DGRC	87
Appendix 23	DIS	89
Appendix 25	List of all national Drosophila meetings to date	90

Appendix 1. ADRC Organizing Committee (Michael Buszczak)

Report of the 2019 Meeting Organizing Committee: Michael Buszczak (chair), Rachel Cox, Helmut Kramer, Harmit Malik

The 2019 Organizing Committee was assembled in 2018. Michael Buszczak (MB) was invited by Deborah Andrew in March 2018 to chair the organizing committee. Michael invited Rachel, Helmut and Harmit 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 all stages of planning and participated in conference calls and group emails. In preparing this report, we have modeled it directly after the 2018 organizing committee report, to make comparisons between the two years easier.

Interaction with the GSA Office

We wish to thank Suzy Brown, Sonia Hall, Tracey Depellegrin, Cristy Gelling and the rest of 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 including the New Faculty (formerly known as Early PI) Forum and Grant Writing Workshop.

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 would convey exciting and excellent science, with speakers representing the entire 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 2018**. The Platforms talks were set by **December 2018**. Special events and the overall timing of Events was decided by **February 2019**. 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 #DROS19 Meeting mobile app.

Keynote Speaker. For the opening night, there was consensus against holding a panel and preference for a single Keynote Speaker. Sixteen Keynote speaker candidates, some of whom were suggested by people outside of the organizing committee, were considered. After preliminary discussions, this list was narrowed down to six. All of these candidates are exceptional senior scientists. There was a continued interest in addressing the gender imbalance seen for this position since 2001; 11 males, 2 female and 5 panels. After a brief discussion, Mariana Wolfner was selected by consensus and invited by email (MB). She accepted our invitation in **June 2018**. The title of her talk is “What’s love got to do with it? Stimulating reproduction and activating eggs in Drosophila”.

Plenary Speakers. Nominations for plenary speakers were mostly restricted to those who had not previously presented in a Plenary session at the Fly Meeting in the past 10 years. 59 candidate Plenary Speakers were initially nominated by the members of the organizing committee in **April 2018**. In **May 2018**, online voting (Google docs and e-mail) by the four co-organizers narrowed this list to 18 potential speakers. These candidates were discussed during a teleconference on May 8. The members of the organizing committee considered diversity of scientific sub-fields and geographical locations in their discussion. Eight plenary speakers were selected by consensus. Further online discussions over the next two weeks resulted in the selection of four more potential speakers, with a small number of alternates. Invitations were sent by email in mid-May. One of the invited speakers from Australia could not attend the meeting. An alternative speaker was selected by consensus. All invited speakers (John Abrams, Gwyneth Card, Bernardo Carvalho, Angela DePace, Angela Douglas, Rick Fehon, Liz Gavis, Bassem Hassan, Barbara Mellone, Mala Murthy, Aurelio Teleman, Hongyan Wang) committed by **June 2018**.

The 2019 organizers implemented several changes to the format for the first time stemming from suggestions from previous organizers and the 2016 Meeting Rejuvenation Committee Report (also see 2017 & 2018 reports, section on *Major changes/additions to the Meeting*). For 2019, the organizers decided to make a couple of changes to the 2018 format, based both on responses to a community survey that was sent out by GSA after the 2018 meeting and

suggestions by previous organizers. Specific changes that the 2018 committee made and were kept largely intact for 2019 include:

- Updates to Abstract Categories and Keywords
- PI Early Career Forum (re-named “New Faculty Forum”)
- Q&A sessions on peer-review and publishing
- Fundraising efforts by the Organizers
- Having Platform Sessions (i.e. the number of talks in each) roughly reflect the distribution of abstracts.

The 2019 committee did make a number of significant changes to the format.

First, we decided unanimously to rebrand the stand-alone “Techniques & Technology” Session as an independent Plenary Session with a mix of invited speakers and talks selected from abstracts. The organizing committee asked Hugo Bellen and Julie Simpson to chair this session. They agreed and recruited Lena Riabinina to help assist with their efforts. The three organizers independently invited potential speakers and the final list was presented to the organizing committee in **December, 2018**. The Techniques & Technology session is scheduled for the Saturday evening time slot, so not to conflict with other platform sessions.

This year, the organizing committee decided to replace one platform talk in each session with a round of “poster previews”, also known as “lightning talks” – 3-4 two-minute brief talks designed to highlight the chosen presenter’s poster. This was first recommended by one of last year’s organizers (Pam Geyer) and was enthusiastically embraced by some members of the committee who had attended other meetings where they occurred. This format appears generally well-received. There were several reasons for adding the lightning talks, with some potential drawbacks. After the meeting, we will be able to evaluate how successful and popular they were. For the majority of platform sessions and topics, there are many deserving abstracts submitted for which the presenter has requested a platform talk, but there are simply not enough slots to accommodate everyone. GSA meeting attendees are young consisting primarily of trainees and the fly meeting has a very large poster session. These short formats give the opportunity for more young scientists to highlight their work and entice people to view not only their poster, but all the posters. The organizing committee felt the lightning talks would be minimally disruptive and while taking away one 15-minute platform slot per session, would add 3-4 highlighted topics. The organizers, with the help of Suzy et al, gave very explicit instructions – two slides with minimal data (no animations), no questions afterwards. This could potential place an added burden on session chairs to keep this 15-minutes moving efficiently, however, they are at the end of the session to help keep them on time with the hope of not running over. And finally, we anticipate that the lightening talks will be fun – dynamic and fast at the end of the session when audience interest and focus may be flagging.

In **June-July 2018**, co-chairs for each Platform Session were nominated, discussed and decided by consensus. The co-chairs were then 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 2018**. The co-chairs of three sessions did not select a junior co-chair.

The abstract deadline was **November 15, 2018**. From the submitted abstracts, the Organizing Committee allocated the number of talks per Platform Session and sent the co-chairs guidelines for abstract review and talk selection. Co-chairs deliberated together to provide ranked lists of selected abstracts for talks, with the opportunity to review abstracts that listed the topic as a primary or secondary choice, by **December 10, 2018**. The Organizers reviewed the ranked lists to remove duplications across Platforms and to ensure diversity in presenter gender, career stage and individual laboratories represented. Final Platform talks were assigned by **December 18, 2018**.

2019 Fly Meeting Registration and trends

Pre-registration is **down by 17% compared to 2018**, with **1114 pre-registrants** as of March 6, 2019. For historical comparison, earlier Fly Meeting pre-registrations were: 1343 (2018), 1121 (2017), 997 (2016/TAGC), 1517 (2015), 1431 (2014), 1555 (2013), 1537 (2012), 1328 (2011), 1516 (2010), 1383 (2009), 1343 (2008), 1345

(2007). This downward trend is a concern and possible contributing factors are discussed in the GSA report to the Fly Board.

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. Everyone had to cover their own lodging and travel costs. The Larry Sandler Award Winner receives complementary airfare, registration, lodging, and GSA lifetime membership. Victoria Finnerty Memorial Fund travel grants were awarded to 14 undergraduate researchers presenting posters.

Detailed description of program components

Opening Session and Keynote Speaker. The 2019 Meeting will follow the traditional program on the first night, with introductions and a brief historical perspective, announcements from GSA, the Sandler lecture and a Keynote lecture.

Plenary Speakers. As in previous years, the criteria for choosing Plenary Speakers were scientific importance and novelty, breadth of topics, ability to engage the audience, and a balance in gender, career stage, and foreign/domestic location. In addition, we wanted to avoid inviting people who have presented plenary talks in the past. The 2017 report of the organizing committee noted that a concern was raised after the 2016 meeting because 8/12 speakers were non-US-based. This concern was discussed again at the 2018 Fly Board meeting. In addition, members of the Fly Board recommended that the 2019 organizers consider gender and ethnic diversity when selecting speakers. We made a sincere effort to consider these factors when making our final decisions. Plenary speakers are a diverse group that we believe reflect the *Drosophila* community; over half are female and 33% non-Caucasian. 50% of the speakers are senior investigators (e.g. full professors) and 67% are US-based. All twelve are first-time plenary speakers. We believe future organizers should continue to emphasize gender and ethnic diversity in their decision-making process. A number of plenary speakers made scheduling requests based on travel and teaching. These requests were accommodated.

Abstract Categories and Keywords. The 2019 Organizers collectively made the decision to merge or expand a number of specific categories. This reorganization resulted in 16 final abstract categories (versus 19 categories in 2018). The 2019 organizers elected to alter the composition of categories based on a number of factors, including the (1) number of abstracts in recent years, (2) anonymous suggestions made through the GSA survey sent out after the 2018 meeting, (3) suggestions from previous organizers and (4) direct requests by members of the community. First, a number of individuals independently approached both the 2018 and 2019 organizers requesting that the Microbiome Workshop be included in a platform session. Successful and highly attended workshops in this area over the last several years appeared to justify this request. We elected to pair this subject area with Immunity (previously paired with Cell Death) to create a new category called Immunity and the Microbiome. Next, we created a new category called Cell Stress and Cell Death, intended to include abstracts focused on autophagy and other stress response pathways with cell death. We believe that this represents closer subject pairing than combining Cell death with Immunity. Next, we combined “Evolution and population genetics” and “Evolution in Development” into one “catch all” category. We reasoned that this would give the session chairs the most flexibility in determining which abstracts to select for talks and how they should be grouped into the allotted sessions. We anticipated that this category would be given multiple sessions based on the number of abstracts received in recent years. We took a similar strategy with Models of Human Disease. As organizers, we sought to recruit two co-chairs who had complementary expertise in the different sub-areas of their categories (i.e. “Evolution and population genetics” and “Evolution in Development”; “Models of Human Disease: Neurodegeneration and Neurological Disorders” and “Models of Human Disease: Developmental and Physiological Disorders”). Next, we expanded the “Stem Cells” category from 2018 to include “Stem cells, regeneration and tissue injury”. We also expanded “Gametogenesis” to “Reproduction and Gametogenesis”. Finally, we decided not to have a stand-alone “RNA Biology” category. This category had the fewest number of submitted abstracts several years running. In addition, we reasoned that many of the abstracts directed to this category would be appropriate for “Regulation of Gene Expression”. Other categories remained unchanged. The 16 categories are also used for poster sessions. The **2019 Abstract Categories** are in **Table 1**.

Submitted abstracts. 832 abstracts were submitted under 16 categories and associated with keywords. Totals in recent years were 889(2018), 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, 2019 reflects an **6% decrease in abstract submissions over 2018**, in line with a decrease in pre-registrations in the same time period. There were **384 requests** in the primary category for **143 Platform talks**, which resulted in a **37% success rate**. This was slightly lower than the 38% success rate in 2018. However, we have introduced the new 2-minute lightning/poster preview talks at the end of each session, which in effect increases the number of speakers presenting at the podium. The number of total abstracts varied across sessions (see **Table 1**).

The highest number of abstracts was submitted in “Models of Human Disease”, with 91 abstracts as a primary choice. The lowest number of abstracts was in “Cell Stress and cell death”, with 24 abstracts as a primary choice. The corresponding categories from 2018 were “Physiology, metabolism and aging” (92 abstracts) and “RNA Biology” (18 abstracts). The fraction of abstracts in a given category that requested talks also ranged widely, from 64% in “Signal Transduction” to 38% in “Reproduction and Gametogenesis” (In 2018, the range was from 71% in “Stem Cells” to 38% in “Models of Human Disease: Developmental and Physiological Disorders”).

Table 1. Categories and abstracts submitted

Received	Request Platform	%Request Platform	Selected	% Selected	Poster	Session
24	15	63%	6	40%	9	01. Cell Stress and cell death
38	19	50%	7	37%	19	02. Immunity and the microbiome
84	44	52%	14	32%	40	03. Evolution
30	14	47%	6	43%	16	04. Stem cells, regeneration and tissue injury
60	23	38%	7	30%	37	05. Reproduction and gametogenesis
56	26	46%	9	35%	30	06. Regulation of gene expression
47	23	49%	9	39%	24	07. Chromatin, epigenetics and genomics
64	26	41%	13	50%	38	08. Patterning, morphogenesis and organogenesis
25	16	64%	6	38%	9	09. Signal transduction
50	22	44%	6	27%	28	10. Cell biology: Cytoskeleton, organelles and trafficking
36	14	39%	6	43%	22	11. Cell division and cell growth
76	31	41%	13	42%	45	12. Physiology, metabolism and aging
54	23	43%	9	39%	31	13. Neural development and physiology
52	24	46%	10	42%	28	14. Neural circuits and behavior
91	40	44%	14	35%	51	15. Models of human disease
36	20	56%	4	20%	16	16. Techniques and technology
9	4	44%	4	100%	5	17. Educational Initiatives
832	384				448	Total

Platform Session organization. Eight categories that had the most abstracts were given two split sessions (I & II). Individual sessions contained either 7 or 6 talks based on the organization of the day. “Evolution” and “Models of Human Development” received the most abstract submissions and were given 14 platform talks each (+ additional lightning talks), split into two sessions on different days. Next, “Patterning, morphogenesis and organogenesis” and “Physiology, metabolism and aging” were given thirteen talks each (+ additional lightning talks), which were also split into two separate sessions. “Regulation of gene expression” and “Chromatin, epigenetics and genomics” will each have one full 6 talk session and share one split session (3 talks each). “Neural development and physiology” and “Neural circuits and behavior” will also share one split session, in addition to their respective full sessions. The decision to pair these different sessions together was based on shared interests, and allowed us to include more talks in areas that received more abstract submissions. Eight categories were assigned a single session (6 or 7 talks; + additional lightning talks). “Techniques & Technology” has 8 talks, one fewer than in 2017, to fit into the new time slot on Saturday evening. Four of the talks were invited speakers and 4 were selected from the submitted abstracts. “Educational Initiatives” will be held Thursday evening and will feature four talks.

The 2019 Organizing Committee designated two co-chairs to each session. This is different from the practice of the 2018 organizers who assigned one chair, who, in turn, recruited a co-chair directly. The chairs were chosen for the scientific excellence but also to ensure diversity across many dimensions including gender, geography and institution type. The co-chairs were then given the choice of inviting a junior co-chair, typically a postdoctoral trainee or a new faculty, for each session. All but three sessions chose to do so. The reason for the junior researchers is to give them exposure, allow them to network and interact with more senior colleagues, and to help in judging the poster session. The 2019 **Platform Session co-chairs and junior co-chairs** who selected abstracts for Platform presentations are listed with affiliation by session in **Table 2**. A number of session chairs made scheduling requests based on travel and teaching. These requests were accommodated.

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 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, 2018. 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 Organizers ensured that there was a balance in gender and career stages of the selected abstract

Table 2. 2019 Drosophila Meeting Platform Sessions and Chairs

Session	Co-Chair	Co-Chair2	Junior co-chair
01. Cell Stress and cell death	Don Ryoo ; New York University School of Medicine	Gabor Juhasz ; Eotvos Lorand University	Tamas Maruzs ; Biological Research Centre, Hungarian Academy of Sciences
02. Immunity and the microbiome	Nichole Broderick ; University of Connecticut	Neal Silverman ; University of Massachusetts Medical School	
03. Evolution	Amanda Larracuente ; University of Rochester	Erin Kelleher ; University of Houston	Emily Behrman ; Janelia Research Campus
04. Stem cells, regeneration and tissue injury	Susan Parkhurst ; Fred Hutch	(Lucy) Erin O'Brien ; Stanford University School of Medicine	Mitsutoshi Nakamura ; Fred Hutch
05. Reproduction and gametogenesis	Hilary Ashe ; University of Manchester	Erika Bach ; New York University School of Medicine	Salvador Herrera ; New York University School of Medicine
06. Regulation of gene expression	Michael Eisen ; University of California, Berkeley	Scott Barolo ; University of Michigan	
07. Chromatin, epigenetics and genomics	Xin Chen ; Johns Hopkins University	Erica Larschan ; Brown University	Leila Rieder ; Emory University
08. Patterning, morphogenesis and organogenesis	Jennifer Zallen ; Sloan Kettering Institute	Juan Riesgo-Escovar ; Universidad Nacional Autónoma de México	
09. Signal transduction	Jessica Treisman ; NYU School of Medicine	Ken Moberg ; Emory Univ School of Medicine	Helen Attrill ; University of Cambridge
10. Cell biology: Cytoskeleton, organelles and trafficking	Elizabeth Chen ; UT Southwestern	Blake Riggs ; San Francisco State University	Donghoon Lee ; UT Southwestern Medical Center
11. Cell division and cell growth	Savraj Grewal ; University of Calgary	Mary Lilly ; NICHD	Yingbiao Zhang ; NICHD
12. Physiology, metabolism and aging	Akhila Rajan ; Fred Hutch	Tânia Reis ; University of Colorado Medical School	Elizabeth Rideout ; University of British Columbia
13. Neural development and physiology	Karen Chang ; University of Southern California	Robin Hiesinger ; Free University Berlin	Laura Alto ; UT Southwestern Medical Center
14. Neural circuits and behavior	William Joiner ; University of California, San Diego	Ellie Heckscher ; University of Chicago	Yi-Wen Wang ; University of Chicago
15. Models of human disease	Rolf Bodmer ; Sanford Burnham Prebys Medical Discovery Institute	Juan Botas ; Baylor College of Medicine	Georg Vogler ; Sanford Burnham Prebys Medical Discovery Institute
16. Techniques and technology	Hugo Bellen ; Baylor College of Medicine	Julie Hayner Simpson ; UCSB	Lena Riabinina ; University of Manchester, UK

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. We followed the rule that no one lab would present more than two platform talks, and these two talks would be in different sessions.

Poster Sessions. There are currently **689 abstracts** scheduled to be presented as posters. There were 832

abstracts submitted in total, including the 143 abstracts selected for Platform talks. Late abstracts were accepted through **February 1, 2019**. 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). This remains the same from the 2018 meeting. Postdoctoral poster awards will not be given, since several of the judges are the Postdoc trainees functioning as Platform Session co-chairs. Awards will be given based on merit only, so there is the option that fewer than six awards will be given. The prizes are \$500 for 1st place, \$300 for 2nd place and \$200 for 3rd place.

Based on the recommendations of the previous organizers and GSA and what was done in 2018, posters will be judged initially by the junior co-chairs and other post docs who have volunteered to help judge to select the best posters in their group. 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 instead of the entire group in that category. The selection will be based on science and poster design, not on the poster presentation, given the time constraints of the meeting. The judges will communicate the recommended posters for each session to Michael Buszczak by Friday. All 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 examine the winning posters during the final poster session on Saturday afternoon. The winners will be recognized after the Technology and Techniques Plenary session Saturday evening.

Workshops. Workshop applications and selection criteria were similar to past meetings. Thirteen applications were received and reviewed. One application, “Drosophila Polytene Chromosome Protocol for Undergrad Labs”, was viewed as impractical for the venue and rejected. Two of the workshop applications, “Using Drosophila to bring authentic course-based undergraduate research experiences (CUREs) into the undergraduate classroom” and “Design a CRISPR-Cas9 undergraduate lab course to generate knock-in alleles for the research community”, went to the education committee for consideration of whether they should be combined into one. In the end, they were kept separate in the final program. The other ten applications were approved. In addition, GSA will present a career-oriented Workshop for a total of twelve listed Workshops. The Organizers scheduled Workshops at times in the program to avoid parallel Workshops covering overlapping interests. The two major Workshop Sessions will be Thursday night 7:45- 9:45 PM and Friday afternoon 2:15- 4:15 PM. The Ecdysone Workshop, which will take place at its historic pre-meeting time on Wednesday 2:00-5:00 PM.

Workshops listed in order of the program: (1) Ecdysone Workshop (Wednesday); (2) Spotlight on Undergraduate Research (Thursday); (3) Equity and inclusion in the Drosophila Research Community (Thursday); (4) Lipid Signaling in Drosophila (Thursday); (5) Everything you ever wanted to know about sex (Thursday); (6) Intro to the Drosophila microbiome: How can I control the microbiome research (Thursday); (7) Design a CRISPR-Cas9 undergraduate lab course to generate knock-in alleles for the research community (Thursday); (8) Collaborating with clinical researchers: expanding opportunities for Drosophila biologists in rare disease diagnosis and therapeutic research (Friday); (9) Feeding behavior, nutrition and metabolism; (10) Developmental mechanics (Friday); (11) Using Drosophila to bring authentic course-based undergraduate research experiences (CUREs) into the undergraduate classroom (Friday); (12) Maximize the impact of your curriculum vitae and resume workshop.

In previous years, workshop requests were hard to accommodate because of limited space. Several workshops have become somewhat institutionalized (Ecdysone, sex, feeding, PUI, etc.). There was some discussion about this last year and it may be something for additional discussion (i.e. – should some become platform sessions? Should some be every other year? Should there be a different evaluation system for the workshops? Ranking? Etc.) This year, the organizers agreed that workshops should not be de facto platform sessions by another name. We included instructions in the workshop application that the applicants should explain what added value the workshop would bring to the meeting. In addition, we emphasized that workshops should foster interactions between participants. All the applications made some effort to address these points.

PI Early Career Forum. This new event was created in 2017 among concerns that “while certain (older) 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 foster community-building while also helping young PIs start their career. The 2017 & 2018 events were well-attended (49 (2017) & 36 (2018) registered attendants). The 2019 event is being organized by Sonia Hall of GSA. A report from Sonia is included in the report from GSA.

Science Slam. We elected not to repeat Science Slam, which began in 2017. Several members of the 2019 committee attended the event in 2018 and were disappointed by the turnout and participation.

Several other special events were considered, including a Saturday night music concert and a fun run to be scheduled one morning before the start of events. Logistical and financial considerations made these events impractical. However, opportunities to include similar types of enhancements should be considered for future meetings.

Fundraising

The organizing committee generated a fund-raising letter modeled after the one used last year. MB obtained a list of local vendors/ representatives in the Dallas area from a colleague at UT Southwestern. MB e-mailed a request for sponsorship letter to these representatives. Members of the GSA office authored a second Request for Sponsorship letter. This letter was sent out to over 60 scientific product companies through MB’s e-mail account. GSA hired Sponsorship Boost to try to enhance our fund-raising efforts. MB also contacted the Center for Regenerative Science and Medicine (CRSM) and the Associate Dean for Graduate studies at UT Southwestern Medical Center. Both elected to sponsor the meeting. MB also contacted Max Guo at NIA. In the past, the NIA has directly paid for the A/V vendor of the Physiology, Metabolism and Aging session. Max asked whether NIA could be actively involved in selecting abstracts for platform talks. By the time of this request, the session chairs had already selected the talks. This list, along with a second list of other aging-related abstracts submitted to other sessions, was sent to Max. In the end, NIA provided funds for the meeting. Harmit Malik (HM) contacted a number of journals including PLoS, which elected to provide sponsorship funds. David Bilder was able to secure sponsorship funds from Genesee Scientific to cover the cost of a poster, designed to commemorate the 15th annual image award competition and the 60th annual Drosophila Conference. This poster will be provided to every attendee of the meeting. In total, we were able to secure funds from 7 different sponsors.

Planned assistance to future Drosophila Conference Organizing Committees

All of the material available to the 2019 organizers will be placed in a Dropbox folder. The chairs of future organizing committees 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 suggest the following aspects of this year’s conference to be evaluated for future conferences.

- Abstract categories: Further tuning may help to adjust the categories to emphasis new developments (e.g. in metabolism, single cell techniques, and improved imaging methods or new developments in understanding diverse fly behaviors)
- Lightning Talks: An experiment that has proven successful in smaller, more focused meetings; we hope they will work as well for the fly meeting with its concurrent sessions. GSA should gauge the success of these lightning talks through post-meeting surveys.
- Technology Plenary session: We believe a major topic that brings Drosophila researchers with distinct interests back to the fly meeting (as opposed to specialty meetings) is a shared interest in new technological developments. We expect therefore that this new stand-alone plenary session should prove popular.

- Workshops: We attempted, by means of application instructions, to steer people away from de-facto specialty podiums session towards more integrated formats with the goal to foster interactions and discussions. Hopefully, implementation will follow this spirit.
- Encourage more participation by early stage investigators/ trainees. Workshops organized by the GSA (grant writing, new Faculty Forum) and inclusion of postdocs as session chairs and poster judges are aimed to entice the continued participation of early stage investigators at the fly meeting. We think this is vital for the future of the meeting.
- This year we had a number of last-minute cancellations by platform speakers which created some organizational problems. We propose that speakers should have to register for the meeting within 3 weeks of notification. If speakers do not meet this deadline, his/her place will be lost and given to the next person on the priority list.

Appendix 2. Sandler Lectureship (Daniel Barbash)

Report on 2019 Larry Sandler Award

2019 Committee:

Daniel Barbash (Chair)

Leslie Griffith

Barbara Mellone

Benjamin Ohlstein

Luis Teixeira

2020 Chair: Barbara Mellone

Process:

The committee received **27 nominations**, a large increase over last year's total of 19. Shortly before the deadline the Chair asked several prominent colleagues to send reminders out on Twitter, which may have helped increase the number of nominations.

We ranked applicants using a 4-point voting system, and then met via Zoom to discuss, focusing on the top 6. From these, we chose 3 to review further by reading the full theses. We then again met by Zoom to choose a finalist. After brief discussion, we settled on a unanimous winner. After more extensive discussion, we decided to consider the remaining two as co-runner-ups.

2019 winner: Dr. Laura Seeholzer, Ph.D. Rockefeller University (mentor Dr. Vanessa Ruta)

Student supplied abstract:

Animals display an extraordinary diversity of behavior both within and between species. While there is increasing insight into how learning and experience modify neural processing to produce variations in individual behavior, far less is known about how evolution shapes neural circuitry to generate species-specific responses. Cross-species comparative studies have identified genetic loci that explain behavioral diversity, but only rarely examined the neural substrate upon which this genetic variation acts.

In my Ph.D., I studied rapidly evolving species-specific *Drosophila* courtship behaviors as a model system to understand how nervous systems evolve to underlie behavioral adaptation. Several species in the *Drosophila melanogaster* subgroup exhibit pre-mating isolation due, in part, to the fact that *D. melanogaster* females produce 7,11-heptacosadiene (7,11-HD), a pheromone that promotes courtship in *D. melanogaster* males but suppresses it in *D. simulans*, *D. yakuba*, and *D. erecta* males. I compared pheromone-processing pathways across species to define how males endow 7,11-HD with the opposite behavioral valence to underlie species discrimination.

Drosophila males rely on sensory neurons in their foreleg tarsi to taste cuticular pheromones. Surprisingly, we found that *D. melanogaster* and *D. simulans* males use an anatomically and functionally conserved population of ppk23+ sensory neurons to detect 7,11-HD, suggesting that species-specific behaviors were not due to changes in the sensory periphery, a commonly described mechanism of behavioral adaptation. Instead, since optogenetic activation of ppk23+ neurons promotes courtship in *D. melanogaster* males but suppresses it in *D. simulans* males, we hypothesized there must be changes in the central neural circuits that process 7,11-HD.

In *D. melanogaster*, 7,11-HD activates courtship-promoting P1 neurons; a neural population we found also promotes courtship in *D. simulans* males. Further, 7,11-HD signals in both species equivalently propagate to neurons that form a feed-forward inhibitory circuit onto P1 neurons. However, while in *D. melanogaster* males this feed-forward inhibitory circuit drives net excitation of P1 neurons to

promote courtship towards conspecific females, we found that in *D. simulans* males the inhibitory branch onto P1 neurons is capable of suppressing the excitatory branch. Thus, a change in the balance of excitation and inhibition onto courtship-promoting neurons transformed an excitatory pheromonal cue in *D. melanogaster* into an inhibitory one in *D. simulans*. My results reveal how species-specific pheromone responses can emerge from diversification of central circuitry and suggests that evolution can exploit flexible circuit nodes to generate behavioral variation.

To explore the neural basis of parallel behavioral evolution, I also began characterizing the pheromone processing pathways in *D. yakuba* and *D. erecta* males, two species that derived their aversion to 7,11-HD independently from *D. simulans* males. Interestingly, preliminary analysis hints that both species also rely on changes in central circuit processing to suppress courtship towards *D. melanogaster* females. Together, these studies represent one of the first systematic comparisons of neural circuits across *Drosophila* species and mark a new advance in the study of behavioral evolution by revealing how changes in central circuitry can alter discrete behaviors.

2019 co-runner-ups:

Dr. Amy Strom, UC Berkeley (Mentor Dr. Gary Karpen)

Dr. Julianna Bozler, Dartmouth Medical School (Mentor Dr. Giovanni Bosco)

Comments and suggestions on selection process.

The process ran similarly to previous years, although a bit behind schedule. Also, the Chair (Barbash) forgot to distribute the suggested information on gender bias to the committee; he will make sure to forward that information to next year's Chair. Despite that, the top 6 scoring nominees were all women.

The Committee all felt that the process ran smoothly. In particular, they felt that once seeing the full theses, the relative strengths and weaknesses became clear, despite all of them representing excellent work.

The Committee did feel that choosing the initial shortlist was more challenging, due to the relatively little information available from the initial nomination process. One possible change would be to request more letters of recommendation. Another possibility would be to ask the PIs to be more specific in their nomination letters, to address defined questions such as: describe the process of how this project was chosen by the student; address the specific role(s) of other co-authors; explain the significance of the student's work in the context of your larger research program. Similarly, it might be beneficial to ask the students to fill out a ~1 page information sheet where they explicitly describe the background and significance of their thesis. A concern about these suggestions though is that any additional effort required might reduce the number of nominations.

Other ideas were briefly discussed, such as Skype interviewing the short-listed nominees. However this idea raised significant concern that it would inappropriately lead to a focus on personality and interview skills, rather than scientific contributions. Reviewing more of the full theses was also rejected due to the significantly increased work load.

Nominees for 2019

Anreiter_Ina	F	Marla B. Sokolowsk	F
Bozler_Julianna	F	Gio Bosco	M
Brand_Cara	F	Daven Presgraves	M

Chen_Jun	F	Rongwen Xi	M
Deady_Lylah	F	Jianjun Sun	M
Geissmann_Quentin	M	Giorgio F. Gilestro	M
Hope_Matthew	M	Ilaria Rebay	F
Johnson_Matthew	M	Michael Welte	M
Kelpsich_Daniel	M	Tina Tootle	F
King_Anna	F	Amita Sehgal	F
Li_Josh	M	Sean Millard,	M
Li_Liyang	F	Kausik Si	M
Liang_Xitong	M	Paul Taghert (sent late)	M
Luo_Junjie	M	Craig Montell	M
McLaughlin_Colleen	F	Heather Broihier	F
Ordonez_Dalila	F	Mel Feany	M
Palmer_William	M	Darren Obbard	M
Parhad_Swapnil	Mw	Bill Theurkauf	M
Reimao_Pinto_Madalena	F	Stefan L. Ameres	M
Schaefer_Kristi	F	Mark Peiffer	M
Seeholzer_Laura	F	Vanessa Ruta	F
Seller_Chuck	M	Pat O'Farrell	M
Strom_Amy	F	Gary Karpen	M
Suisse_Annabelle	F	Jessica_Treisman	F
Watanabe_Louis	M	Nicole Riddle	F
Xu_Jiajuie	M	Rick Fehon	M
Zulueta-Coarasa_Teresa	F	Rodrigo Fernandez-Gonzalez	M

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Email to rejected nominations: Thank you for nominating your student for the 2019 Larry Sandler Award Memorial Award. We had an extremely strong pool of 27 applications this year, and it was a challenging process for the committee to choose a winner. I am sorry to tell you that your student was not selected. On the behalf of the committee, I thank you for taking the time to support your excellent student and for helping to keep the Sandler Award selection process a true reflection of the breadth and strength of Ph.D. research in our community.

Email to winner:

Dear Dr. Seeholzer,

On behalf of the 2019 Sandler Award Committee, I am delighted to inform you that you have been selected as the recipient of the 2019 Larry Sandler Memorial Award!

As you no doubt know, the goal for this award is to identify the "best" Ph.D. thesis in Drosophila research from the previous year. In this round we had 27 nominations, which made the competition extremely tight. The committee unanimously felt that your beautiful work on "Neural Circuit Mechanisms Underlying Behavioral Evolution in Drosophila" stood out as especially significant and deserving of this recognition. It also helped that we received very strong and supportive comments from your advisor, Dr. Vanessa Ruta. Many congratulations on executing this spectacular set of experiments and on a superb thesis.

As the recipient of this award, you will have the honor of presenting your thesis work in the Larry Sandler Memorial Lecture on Mar 27th, the opening night of the 60th Annual Drosophila Research Conference in Dallas, TX. You will give your plenary lecture in front of the entire fly community present at the meeting. In addition to sharing your work with the field, we hope that your talk will help to inspire other students just starting or in the midst of their Ph.D.s. Ms. Suzy Brown (cc'ed here) of the GSA will be touch to make (and pay for) your travel arrangements to Dallas. ?Again, please accept our warmest congratulations. You now join a long list

of excellent scientists who have gone on to have successful careers (<http://conferences.genetics-gsa.org/drosophila/2019/conference-and-travel-awards>).

The Sandler Award winner has traditionally been presented as a surprise to the community, therefore please wait until you have received the award to make any public announcements.

Please don't hesitate to let me know if you have any questions as you prepare for your talk in Dallas. I look forward to meeting you in person in March.

Sincerely,

Daniel Barbash (Chair)
Leslie Griffith
Barbara Mellone
Benjamin Ohlstein
Luis Teixeira

Email to runner-ups:

Dear Julianna,

I am writing to inform you that you have been selected as one of two Runners-up for this year's Larry Sandler Memorial Award.

Although you are not the winner for this year's award, I nevertheless want to congratulate you for executing a spectacular thesis. This year's competition was intense: we received 27 nominations, several of which were truly outstanding and deserving of the Larry Sandler Award. The committee struggled to narrow this down to even a top three. We truly enjoyed reading about your work and accomplishments and have no doubt that you will continue to do superb research in the future. I should add that your advisor was extremely supportive and said glowing things about you and your work.

On behalf of this year's Sandler Award Committee, we congratulate you on being selected as a Runner-up, and wish you the very best of luck for continuing success. Suzy Brown of the GSA will be in touch with you soon regarding your complimentary conference registration.

Best wishes,
Daniel Barbash (Chair)
Leslie Griffith
Barbara Mellone
Benjamin Ohlstein
Luis Teixeira

FlyBoard Report from GSA

59th Annual Drosophila Conference

A total of 1,455 (paid) people attended the 59th Annual Drosophila Research Conference in Philadelphia in 2018. GSA Executive Director Tracey DePellegrin and other GSA staff worked with the meeting organizers to modify the conference survey to elicit actionable items and, in doing so, also doubled the response rate from previous years. This survey format will be used across all GSA meetings to help inform ways to make the conferences more valuable to potential audiences.

Some of the important feedback from the survey includes:

- When asked about their overall assessment of the meeting, 11% reported that it greatly exceeded expectations; 38% reported that it exceeded expectations; 47% reported that it matched expectations.
- 80% thought that it would be okay to hold workshops and platform sessions concurrently, provided that the topics do not overlap and the number of concurrencies are kept to a minimum.
- Nearly half the respondents were not able to attend all the workshops that they wanted to attend because they were scheduled concurrently with other workshops.
- Nearly 70% thought the mix of platform sessions to workshops was "about right."
- Approximately 50% either agreed or strongly agreed that there should be more dedicated poster time.
- 42% indicated that they would like more professional development programming.
- 92% visited the posters (while the posters were attended).
- 90% "learned information that may inspire my own science."
- 85% "had a science-related conversation with someone I'd never met."
- 68% "met colleagues with whom I may likely form collaborations."

Current registration and abstract stats

Attendance for the 60th Annual Drosophila Research Conference is down compared to last year as well as previous recent years. Attendance is also lower compared to other recent GSA Conferences. We first identified lower attendance as a concern when abstract submissions at the original deadline were less than expected. The deadline was extended for poster submissions, and that provided an increase in total abstracts. E-mail and social media marketing efforts were increased, with a focus on encouraging attendance by locals and researchers outside the fly community. FlyBase and many others in the fly community provided additional targeted assistance to get the message out. Despite these efforts, however, registration numbers remain lower than usual.

An analysis of registrants by region suggests that the 2019 meeting location is a substantial contributor to lower registration numbers (Figure 1). For all years, registrants living near the meeting site attend in greater numbers, but that local effect has been much larger for previous years than it is for Dallas. It seems highly likely that other meeting locations drew more local and regional attendees from larger population centers. That is good news in that it can explain the worrying numbers from this year, but it also highlights the fact that the attendee pool is clearly stagnant. Meeting attendance does not seem to grow; it is just shuffled according to location and timing. (Note that reduced attendance in 2017 was likely due to the summer timing of TAGC16, which took place only a few months before the abstract deadline for ADRC 2017.)

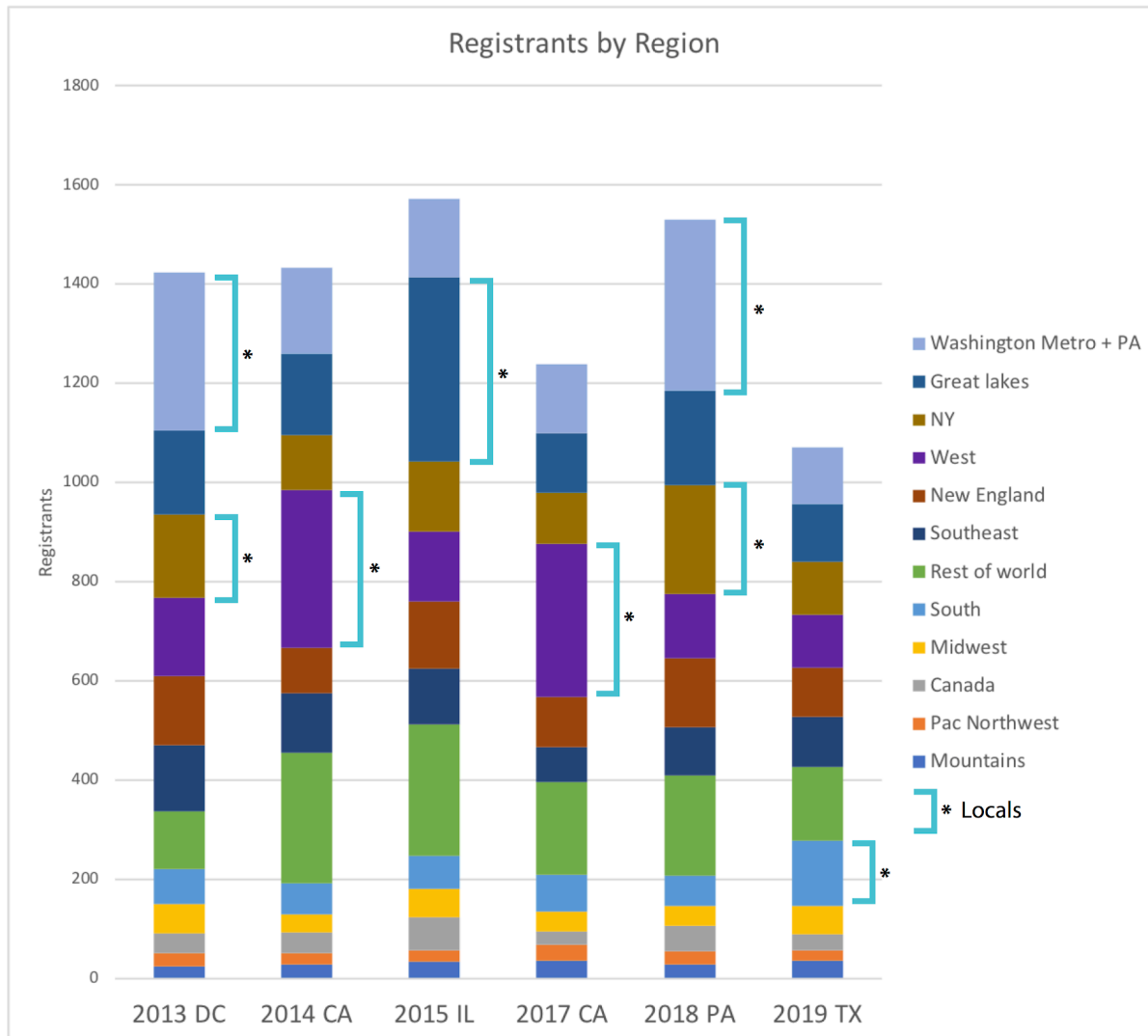


Figure 1: ADRC registrants in recent years, excluding The Allied Genetics Conference 2016. Registrant addresses were categorized into US OMB ten standard federal regions, Canada, or Rest of the World (i.e., locations outside of the US or Canada). Regions within driving distance of the conference location are indicated with an asterisk. We gave the federal regions brief nicknames to make it easier to interpret the graph:

New England: Region I — Connecticut, Maine, Massachusetts, New Hampshire, Rhode Island, Vermont

New York: Region II — New Jersey, New York, Puerto Rico, US Virgin Islands

Washington Metro + PA: Region III — Delaware, District of Columbia, Maryland, Pennsylvania, Virginia, West Virginia

Southeast: Region IV — Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, Tennessee

Great Lakes: Region V — Illinois, Indiana, Michigan, Minnesota, Ohio, Wisconsin

South: Region VI — Arkansas, Louisiana, New Mexico, Oklahoma, Texas

Midwest: Region VII — Iowa, Kansas, Missouri, Nebraska

Mountains: Region VIII — Colorado, Montana, North Dakota, South Dakota, Utah, Wyoming

West: Region IX — Arizona, California, Hawaii, Nevada, American Samoa, Guam, Northern Mariana Islands

Pac Northwest: Region X — Alaska, Idaho, Oregon, Washington

To explore some of the other potential reasons for the flat or declining trend in attendance, we initiated a series of one-on-one conversations with leadership and past organizers, who suggested explanations including:

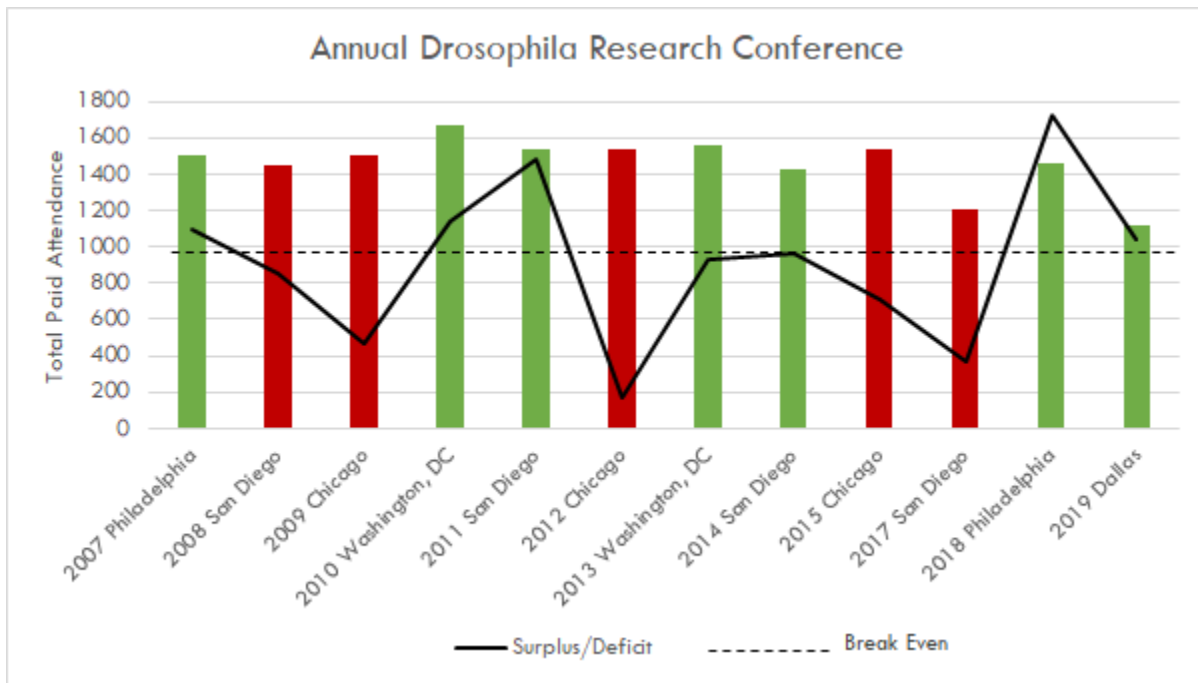
- Preference for smaller meetings
- Labs no longer identify solely as a *Drosophila* labs (some of that relates to access to funding)
- PIs no longer send their “whole lab” to the fly meeting.
- Long- time fly researchers are starting to retire and the focus is shifting away from a specific organism to a more topical approach to research.
- Competing meetings are becoming more attractive (i.e. CSH Neurobiology of *Drosophila*)

Lower attendance can also pose a fiscal challenge. While GSA is responsible for any financial risk associated with the meeting (since the \$164,000 reserve was returned to the fly community at the end of 2017), shrinking attendance numbers almost certainly increase this risk.

The finances of scholarly conferences are complex and highly variable, and ensuring a positive return depends on multiple factors, including: attendance (which in turn is influenced by location, airfares, driving distance from home or institution, whether location is seen as an attractive destination, hotel rates, venue), hotel or venue expenses (there are hundreds, but see below for examples of Audiovisual (AV costs) including costs for food and beverage, special events, hiring of required security, registration personnel, meeting room and exhibit space rentals; insurance; staff time; posterboards; fees charged for credit card usage, and advertising. The revenue side includes sponsorship and exhibit fees, registration fees, advertising, and abstract submission fees, and any minimal charges designed to offset special event costs (charges do not cover costs, but simply offset catering or rental).

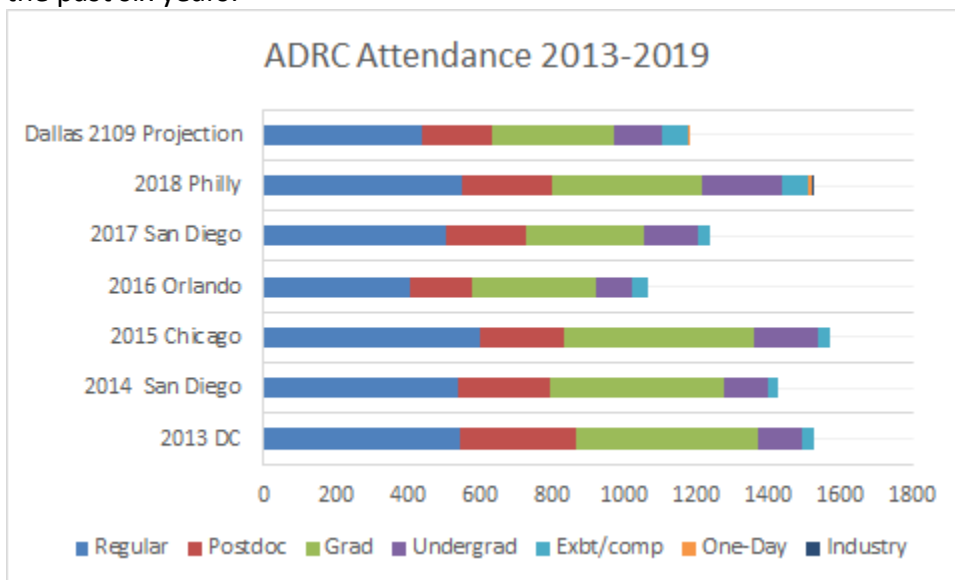
To illustrate, some major expenses, such as A/V, are the same regardless of the number of people. Increased attendance spreads this expense over a greater number. Another example, which GSA is faced with this year, due to lagging registration numbers, is the potential for attrition penalties. Attrition is a contract clause that represents GSA’s guarantee to the hotel that attendees will purchase or use a certain number of sleeping rooms. In return, the hotel may offer special concessions and a lower guest room rate. But if our actual sleeping room numbers fall below our contractual commitment, then an attrition penalty is typically charged. Lower attendance, then, means we may not meet our contractual commitment on our sleeping room block, which means a financial penalty for GSA. This year, GSA was facing having to pay upwards of \$40,000 in penalties. After much negotiations, we feel confident that this penalty will be waived, but regardless, that specific penalty is not our main concern and doesn’t need to be yours. But it does mean that GSA and FlyBoard need to continue to innovate to make the conference one that cannot be missed. And if the landscape is changing for this type of meeting, we need to understand why and what the future holds.

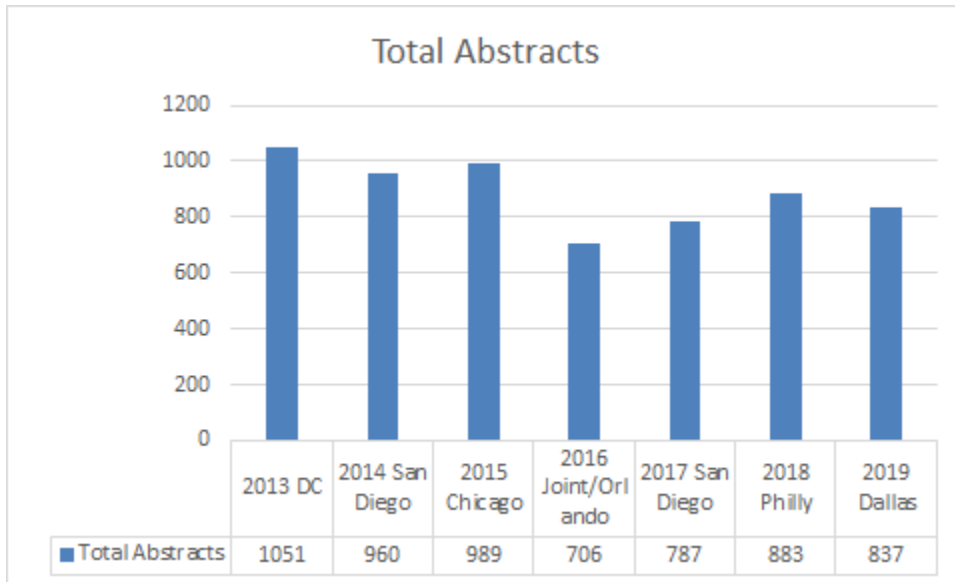
The following chart illustrates attendance by meeting and whether the meeting received a surplus or deficit.



Scientific conferences continue to evolve in response to community needs. As part of GSA’s ongoing strategic planning efforts and because GSA Conferences are a defined Pillar (core part) of GSA’s strategic framework, in 2019-2020 we will conduct research into each our community meetings. This will include collecting satisfaction and attendance information for attendees and non-attendees, a competitive analysis (of other meetings), discussions with stakeholders, and other data. We’ll share this data with community leaders to form a plan together about how to keep your meetings healthy, robust, and operating in accordance with your own goals and missions. We want to look into the future, including formulating short, medium, and longer-term plans.

The following graph depicts additional data relating to conference attendance and abstract submissions for the past six years:





Conference Rejuvenation Committee (2016)

In 2016 Howard Lipshitz, Denise Montell, and Leanne Jones were appointed by then President David Bilder to form an ad hoc committee and provide recommendations to rejuvenate the Drosophila conference. Full information on the results and recommendations can be found at beginning on page 18 here:

https://wiki.flybase.org/mediawiki/images/c/c2/2016_FlyBoard_Meeting_Minutes.pdf.

The committee had the following recommendations, reproduced here from the 2016 report. Items in blue are updates that have been made to the conference since then. Text in italics is taken directly from the report, and includes direct quotations. The information covered below may inform strategic discussions about future Drosophila conferences.

For PIs

- *Social event for PIs/communication with the board: A reception for PIs to meet with the Board (at the hotel, pay ahead with registration) — catch up with colleagues and have a discussion with Board members. This could be held after the Board meeting and before the opening session.*
- *Lunch with Postdocs/students (students register ahead of time to have lunch with PIs/speakers from the meeting)* **This is being done as a community building lunch with topical tables led by PIs and other leaders.**
- *Make the meeting effective for recruiting students/postdocs: Journal-sponsored “Meet Up lounge?” Market this feature to PIs.*
- *Add more opportunities to talk: Replace historical session (which has gotten stale) with an up-and-coming PI plenary session and/or make the workshops more prominent. We discussed the need to work in some quality control to the workshops if they become more prominent. **The historical session has changed; at times it is a panel discussion and other times it is a keynote speaker, as is the case this year with Mariana Wolfner.***

For trainees

- *Lunch with PIs* **This is done through the Community lunch.**
- *Career development session (non-academic careers)* **CV/Resume Workshop**
- *Social event (dance party hosted by a company? Zeiss? Genesee?)*
- *Hold a plenary session in which 3-4 Sandler Award finalists speak*

- Create a “big sib” program so newcomers know someone
- **New Faculty Forum**
- **Grant Funding Workshop**
- **Poster Invitations**
- **GENETICS Peer Review Workshop**

For all attendees

- *Many people (PIs and students) would appreciate more opportunities to present their work. Yet some people don't like too many concurrent sessions, and the schedule is already so compressed that it is hard to find time for social events with lab members, so there are certainly challenges to this. Eliminating the historical session (or holding it only every 5 or 10 years when there is a good reason to do it) is one way to gain another plenary session. Other than that, offering some very short “flash” talks to advertise posters might be an option. **Poster preview talks will be happening in each session this year.** Another possibility would be to add a “Doorstep” meeting on a specialized topic for one day or ½ a day prior to the opening of the meeting. ASCB is trying this this year: <http://www.ascb.org/doorstep/>. The Ecdysone Workshop is a micro example of this, but one could hold a Drosophila Neuroscience doorstep meeting or a Cancer Biology of Drosophila meeting or some other topic-oriented meeting. This could change each year to bring a little small/topic-oriented flavor.*
- *Re-vitalize the topics for posters and concurrent sessions (e.g., “mandatory” change of at least 20% of session topics each year) **Changes were made to reflect submissions in the previous year.***
- *Introduce a Grad Slam competition along the lines of the one that The University of California holds annually <http://www.graddiv.ucsb.edu/profdev/grad-slam>. It starts with each campus holding preliminary rounds of competition to identify the best grad student 3-minute presentation about their research. Each campus then holds a final round. The winners from each campus go to a UC wide competition. Leanne and Denise have attended these events and find them inspiring. There is significant prize money attached (the UCSB winner this year won \$5,000 and is a fly person). **The ScienceSlam was introduced in 2017 and repeated in 2018. It is not scheduled for 2019.***
- *Better social media presence - We discussed pros and cons of this. Young people might get more engaged. Some people might worry about their unpublished results appearing on Twitter and Facebook. But those are always concerns with or without social media when presenting unpublished work at conferences. The Social media presence is stronger than in previous years. **GSA staff live tweet the meeting and encourage attendees to tweet about sessions, except in cases where the speaker opts out.***
- *Food/drinks at poster sessions **Opening reception is now held with posters and a cash bar is available at night during posters.***
- *A major benefit of the model organism meeting is the techniques session, which is usually overflowing. This should probably be a plenary session with nothing running concurrently. **This session is being held as a plenary session this year.***

David Bilder had related questions and suggestions as an addendum to the minutes, to which the Committee responded specifically. This can be found at:

https://wiki.flybase.org/mediawiki/images/c/c2/2016_FlyBoard_Meeting_Minutes.pdf beginning on page 20.

FlyBook

FlyBook continues to serve as an excellent resource to the community, thanks to the dedicated editors who recruit and oversee the review of chapters for each section! To date, 30 of the 50–60 expected chapters have been accepted for publication. Additionally, a new section has been added, “Parasites, Viruses, and Microbiomes,” which will be headed by Dr. Bill Sullivan, who will begin to commission chapters in the coming year. Finally, the *GENETICS* site has been updated with a new format and organization of FlyBook chapters.

Special Programming (Professional Development)

2018 Special Event Summary:

New Faculty Forum

Attendees: 35 registered (18 postdocs, 17 faculty)

The goal for 2018 was to provide meaningful interactions with established faculty and peers while also providing useful information related to laboratory budgeting, curriculum design and development, and best practices for running a research lab.

What were the three most striking things that you learned?

Lab management – general (11), use of active learning (11), lab management – budgeting (9), tips for training trainees (7), recognition of shared experiences (6), lab management – personnel (4), improved sense of community (3), networking (3), identified new resources/techniques (2), identified community support (1)

What did you find most helpful about today’s workshop?

Networking (8), discussion with established investigators (7), active learning (5), community building (3), general advice (2), budgeting advice (2), career development (2)

Example Comments:

“Good advice for new PIs, I wish I attended sooner!”

“the scientific talks didn’t fit with the rest of the schedule.”

“A great workshop”

“thank you”

***GENETICS* Peer Review Workshop**

Attendees: 25 registered (11 grad students, 9 postdocs, 5 regular members)

This four hour, 2-part workshop introduced participants to the principles and best practices of scientific reviewing. In part one, the participants worked in small groups, guided by a facilitator, to review a manuscript. Participants chose between three different papers from different sub-disciplines so that they could pick the paper most relevant to their scientific expertise. Participants began by dissecting the manuscript to identify the author’s main claims, evaluate the data analysis and figures, and critique the writing and scholarship. These interactive activities were followed by time for each participant to individually draft a “typical” review,

including a summary and major and minor points. As a group, they wrapped up the first session by evaluating whether their requests for the author were realistic.

In part two, the participants returned to their groups to compare their reviews to evaluate the strengths and weakness of their reviews and identify areas for improvement. The participants were then joined by the Editor in Chief of *GENETICS* and four *GENETICS* editors (including Senior Editors). The editor in chief of *GENETICS* gave a 10-minute presentation to discuss review best practices, and then facilitated a panel discussion with editors to answer questions from the workshop participants about the role of the editor, reviewer workflow, determining *GENETICS* and *G3* journal scope.

What were the three most striking things that you learned? (from 3 or more respondents)

Strategy/approach for reviewing (10), role of reviewers/editors/staff (6), effective reading of manuscript (5), writing of review (5), process of peer review (4)

What did you find most helpful about today's workshop? (from 3 or more respondents)

Strategy/approach for reviewing (5), interactive activity (5), process of peer review (3), effective reading of manuscript (3)

Did this workshop take you beyond what you already knew?

Yes (11), No (1)

Participants reported learning growth in understanding a strategy to use to approach reviewing a manuscript and the process of how a manuscript moves from submission to publication.

Example comments:

"real reviewers would benefit from more structure such as was taught here"

"it helped to have a bad paper and really get into how to write a review to help the authors do better"

"it gave me a plan when reading papers"

"... also gives me guide posts for writing my own papers"

"it has taught me not only how to review but how to make a reviewer's job easier"

"I have some experience with reviewing, so I was expecting bit more from the process"

"it was great"

"I'm really happy you have started offering this workshop"

"it was useful and fun – thank you"

"I learned a lot about the interplay/history of different journals and their relative impacts."

"panel discussion and breakout tables were great!"

Community, Connections, and Lunch

Attendees: 167 registered

Event Summary:

This year, we redesigned the optional lunch event available at the *Drosophila* conference. To increase participation in this event, we worked to identify ways to make the experience more meaningful to a wider

audience. The overarching goals of the event were to 1) deepen connections between researchers within the community; 2) provide visibility for mid-career scientists; 3) provide a platform for more scientists at the meeting.

What were the three most valuable aspects of the event?

Networking with experts (20), diverse attendance (19), discussion with experts in field (10), received suggestions for future work (9), met new people with similar interests (8), small tables (8), variety of topics available (7), meaningful interactions with early career scientists (7), research discussions (5), feedback from experienced people (5), casual setting (5), able to change topics/choose tables (5), food (5), time to talk (2), hearing common concerns (2)

Example Comments:

These discussion tables are awesome opportunities to dive deeply into topic area of interest and should continue to be offered."

"kudos and thank you [staff]"

"very well done"

"eliminate the fee, lunch was not worth this much but the discussion was."

"really great overall, didn't feel like the book reading at the end was necessary."

"the expert format to drive the conversation was great"

"like the diversity of participants"

"great exchange of ideas"

"having professionals in different positions and different points in their career was extremely helpful in getting a variety of perspectives."

"unexpected and valuable encounters and conversation"

"met new friends in similar field"

"great diversity of people at the table"

Professional Development Toolkit

Event Summary:

This year, we invited two speakers that work in the area of career and professional development for PhD trained scientists. The two-part session consisted of presentations on transferable skills. This workshop was designed to highlight the strength of PhD training in preparing well-rounded scientific professionals.

Are career and professional development programs widely available on your campus? Please describe.

Yes (8), no (3), somewhat (6), I don't know (2)

Example comments:

"We have a career development office but too general to be helpful."

"Departmental resources are really limited"

"Mostly gain skills through professional development and scicomm at conferences"

“we have a SACNAS chapter that holds professional development/career development seminars 1-2x per semester”

“I am not aware of them, but I would greatly benefit from such programs on a regular basis.”

“we have a career office but it is mostly focused on undergrads or masters in non-science majors”

“clubs host events; happy hours/networking opportunities; internship opportunities

“mandatory PD plan for all grad students & mandatory PD hours to graduate”

Do barriers exist on your campus that prevent your participation in career and professional development?

Please describe

Poor time management/prioritization (8), lack of access (2), poor campus culture toward professional development (2), poor quality of offerings (2)

Example Comments:

“I’m at the medical campus so sometimes it is difficult to travel to the main campus”

“employees don’t really have accessible career services”

“programs are available, but not useful to science careers and directed at undergraduates”

“nobody cares, postdocs just stay in the lab doing experiments career development is secondary”

“we have a very small program that is new. So the professional development aspect is very underdeveloped”

GSA Committee on Conferences Childcare

Many scientific conferences fail to provide adequate support for attendees who are primary caretakers of dependent children. Solutions are needed to provide support for a wide range of parental needs—including considerations for pregnancy, breastfeeding, and childcare, which encompasses both practical and monetary considerations. Additionally, scientific conferences need a shift in culture that clearly communicates this support. Ensuring that scientific conferences are family friendly and that primary caretakers do not face a career penalty for raising children will benefit the larger scientific endeavor.

In 2018, GSA formed a Committee on Conferences Childcare to explore and address these challenges. The scope of this committee is to: 1) assess the current offerings for family support and childcare available at GSA Conferences, using the recommendations made in Calisi *et al.* to guide the assessment; 2) make recommendations to the Board of Directors for ways that GSA Conferences can better serve primary caretakers and make our meetings equitable; 3) explore fundraising opportunities that would allow GSA Conferences to expand childcare offerings; 4) clearly and explicitly communicate current and planned policies to GSA members and meeting attendees.

While the committee was populated in summer 2018, the Chair originally appointed was unable to complete responsibilities due to unforeseen circumstances. GSA felt it was important to invest the time and thought into identifying a Chair. GSA has enthusiastically appointed Tânia Reis, who is quickly moving forward with convening the committee to discuss recommendations for TAGC 2020 as well as GSA’s Community Meetings. Committee members include a mix of career stages:

- Thomas Merritt, Laurentian University
- Julie Claycomb, University of Toronto

- Sean Curran, University of Southern California
- Gillian Stanfield, University of Utah
- Maureen Peters, Oberlin College
- Rhea Datta, Hamilton College
- Elisabeth Marnik, MDI Biological Laboratory
- Madhumala Sadanandappa, Dartmouth College

Code of Conduct for GSA Conferences

The GSA Board of Directors recently approved the following Code of Conduct for all GSA Conferences:

January 2019

The Genetics Society of America Conferences foster an international community of geneticists and provide an opportunity to discuss scientific advances and form new collaborations.

GSA values your attendance and wants to make your experience productive and inspiring by fostering an open exchange of ideas in a professional setting. Our Code of Conduct was established to communicate a transparent set of standards and guidelines for acceptable behavior at GSA Conferences and to provide a positive, safe, and welcoming environment for all attendees, vendors, volunteers, and staff.

All conference participants (regardless of their role) are expected to follow the Code of Conduct while attending any portion of the meeting, including but not limited to meeting rooms, the exhibit/poster hall, meeting areas in the official conference venue, and social events provided by the meeting or vendors.

Unacceptable Behaviors

Unacceptable behaviors include, but are not limited to:

- Intimidating, harassing, abusive, discriminatory, derogatory, or demeaning speech or actions by any participant and at all related events
- Harmful or prejudicial verbal or written comments or visual images related to gender, gender expression, gender identity, marital status, sexual orientation, race, religion, political orientation, socioeconomic, disability or ability status, or other personal characteristics, including those protected by law
- Inappropriate use of nudity and/or sexual images in public spaces (including presentation slides and posters)
- Deliberate intimidation, stalking, or following
- Violating the rules and regulations of the conference hotel
- Sustained disruption of scientific sessions or other events
- Unwelcome and uninvited attention or contact
- Physical assault (including unwelcome touching or groping)
- Real or implied threat of physical harm
- Real or implied threat of professional or financial damage or harm
- Harassing or unwanted photography

- Photographing slides of oral presentations and posters without permission
- Recording of scientific and other sessions without permission

Taking action or making a report

- If you feel threatened, witness someone being threatened, or observe behavior that presents an immediate or serious threat to public safety, please contact venue staff/security or call 911 immediately.
- GSA staff is available to assist participants in contacting hotel/university security or local law enforcement, and otherwise assist those experiencing harassment.
- If you see someone taking photographs or videos of a presentation or poster (where permission has not been granted), you may choose to remind them of the Code of Conduct policy and ask them to stop photographing the presentation or poster.
- You may also report unauthorized photography to GSA Staff.
- Need to file a complaint? Please contact any member of GSA Staff (indicated by red ribbon on their badge) or email Tracey DePellegrin at tracey.depellegrin@genetics-gsa.org. All reports will be handled confidentially.

Consequences of non-compliance

Anyone asked by GSA, the venue or security staff, or law enforcement officers to stop unacceptable behavior is expected to comply immediately. Retaliation toward GSA or toward someone reporting an incident or after experiencing any of the following consequences will not be tolerated and may result in additional sanctions. The consequences of non-compliance with GSA's Code of Conduct may include:

- Immediate removal from the meeting without warning or refund
- Restrictions from future GSA meeting attendance
- Termination of GSA membership or positions on GSA Boards or Committees
- Incidents may be reported to the proper authorities

TAGC 2020

The Allied Genetics Conference (TAGC) 2020 will be held April 22–26, 2020 at the Gaylord National Resort & Convention Center. As directed by the Board in 2018, Hugo Bellen is the Fly Community's representative on the Allied Program Committee (APC). Lynn Cooley and Hugo will co-chair the Fly Community Program Committee, which will be responsible for the *Drosophila*-specific programming. The other committee members are Brian Oliver and Helen McNeill

TAGC Organizing Committee (aka Allied Program Committee - APC)

Mark Johnston, University of Denver, Co-Chair
 Molly Przeworski, Columbia University, Co-Chair
 Phil Batterham, University of Melbourne
 Hugo Bellen, Baylor College of Medicine
 Kirsten Bomblies, John Innes Centre
 Maitreya Dunham, University of Washington

Phil Hieter, University of British Columbia
Emily Lescak, University of Alaska
Sally Moody, George Washington University
Mary Mullins, University of Pennsylvania
Steve Munger, The Jackson Laboratory
Dmitri Petrov, Stanford University
Piali Sengupta, Brandeis University
Kailene Simon, Sanofi

Participating Communities*

C. elegans

Drosophila

Mammals

Population, Evolutionary, and Quantitative Genetics

Yeast

Xenopus

Zebrafish

*We expect to see and welcome participation from other communities as well including plant, agricultural, human, etc.

There has been a lot of activity in the last year, and I encourage you to visit the conference website for updated details: <http://conferences.genetics-gsa.org/tagc/2020/index>.

The feedback from 2016 was an overwhelming (85%+) desire to have more topical sessions, and this was supported by Board discussions. This is the TAGC 2020 framework the APC has designed. TAGC will feature an equal amount of topical and community specific sessions. There will be an opening keynote session on Wednesday night followed by individual community mixers, making it easy to find your colleagues in Drosophila research. There will also be a designated meeting spot for fly people, and we'll make it easy to spot Drosophila people and posters via signage and badges.

Submitted abstracts will be considered for one of three session types:

- Poster
- Platform (Community)
- Platform (Thematic)

Poster and Thematic Sessions will feature research from all communities, while Drosophila Community Sessions will be dedicated to research on fruit flies.

Community Sessions and Thematic Sessions are held at different times, so you won't need to choose between your favorite topic and the Drosophila sessions.

More details will be forthcoming, but mark your calendars now to attend TAGC 2020!

Appendix 4. GSA & the Fly Board (Denise Montell)

Hello Drosophila Board!

I hope you have a great meeting and thank you for volunteering your time and energy to the FlyBoard.

The GSA is facing some interesting - in fact unprecedented - challenges. First, the push for open access publishing, which is laudable in many respects, represents a challenge for most scientific societies (especially those that do not have large, annual meetings in the range of ~8-20K attendees). Most societies including GSA have historically relied on income from science publishing to do all the great things they do. Second, attendance at most of our organism-specific meetings is steady, but for some, the trend is downward.

GSA is developing plans to best serve its members. You are the GSA, so we need your ideas and your help. Here is what we are thinking.

First we will be evaluating all GSA conferences in more depth than usual to identify what the communities need most. At the moment it seems that early career researchers are less identified with a single model organism than in the past. In 2016, GSA held its first TAGC meeting to bring more people together while still offering model-organism-specific programming. TAGC 2020 (next April in DC) could be a big win/win/win for GSA and our communities. Please plan to attend and spread the word. The more attendees representing a diversity of topics, the more intellectually satisfying and financially sustainable the conference will be.

Secondly GSA has crafted a strategic plan that includes launching a fundraising campaign, something that GSA has never before done. A high priority will be to use the funds from the campaign to expand our early- and mid-career investigator programs, amongst other things. The mission is to provide value to investigators at all stages of their careers, and early and mid career investigators need extra support.

The overarching goals are to serve the community and maintain fiscal viability. Your suggestions for new topical conferences are welcome. Neurogenetics has been suggested. If you can think of other cross-cutting conferences we would love to hear from you.

See you at TAGC20!

Denise

Appendix 5. Treasurer’s Report (Michelle Arbeitman)

Larry Sandler Fund					
	Investment Gain/(loss)/transfer	Travel Expenses	Other Expenses	Net Income	Fund Balance
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	(2,212)	753	107	(3,072)	72,407
ytd 2/15/19	2,062			2,062	74,469

*Includes \$20,000 transfer from meeting fund

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	2,560	6,000	4,945	21,501
2019		6,000	5,100	22,401

2019 Awards: 15, totaling \$5000
 2 @ \$600
 6 @ \$400
 6 @ \$200
 3 @ \$100

Investment Activity - Drosophila Reserve Fund					
LifeStrategy Mod Growth					
	Deposit/(Withdrawal)	Dividends	Capital Gain/(Loss)	FMV Gain/(Loss)	Balance
6/2018 Initial Investment	161,427				161,427
Jul- Dec 2018 activity		2,374	2,180	(12,192)	153,789
Add'l Investment (per audit)	3,048				156,837
2/15/19 ytd activity				9,180	166,017

Treasurer Report 2019 ADRC Fly Board meeting

- 1) A mechanism to distribute travel awards funded by the Drosophila reserve fund should be decided on in the coming year. Continue discussion on named awards.
- 2) The custodial agreement needs to be signed (attached).

Information from Mary Adams at Genetics Society of America:

Also attached for the Board’s review and signature is the custodial agreement governing GSA’s holding and administration of the Drosophila Reserve Fund. Would you please fill in the official name the fund should be listed as (in 2 places on the first page, and above the signature line on page 3), as well as the current principal’s name and contact info (page 1). The signature of an authorized representative is required on page 3. Page 4 lists the custodial policies, which includes an annual fee to GSA equal to 1.5% of the account balance. Please let us know if you have questions regarding any of the documents.

GSA FISCAL SPONSORSHIP AGREEMENT

This Agreement is made by and between The Genetics Society of America, Incorporated (“GSA”), and _____ (“Community”). GSA is a Maryland nonstock corporation, qualified as exempt from federal income taxation under Section 501(c)(3) of the Internal Revenue Code (“IRC”) and classified as a public charity under IRC Sections 509(a)(1) and 170(b)(1)(A)(vi). Community is an unincorporated scientific society in the field of genetics.

RECITALS

A. Community provides funding for its members to attend professional meetings and conferences with funding provided in the form of travel awards and coverage of meeting expenses (“Community’s Activities”). GSA has determined that Community’s Activities are in furtherance of GSA’s own tax-exempt purposes.

B. GSA has approved the establishment of a restricted account to receive donations of cash earmarked for support of the Community known as _____ and to make disbursements in furtherance of the Community's Activities. Currently, the principal officer of the Community is _____ *[insert name and contact information]*.

C. GSA desires to act as the fiscal sponsor of the Community, by receiving and holding funds on behalf of the Community beginning on the Effective Date. GSA has determined that acting as Community’s fiscal sponsor will further the charitable, scientific and educational goals of GSA.

NOW, THEREFORE, THE PARTIES HEREBY AGREE AS FOLLOWS:

1. Term of Agreement. On June 28, 2018 (the “Effective Date”), GSA shall begin to receive and hold funds on behalf of the Community.

2. Community Activities and Sponsorship Policies. All processing and acknowledgment of cash and disbursements of Community funds shall be the ultimate responsibility of GSA and shall be conducted in the name of GSA, beginning on the Effective Date. The Community is responsible for the conduct of all Community Activities which must at all times be in furtherance of the tax-exempt purpose of GSA. The Community shall abide by the Sponsorship Policies of GSA set forth on the attached Exhibit 1, which may be amended from time to time by GSA and which include administrative fees to be paid to the general fund of GSA from the restricted account described in Paragraphs 3 and 4 below.

3. Restricted Fund/Variance Power. Beginning on the effective date, GSA shall place all gifts, grants, contributions, and other revenues received by GSA and identified with the Community into a restricted account to be used for the sole benefit of the Community's mission as that mission may be defined by the Community from time to time with the approval of GSA. GSA retains the unilateral right to spend such funds so as to accomplish the purposes of the Community as nearly as possible within GSA's sole judgment, subject to any donor-imposed restrictions, as to purpose, on the charitable use of such assets. The parties agree that all money, and the fair market value of all property, in the restricted account be reported as the income of GSA, for both tax purposes and for purposes of GSA's financial statements. It is the intent of the parties that this Agreement be interpreted to provide GSA with variance powers necessary to enable GSA to treat the restricted account as GSA's asset in accordance with Interpretation No. 42 of Statement No. 116 issued by the Financial Accounting Standards Board, while this Agreement is in effect.

4. Restricted Fund Management / Performance of Charitable Purposes. All of the assets received by GSA under the terms of this Agreement shall be restricted for use by the Community at their behest. GSA may hold the funds in any investment vehicle that is in compliance with the Maryland Prudent Management of Institutional Funds Act. GSA may hold the funds in cash, co-mingled with GSA's funds, or invested in a GSA investment account. All disbursements by GSA to or for the benefit of the Community may only be used in furtherance of the tax-exempt purposes of GSA. The Community shall not use any portion of the assets to participate or intervene in any political campaign on behalf of or in opposition to any candidate for public office, to induce or encourage violations of law or public policy, to cause any private inurement or improper private benefit to occur, nor to take any other action inconsistent with IRC Section 501(c)(3).

5. Termination. Either GSA or the Community may terminate this Agreement on 30 days' written notice to the other party, so long as another nonprofit corporation which is tax-exempt under IRC Section 501(c)(3), and is not classified as a private foundation under Section 509(a) (a Successor), is willing and able to sponsor the Community and is approved in writing by both parties by the end of the 30-day period. If the parties cannot agree on a Successor to sponsor the Community, the Community shall have an additional 30 days to find a Successor willing and able to sponsor the Community. If a Successor is found, the balance of assets in GSA's restricted account for the Community, together with any other assets held or liabilities incurred by GSA in connection with the Community, shall be transferred to the Successor at the end of the notice period or any extension thereof, subject to the approval of any third parties that may be required. If the Community has formed a new organization qualified to be a Successor as set forth in this Paragraph, such organization shall be eligible to receive all such assets and liabilities so long as such organization has received a determination letter from the Internal Revenue Service, indicating that such qualifications have been met, no later than the end of the 30-day period or any extension thereof. If no Successor is found, GSA may dispose of the Community assets and liabilities in any manner consistent with applicable tax and charitable trust laws.

6. Miscellaneous. In the event of any controversy, claim, or dispute between the parties arising out of or related to this Agreement, or the alleged breach thereof, the prevailing party shall, in addition to any other relief, be entitled to recover its reasonable attorneys' fees and costs of sustaining its position. Each provision of this Agreement shall be separately enforceable, and the invalidity of one provision shall not affect the validity or enforceability of any other provision. This Agreement shall be interpreted and construed in accordance with the laws of the State of Maryland.

7. Mediation. In the event of any dispute under this Agreement, the parties shall attempt to resolve the matter themselves in an amicable manner. Failing such resolution, any dispute under this Agreement shall be attempted to be resolved first by mediation.

8. Entire Agreement. This Agreement constitutes the only agreement, and supersedes all prior agreements and understandings, both written and oral, among the parties with respect to the subject matter hereof. All Exhibits hereto are a material part of this Agreement and are incorporated by reference. This Agreement, including any Exhibits hereto, may not be amended or modified, except in a writing signed by all parties to this Agreement.

IN WITNESS WHEREOF, the parties have executed this Fiscal Sponsorship Agreement.

Genetics Society of America

[Name of Community]

By: _____

By: _____

Dated: _____

Dated: _____

Exhibit 1

GSA Fiscal Sponsorship Policies

- GSA has no responsibility to raise funds for Community.
- GSA will accept donations in the form of cash or cash equivalents (checks, wires, electronic transfers, etc.) Funds invested in the GSA account at Vanguard will be placed in a fund chosen and designated by Community. GSA will have no input or responsibility in either the choice or performance of the fund.
- Community will designate the person(s) who will have authority to provide instructions and administer the funds through GSA, including requesting withdrawals and/or disbursement of funds.
- Interest and or dividends earned by the fund will reinvest into the fund, and GSA will provide an accounting of the fund on a periodic basis to the appointed persons.
- Liquidation of funds will be upon the written request of the designated persons of Community, with a minimum of 30-day's notice prior to the date the funds are needed. Withdrawals will be sent to the GSA main operating account at Bank of America, and further dispersed by check or wire to payees, as instructed in writing.
- Documentation of expenses in the form of vendor invoices for meeting expenses, or memos and emails listing award winners (including addresses as well as any necessary tax forms) will be required for disbursement of funds. Community will provide GSA with written notice of any change in the persons designated to provide instructions on the funds.
- It is understood that funds of Community may be co-mingled with GSA funds but will be tracked and accounted for separately.
- GSA will charge an annual administrative fee of 1.5% of the account balance, collected in advance, upon receiving the Community's funds, and thereafter on the anniversary date of the fund's establishment.

Appendix 6. Finnerty Award (Amanda Norvell)

Report to the North American Drosophila Board, March 27, 2019, Dallas, TX Amanda Norvell, Finnerty Undergraduate Travel Award Committee

This year we received 29 applications for the Victoria Finnerty (VF) Undergraduate Travel Award and funded the top 14. In order to maximize the number of students who received funding, money was awarded on a sliding scale, according to their ranking.

The awardees are:

- Katherine H. Fisher (Poster #718), Indiana University, \$600
- Kathy H. Le (Poster #278), Johns Hopkins School of Medicine, \$600
- Carolyn W. McGrail (Poster #628), Baruch College (CUNY), \$400
- Nicco L. Ruggerio, (Poster#533), University at Buffalo, \$400
- Issac Wong, (Poster #404), University of Rochester, \$400
- Caroline A. Miller, (Poster #310), Davidson College, \$400
- Taylar J. Mouton, (Poster #222), University of Rochester, \$400
- Brandon Turner (Poster #225), University of North Carolina – Charlotte, \$400
- Caroline Phan, (Poster #308), Davidson College, \$300
- Rebecca Tarnopol (Poster #261), University of Michigan, \$300,
- Helen Margaret Stone (Poster #275), University of Virginia, \$300
- Esther Hyeyoung Kwon (Poster #407), University of North Carolina at Chapel Hill, \$200
- Amanda Petersen (Poster #459), University of St. Thomas, \$200
- Francesco P. Satriale (Poster #182), Bucknell University, \$200

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

This year's selection committee was Amanda Norvell(chair), Dan Cavanaugh, Justin D'Angelo, Scott Ferguson, Geoff Findlay, Jennifer Kennell, Judith Leatherman, Matthew Wawersik.

Appendix 7. Image Award (Nasser Rusan)

Image Award (Nasser Rusan)

This year the Image Award committee has added Elizabeth Chen as their newest member, bringing the total committee members to 5 (including Nancy Bonini, Don Fox, and Mia Levine). Committee members are asked to serve 2-3 year terms, which will allow for steady turnover. It is therefore likely that 2 members of the current committee will be replaced for next year's competition.

New for this past year was an increased presence on Twitter, especially leading up to the submission deadline. Also new is the addition of the *Drosophila* Image Award Poster. The DIA Poster is a David Bilder initiative aimed at highlighting the awesome science from the *Drosophila* community. The hope is that fly labs will display these posters as prominently as the "Learning to Fly" poster.

Results of the 2019 competition

85 total submissions: 62 images and 23 videos. That is a 25% increase over last year.

The winners this year are:

Philipp Schlegel, for an image showing the reconstruction of neurons from an electron microscopy volume of the entire adult fruit fly brain

Anna Franz, for a video showing a fat body cell moving to the site of a wound

The runners-up are:

Joshua Li, for an image showing Splicing reporters revealing cell-type-specific isoform expression crucial for neurodevelopment

Judy Martin, for a video showing a new platform for long-term live imaging of the *Drosophila* adult midgut

Nasser Rusan will present the image awards at fly meeting

Appendix 8. 2020 Fly Meeting at TAGC (Helen McNeill)

TAGC 2020 meeting report

Organizers: Helen McNeill, Brian Oliver, Hugo Bellen and Lynn Cooley

This meeting in Washington is a follow up meeting from the Orlando 2016 TAGC (The Allied Genetics Conference) organized by the GSA. It is co-organized with many model organism communities as well as Population Evolution and Quantitative Genetics (PEQ) section. Suzy Brown is presenting a report about this meeting at the Fly Board. The following focuses on the issues that affect the *Drosophila* portion of the meeting as her report outlines the schedule and general issues.

- after the plenary session on Wednesday there will be a mixer for our community
- there will be a specific gathering site available throughout the meeting where *Drosophilists* can congregate/meet.
- there will be five 2-hour pan-organism sessions with concurrent topics throughout the meeting, with a total of 120 platform talks. We estimate at least 35 of those will go to *Drosophila* people.
- there will be five 2-hour *Drosophila*-specific sessions.
 - one will be on Sunday morning for the Larry Sandler Memorial Lecture and three invited plenary *Drosophila* talks.
 - the remaining four will have two concurrent sessions each, for eight sessions. Each session will have eight talks (12 minutes plus 3 for questions) for a total of 64 platform talks.
- combining the platform talks in the pan-organism and *Drosophila*-specific sessions should come out to close to 100 *Drosophila* talks.
- in addition, there will be a series of *Drosophila* talks in the PEQ section of the meeting (15? maybe more). Hence, the total number of talks in the parallel platform sessions for our community will be about 114 (64 + 35+ 15) versus the typical 168.
- based on the number of abstract submissions per topic (there are about 12 main topics) some of our parallel sessions will have 4 talks (1-hour sessions) whereas others will have 8 talks.
- the poster sessions will be mixed and focus on topics not on organisms
- there will be at least one session on technology for all model organisms
- postdoctoral fellows will assist the chairs and co-chairs in the parallel sessions
- suggestions for chairs and co-chairs would be appreciated

Appendix 9. Drosophila Board Elections (Laura Johnston)

Fly Board Elections committee 2018: 2 year terms

Laura Johnston (Chair)
Carl Thummel 2019
Elizabeth Chen 2019
Tin Tin Su 2020
Noah Whiteman 2020

Drosophila Election Report (Laura Johnston)

The Elections Committee consisted of Laura Johnston (Chair), Tin Tin Su, Noah Whiteman, Carl Thummel, and Elizabeth Chen. Carl and Elizabeth served last year and will rotate off next year, Tin Tin and Noah were new recruits to the committee. Next year's chair will be Debbie Andrews. Laura will remind her to organize the committee and to select two new members to serve 2-year terms.

In choosing candidates for the Fly Board positions, the committee considered several criteria: previous involvement in the fly community, our sense of their level of responsibility, career level (preference for mid or early for Regional Reps, senior for President), institutional and gender balance. The Chair also solicited nominations from outgoing regional representatives and from the elections committee. The Committee then ranked the nominations. The Chair contacted the top-ranked nominees to ask them to stand for election. Some declined, but in most cases we were easily able to come up with two excellent candidates for each position; the exception was the California region, for which we were unable to get acceptance for a second candidate. In this case the Election Committee agreed that the one candidate who had accepted would be appointed to be the regional representative. For the elections, the chair asked the candidates to submit a short biographical paragraph to be included on the ballot. FlyBase (Pepe Urbano and Jim Thurmond) set up a SurveyMonkey website to facilitate voting and vote counting and sent an email (appended below) was disseminated to the fly community by email on Oct. 26. Subsequently it became clear that due to a misunderstanding, we had omitted selection of the next President-elect. The process of selection and acceptance of 2 candidates for President – elect was quickly carried out, and this was added to an amended ballot. The amended ballot, which included candidates for the Regional rep positions and the President-elect, was posted on Nov. 15, and carried a deadline for voting of Dec. 11. The ballot included a statement that *“only scientists who use Drosophila as a research organism are eligible to vote”*, as decreed at the last Board Meeting*. Election emails and candidate statements are appended to the end of the Agenda.

Election results: For comparison, data from previous years is shown with this year's results. The number of votes this year was particularly good, and seems to steadily rising each year, which we take to be a sign of an increase in active community involvement. (Note that the high number in 2016 was due to an anomaly; see * below.)

<u>Year</u>	<u>Votes</u>	<u>Regions up for election</u>
2018	702	Mid-Atlantic, California, Europe, Latin America, Asia
2017	652	Mountain, New England, Primarily Undergraduate Institutions, Australia
2016	1795*	Mid-Atlantic, California, Europe, Latin America, Asia
2015	557	Midwest, Canada
2014	530	Northwest, Southeast, Heartland, Great-Lakes

The newly elected Fly Board members are:

President-elect: **Mariana Wolfner** (begins 2020)
Mid-Atlantic: **Erika Bach** (through 2022)
California: **Leanne Jones** (through 2022) (*appointed by Election Committee*)
Europe: **Nic Tapon** (through 2022)
Latin America: **Helena Araujo** (through 2022)
Asia: **Tatsushi Igaki** (through 2022)

* The turnout for the 2016 election was unusually high, apparently because some of the votes came from outside of the fly community (one of the candidates forwarded the SurveyMonkey link, which was publicly posted on Flybase, to a number of local colleagues). The excess of votes was from this region. To avoid any appearance of bias in future elections the Board voted in 2017 to add this statement to each election ballot, to restrict the vote to the fly community.

→ Item for discussion: [appointment or election of another Trainee rep.](#)

**Ballot Reminder and Addendum Ballot for the election of new representatives
to the National Drosophila Board of Directors**

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.

Please participate in these elections! This is your opportunity to choose the individuals who will help set priorities and secure support for community resources. Remember that you may vote for candidates in **ALL** categories, even though you do not reside in the region represented by the candidates. However, only scientists who use Drosophila as a research organism are eligible to vote.

Please go to each of the URL below and follow the instructions to cast your ballot.

- **Please note that a second Ballot has been added, to elect Regional Representatives from the US Mid-Atlantic region, Europe, Latin America, and Asia.**
- **If you have already voted for President-elect we invite you to vote again, but only for the regional candidates.**

(insert survey link)

Balloting will end December 11, 2018.

Thank you,

The 2018 Drosophila Board Election Committee:

Laura Johnston (Chair)
Carl Thummel
Tin Tin Su
Noah Whiteman
Elizabeth Chen

**Addendum Ballot and Reminder
for the election of new representatives to the National Drosophila Board of Directors**

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

This year we are electing the President-elect, who will serve as President starting with the fly meeting in 2021. In addition, a second ballot has been added to elect a representative for the US Mid-Atlantic region and international representatives for Latin America, Europe and Asia, to serve 3-year terms starting with the fly meeting in 2020.

Remember that you may vote for candidates in **ALL** categories, even though you do not reside in the region represented by the candidates; however, only scientists who use Drosophila as a research organism are eligible to vote.

Please go to each of the URL below and follow the instructions to cast your ballot. Please note there are two steps to the ballot:

- **The first step is to elect the President-elect.** *If you have already voted for President-elect we invite you to vote again, but only for the regional candidates.*

- **The second step is to elect Regional Representatives from the US Mid-Atlantic region, Europe, Latin America, and Asia.**

(insert survey link)

Balloting will end December 11, 2018.

Thank you,

The 2018 Drosophila Board Election Committee:

Laura Johnston (Chair)
Carl Thummel
Tin Tin Su
Noah Whiteman
Elizabeth Chen

Election Biographies.

President-elect (Vote for ONE)

Daniela Drummond-Barbosa, PhD

Johns Hopkins University, Bloomberg School of Public Health, Baltimore, MD

(<https://www.jhsph.edu/faculty/directory/profile/2213/daniela-drummond-barbosa>)

Daniela Drummond-Barbosa was born in Los Angeles, California, and raised in Belo Horizonte, Brazil. She received her Bachelor's degree in Biochemistry and Immunology from the Universidade Federal de Minas Gerais in Belo Horizonte. She next moved to New Haven, Connecticut, to join the Genetics graduate program at Yale University. She did her Ph.D. research with Daniel DiMaio on the interaction between the bovine papillomavirus E5 protein and the platelet-derived growth factor receptor in mammalian cells. Daniela did her postdoctoral training with Allan Spradling at the Carnegie Institution, where she pioneered using *Drosophila melanogaster* as a model to study adult tissue stem cell regulation by diet. In 2002, Daniela joined the Department of Cell and Developmental Biology at the Vanderbilt University Medical Center as an Assistant Professor. In 2009, she relocated her lab to the Department of Biochemistry and Molecular Biology at the Johns Hopkins Bloomberg School of Public Health, where she is now a tenured Professor. Daniela's group identified several mechanisms involving insulin-like peptides, ecdysone, adipocyte factors, and other diet-regulated pathways that modulate germline stem cells and their differentiating progeny in the *Drosophila* ovary. Daniela co-organized the 55th Annual *Drosophila* Research Conference in San Diego in 2014, co-chaired several fly meeting sessions, and served on the Larry Sandler Award Selection committee in 2015 and, as Chair, in 2016. Daniela has also participated in outreach activities and made other contributions to the scientific community, including service as a regular member in American Cancer Society and National Institutes of Health study sections.

Mariana Wolfner, PhD

Stephen H. Weiss Presidential Fellow, Department of Molecular Biology and Genetics

Cornell University, Ithaca, New York (<https://mbg.cornell.edu/people/mariana-wolfner/>)

After immigrating to the US with her parents, Mariana grew up in New York City. She attended Cornell University, and did research there with Gerry Fink, on an organism more typically familiar to *Drosophilists* as flyfood. As a graduate student with David Hogness at Stanford, she began to work with *Drosophila*, identifying genes turned on or off by ecdysone during the larval-to-pupal moult. She joined Bruce Baker's lab at UCSD for her postdoc, cloning the *doublesex* gene. From 1983 her independent lab at Cornell focused initially on the function and regulation of genes expressed sex-specifically in flies, morphing into studying (a) functions and evolution of the seminal proteins that cause dramatic behavioral and physiological changes in the mated females that receive them, and (2) processes that 'activate' a mature oocyte to complete meiosis and begin embryo development. Mariana has been very active in the fly community, including serving as Great Lakes Rep 1990-1993 and then FlyBoard president, co-organizing the 2001 fly meeting, and being on or chairing committees such as for the Sandler Lectureship. She has also served in multiple capacities at GSA (e.g. Board member, Secretary of the GSA Board, and member of several GSA committees) and at AAAS, where she Chaired the Biology Section in 2008-2009. Beyond research, Mariana is passionate about mentoring students, postdocs, and junior faculty, is active in efforts at inclusion and diversity, and serves on numerous editorial boards.

Regional Reps:

Mid-Atlantic Region - Vote for one:

Erika Bach

New York University School of Medicine <http://bachlab.med.nyu.edu>

Erika received her BS in Zoology from the University of Massachusetts, Amherst. After graduating college, she was a technician in Dr. Carl Nathan's lab at Weill Cornell Medical College studying macrophage immune responses. Erika obtained her PhD in Immunology at Washington University School of Medicine in Dr. Robert Schreiber's laboratory, where she studied cytokine/JAK/STAT signaling during mammalian immune responses. For her postdoctoral training, she switched from mouse immunology to Drosophila genetics and was Jane Coffin Childs Fellow in Dr. Norbert Perrimon at Harvard Medical School. During her postdoc, she studied how cytokine signaling regulated organ size in flies. Since 2002, Erika has led her own lab in the Department of Biochemistry and Molecular Pharmacology at the New York University School of Medicine. Erika's research is focused on stem cell dynamics in the Drosophila testis, competitive interactions between cells in developing Drosophila epithelia, and Drosophila hematopoiesis as a model for human myeloproliferative neoplasia caused by dysregulated JAK/STAT signaling. Erika is an active member of local and national fly communities. She has chaired sessions at national fly meetings, was a Chair of the Larry Sandler committee, has written reviews on cell competition and JAK/STAT signaling, and has trained dozens of budding Drosophila researchers (high school, undergraduate, graduate and postdoc) in her laboratory. Erika promotes Drosophila as ideal model to obtain key insights into conserved biological questions and as a low-complexity model for human diseases.

Shubha Govind

City College of New York <http://forum.sci.cuny.cuny.edu/people/science-division-directory/sgovind>

Shubha Govind completed her Bachelors and Masters in Botany from Delhi University and her PhD in Cell Biology from University of Illinois, Urbana Champaign. As a post doc with Ruth Steward at Princeton University and a New Jersey Commission on Cancer Research Fellow, Shubha studied the role of NF- κ B signaling in the development of dorsal-ventral axis of the fly embryo. At CCNY, Shubha's lab pioneered the use of the Drosophila-parasitic wasp co-culture system to investigate cellular immune functions of blood cells. Her group was the first to demonstrate a role for Toll-NF- κ B signaling in larval hematopoiesis and inflammation. Shubha's lab has identified a novel organelle in wasp venom that harbors virulence proteins and is studying how such proteins facilitate parasitic wasp success. Shubha has shared this host-parasite model and related techniques developed in her lab with researchers and educators around the world. She has organized workshops at international conferences (including Annual Drosophila Research conferences), trained more than 75 middle/high school, undergraduate/graduate students, and postdocs in her lab, many from highly-disadvantaged backgrounds. She has been honored for mentoring undergraduate and graduate students by CCNY and doctoral students by the CUNY Graduate Center. Shubha co-developed and has taught the Introductory Genetics course at CCNY for over 15 years. She also teaches a graduate level genetics course, and has introduced new pedagogical approaches to teaching both genetics and genomics at CCNY.

Europe – Vote for one:

Kim Rewitz

University of Copenhagen, Denmark <https://www1.bio.ku.dk/english/staff/?pure=en/persons/407115>

Kim Rewitz received his Master of Science degree in molecular biology from Roskilde University in Denmark. He continued his Ph.D. research in insect endocrinology and developmental timing at the University of North Carolina at Chapel Hill with Dr. Lawrence I. Gilbert, investigating the molecular mechanisms underlying steroid hormone production. His work showed that cytochrome P450 enzymes mediate synthesis of the insect steroid molting hormone ecdysone. After receiving his Ph.D., Kim did his postdoctoral training with Dr. Michael B. O'Connor at the University of Minnesota using Drosophila molecular genetics to identify the PTH receptor, solving one of the major challenges within the insect neuroendocrine community. After his return to Denmark, Kim was appointed a faculty position at the University of Copenhagen and has been running his own lab at the Department of Biology where he is an Associate Professor. His lab focuses on investigating control of development and growth by hormonal and nutritional signals. Kim currently serves at the editorial board of Scientific Reports and has been an active member of the fly community, organizing the International Insect Hormone Meeting and the Ecdysone Workshop at the Annual Drosophila Research Conference. He also serves the community through teaching and mentoring to train the next generation of researchers in Drosophila

genetics. Since his return to Denmark, he has been establishing a fly community in Copenhagen with the goal of promoting model organism research at academia and in medical research using *Drosophila*.

Nic Tapon

Francis Crick Institute, London, UK <https://www.crick.ac.uk/research/labs/nic-tapon>

Nic Tapon did his Bachelor's at Imperial College London followed by a PhD in Alan Hall's lab at University College London working on Rho small GTPases. As a postdoctoral fellow in Iswar Hariharan's lab at MGH Cancer Center, he identified mutations in the TOR regulator Tsc1 and Salvador, one of the first Hippo pathway components to be identified. Nic was a Staff scientist in Pierre Leopold's lab at the University of Nice, France, then started his own group at the Cancer Research UK London Research Institute in 2003. He moved to the Francis Crick Institute in London in March 2016. Work in the Tapon lab is aimed at understanding how tissue size is specified during development and adulthood. In particular, we are interested in the regulation of the Hippo signalling pathway by a variety of upstream signals, such as mechanical forces, cell-cell junctions and nutrient availability. We use several systems such as the wing and eye discs, ovary and abdomen. Nic is a strong believer in supporting and developing the *Drosophila* community. He was on the organising committee of the 2017 European *Drosophila* Research Conference in London and has been treasurer of the monthly London Fly Meetings since 2005.

Latin America – Vote for one:

Helena Araujo

Federal University of Rio de Janeiro, Brazil

<http://buscatextual.cnpq.br/buscatextual/visualizacv.do?id=K4781645H7&idiomaExibicao=2>

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

Mario Zurita

National University of México [Instituto de Biotecnología UNAM](#)

Mario Zurita is a biologist from the National University of México. He performed master studies under the supervision of Dr. Francisco Bolívar working on new molecular cloning vehicles. His PhD was under the supervision of Dr. Paul Lizardi characterizing the genome of the amoeba, *Entamoeba histolytica*. With the support of a McArthur foundation fellowship he performed postdoctoral studies at Stanford University under the direction of Prof. Tag E. Mansour, generating the first molecular studies in parasitic trematodes. After brief period working in México at the Institute of Biotechnology, he performed a second postdoc as PEW fellow, in Harvard University under the supervision of Prof. Fotis C. Kafatos. During these postdoctoral studies he performed several investigations on mosquitoes as well as in *Drosophila*. From 1994 to 1999 Dr. Zurita was Associate Professor at the Institute of Biotechnology from the National University of México and since the year 2000 is full professor at the same institute. From 1999 to 2006 was the regional chairman in México for the PEW Latinamerican fellows program in Biomedical Sciences. President of the Mexican Society for Developmental Biology from 2004-2006 and President of the Latinamerican society for Developmental Biology from 2008 to 2010. Dr. Zurita was Howard Hughes Medical Institute International Scholar for 2002 to 2006. He is author of 58 publications in international journals and his work has more than 2000 citations. He has graduated 12 PhDs and 11 masters in science. Dr. Zurita was member of the editorial board of GENESIS from 2017 to 2014 and is a reviewer of several journals specialized in Molecular and Developmental Biology. His current research work uses *Drosophila* to study the role during development of different factors involved in

transcription and genome stability. These studies have permitted a better understanding of the molecular mechanisms of the role of these factors during development. One of the most important contributions has been to demonstrate that mutations in genes involved in both transcription and DNA repair that are involved in different human syndromes and cancer in humans generate similar phenotypes in *Drosophila*. This has allowed the understanding of how such defects affect the development of a complex organism.

Asia – Vote for one:

Tatsushi Igaki

Laboratory of Genetics, Kyoto University Graduate School of Biostudies, Japan <https://www.lif.kyoto-u.ac.jp/genetics/english/>

Tatsushi Igaki is a Professor in the Graduate School of Biostudies at Kyoto University, where he leads a research group dedicated to using *Drosophila* genetics to build a picture of the cell-cell communications underlying the establishment and maintenance of multicellular systems. He received his PhD from Osaka University in 2003 under Masayuki Miura. He then moved to Yale University as a postdoc to work with Tian Xu. In 2007, he started his own lab at Kobe University Graduate School of Medicine as an Assistant Professor. He secured tenure a few years later and moved to Kyoto University as a full Professor in 2013. He has been an Editor of *Disease Models & Mechanisms* since 2015, and was the chief organizer of 13th Japanese *Drosophila* Research Conference (JDRC 2018) this year.

José C. Pastor-Pareja

Tsinghua University, Beijing, China <http://joselab.life.tsinghua.edu.cn/>

José C. Pastor-Pareja did his Ph.D. in the laboratory of Antonio García-Bellido (Universidad Autónoma de Madrid, Spain). After that, he became a postdoc with Tian Xu (Yale School of Medicine-HHMI). Since 2012, he has been running his laboratory at Tsinghua University, where he is now a tenured Associate Professor, 青千人 (One Thousand Talents) investigator and a member of the Peking-Tsinghua Center for Life Sciences. José has always been a *drosophilist*, except for a short stint with *Arabidopsis* as an undergraduate. His research has focused on tissue morphogenesis, matrix basement membranes, developmental cell biology, tissue damage responses and regeneration. An attendant to the last three Asia-Pacific fly meetings in Korea, China and Japan, José is an active member of the vibrant Beijing area fly community (>30 labs) and the fast growing model organism community in China.

Appendix 10. Primarily Undergraduate Institutions (Amada Norvell)

Report to the North American Drosophila Board, March 27, 2019, Dallas, TX Amanda Norvell, Primarily Undergraduate Institutions (PUI) Representative

There are several events that will likely be of interest to faculty teaching at Primarily Undergraduate Institutions (PUIs) and for undergraduate students attending the meeting.

The New Faculty Forum will have a session focused on undergraduate teaching and it will include discussions about active learning and integrating research experiences into courses, as well as a panel discussion featuring undergraduate students.

The “Spotlight on Undergraduate Research” Workshop will be held Thursday evening. This session, organized by Jennifer Jemc, Kimberly A. Carlson and Eric Stoffregen and sponsored by *UT Southwestern Graduate School of Biomedical Sciences*, will feature undergraduate student presentations on their research.

The undergraduate-focused pedagogy workshop, “Using Drosophila to bring authentic course-based undergraduate research experiences (CUREs) into the undergraduate classroom”, will be held on Friday afternoon. This workshop, organized by Afshan Ismat, Andy Arsham and Justin DiAngelo, will help instructors at Primarily Undergraduate Institutions (PUIs) bring authentic research experiences using Drosophila into the undergraduate classroom.

In addition to these events, undergraduate students may be interested in the “Maximize the impact of your curriculum vitae and resume” workshop. The GSA has also established a mechanism for undergraduate presenters to invite scientists to visit their posters. Finally, in response to a suggestion, undergraduate students attending the meeting will be given ribbons for their badges.

Appendix 11. Advocacy & Communications (Andreas Prokop)

Advocacy report (A. Prokop)

A. Overview of new publications and developments in 2018/19

- Markstein, M. (2019). *Drosophila* workers unite! A laboratory manual for working with *Drosophila*. Course Source, under revision -- [\[LINK\]](#)
- Josh Lisse: Flies in Neuroscience #braintigers -- [\[LINK\]](#)
- Ingham, P. W. (2018). From *Drosophila* segmentation to human cancer therapy. Development 145/21 — [\[LINK\]](#) (part of the new advocacy article series which I initiated as science communications officer of the BSDB: [LINK1](#), [LINK2](#))
- Prokop, A. (2018). What is Developmental Biology – and why is it important? Open Access Government 17, 121-123 — [\[LINK1\]](#); [\[LINK2\]](#)
- Small fly: Big Impact, Part 1 Why the fly (educational YouTube video now also in Arabic (*apart from English, Spanish, Indonesian, soon also Portuguese*) -- [\[LINK\]](#)



- Excellent download statistics of the 4 *Drosophila* advocacy articles during the first year after publication of the special scicomm issue: Illingworth, S., Prokop, A. (2017). Science communication in the field of fundamental biomedical research (editorial). *Sem Cell Dev Biol* **70**, 1-9 [\[LINK\]](#):
 - 1723 for article by H. Bellen and his team about strategies to collaborate with clinicians [\[LINK\]](#)
 - 1242 for article by I. Palacios et al. about the excellent work by DrosAfrica [\[LINK\]](#)
 - 2225 for article by S. Patel and A. Prokop about the concepts and strategies of the Manchester Fly Facility [\[LINK\]](#)
 - 2640 for article by S. Patel and A. Prokop about the droso4schools project [\[LINK\]](#)
- Prokop, A. (2018). Why funding fruit fly research is important for the biomedical sciences. Open Access Government 20, 198-201 — [\[LINK\]](#) and as [GSA blog](#)
- Patel, S., Prokop, A. (2019). Why fruit flies belong in primary and secondary schools. Blog post in “Genes to Genomes” — [\[LINK\]](#)
- Prokop, A. (2018). A novel engaging approach to teaching life cycle and evolution in KS2 classrooms (primary schools). Blog post in “Gedankenexperimente” — [\[LINK\]](#)
- Patel, S., Prokop, A. (2018). An objective-driven long-term initiative to communicate fundamental science to various target audiences – a *Drosophila* case study. Blog post in “Open Research Forum” — [\[LINK\]](#) – mirrored in “PLOS | BLOGS” (ed. J. Organ) — [\(LINK\)](#)
- Prokop, A. (2018). How to communicate basic research in schools - a case study using *Drosophila*. Blog post in “PLOS | BLOGS” -- [\[LINK\]](#)

B. Fly advocacy in under-resourced countries

The key idea is to promote fruit fly research as a means to release funds for infrastructure investments by reducing the cost for cutting-edge biomedical research and training (*"keeping 400 fly stocks requires one stand-alone incubator and £100 a month to pay for food vials and 4-6hrs of work; maintaining the same number of mouse strains readily accessible would take at least £12,000 a month and a vast housing facility"* [Ref]).

- TReND in Africa runs regular neuroscience courses partially involving *Drosophila* [website]
- DrosAfrica: administrative problems caused cancellation of the 2018 Tanta workshop in Egypt [website]

C. Overview of the Manchester Fly Facility



Since its launch in 2011, the Manchester Fly Facility has owned its brand as the worldwide only initiative systematically advocating *Drosophila* research, sharing its many high quality resources via online platforms, its [YouTube channel](#); its main [website](#) is linked from the 'PUBLIC, TEACHERS, STUDENTS' tab on [flybase.org](#);

its six main areas of science communication engagement reach a range of target audiences; these include:

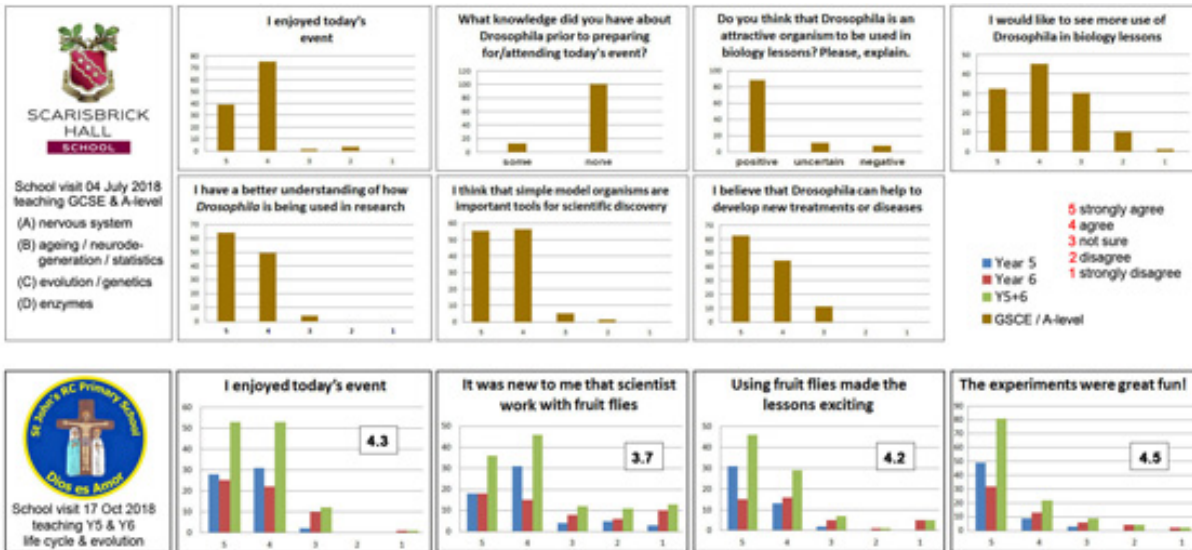
- the development of resources for fly training (>30K downloads across three platforms: [Orig.Ref](#): >34K full views, >8.7K downloads - [Repository1](#): >26K views, >13K downloads -- [Repository2](#): >14K views, >10K downloads). This training was further enhanced through the development of e-assessment strategies suitable for larger university courses ([Ref](#)).
- science fair resource development ([Repository3](#)) and presentation (24 [events](#) since 2011);
- science fair organisation (e.g. '[Brain Box](#)' with 5.4K visitors on a single day);
- educational movies ([YouTube](#); *the flagship educational movies have ~28,000 views, one of them translated by others into Spanish, Indonesian, Arabic, soon also Portuguese*);
- school resource development ([Repository4](#), [Repository3](#)) and engagement (~90 [school events](#) since 2011)
- inspiring other drosophilists and teachers about the concepts and resources through publicising all our strategies and resources ([Publ.List](#)): 5 fly-relevant articles in scientific journals, 2 in school journals, 3 websites, 8 online resources, 5 blog posts (PLoS, GSA, The Node), and 3 plenaries/workshops on international conferences.

Further implementation strategies include:

- The launch of the 'droso4schools' initiative ([Ref](#)): we sent placement students as teaching assistants into schools to collaborate with teachers on the development of curriculum-relevant biology lessons using didactic strategies familiar to teachers. All lessons capitalise on the fact that fruit flies are the conceptually best understood animals (ideal to convey curriculum-relevant contents), are feasible to use for micro-experiments in schools (bringing life and memorable experiences into biology lessons), and offer numerous anecdotes and examples (illustrating the relevance of learned contents).
- International collaborations with groups in Indonesia ([website](#); *the key liaison in Indonesia has now unfortunately been silenced due to uni-internal malevolence*), Nigeria (*Rashidat Abdul Azeez is in the process of establishing a droso4schools-like school program in Nigeria, and potential funds are currently being applied for*) and Croatia (*Rozi Andretić obtained university funds to establish droso4schools in Croatia*).

metrics from 17/03/2019				
site (launch date)	views	visitors	Downloads	Altmetric
droso4schools (04/15 - LINK)	~63.7K	~33.8K	n.a.	n.a.
Manchester Fly Facility (~Feb 2013 - LINK)	~59K	~21.7K	n.a.	n.a.
Figshare: Biology lessons (24/03/15 - LINK)	~4.9K	n.a.	~1K	43
Figshare: Mating scheme (16/01/13 - LINK) * main article in G3 [LINK]	~26.3K *~43.5K	n.a.	~13.2K *8.8K	62 *48
Figshare: 2nd Yr practical (10/02/13 - LINK)	~14.4K	n.a.	~10.8K	34
Figshare: Outreach (27/11/16 - LINK)	~3.5K	n.a.	~330	103
Figshare: Man Fly resources (07/03/15 - LINK)	~7.6K	n.a.	~10K	n.a.
YouTube film 1 (20/12/14 - LINK)	>18.3K	n.a.	n.a.	n.a.
YouTube film 2 (01/04/15 - LINK)	~9.8K	n.a.	n.a.	n.a.

- It seems that our resources are being used worldwide, as can be extrapolated from our [impact document](#) (section 6.2.1.) which lists the examples that we know about: 30 researchers from 9 countries (Eur, N-, S-Am, Asia) using our resources.
- Clear impact is achieved in schools, as illustrated by our Scarisbrick Hall secondary and St. John's primary school evaluations (see below; [evaluation1](#), [evaluation2](#)), which show a complete turn-around of pupils from not knowing anything about flies to wanting to see flies in biology lessons and agreeing to the importance of their uses in research. We got money to intensify our evaluation in 2019. To illustrate the effects we can have:
 - one teacher commented: *"I can't tell you how excited I was to find all of the different ways that we could use these animals - I'm afraid we were thinking that we would have to confine ourselves to genetic crosses but your support material has certainly broadened our horizons"*
 - a student wrote in an evaluation form: *"I never really thought that a fly could be useful, but I see the potential now"*



- Extrapolating from these local achievements, similar results can be expected worldwide: our [impact document](#) (sections 6.2.3. and 6.3) lists the examples we know about: 23 researchers and 26 teachers from 15 countries (N-, S-Am, Eur, Aus, Afr, Asia) using our resources for science education; some lesson were translated into Spanish and Indonesian, and the [impact document](#) (sections 7-9) lists numerous supportive teacher comments.
- Policy impact: the most efficient way forward would be to establish the use of *Drosophila* in biology lessons as a national standard, thus no longer relying on the willingness of teachers to engage in this way of teaching. We are now in conversations with AQA (the biggest national examination board) and collaborate with others in an effort to politicise the idea of universities re-gaining influence on the school curriculum in the UK - which currently lies primarily in the hands of private companies that mostly exclude universities from the process.

D. Future directions

As explained to Fly Board before and detailed in a [PLoS blog](#), [GSA blog](#) and our [special issue editorial](#), fundamental science is of enormous societal relevance (e.g. school curriculum); as basic scientists we are well placed to capitalise on this. However, for the communication of fundamental science there are usually no 'natural' target audiences that would be attracted for any other reasons than curiosity. Therefore, the challenges for communicating fundamental science are disproportionately greater than faced by medical or applied researchers. This requires clever strategies and engaged networks of science communication that include not only researchers but also learned societies, publishers and funding organisations. Speaking from experience, I would say that we need to think big or any effort invested will have very limited reach and impact! For example, as communications officer of the BSDB, I have managed to kick-start a campaign advocating Dev. Biol., which was then joined by the Company of Biologists. However, this campaign will become truly effective only if DB societies worldwide ([LINK](#)) start collaborating on this by sharing arguments, strategies, resources and using them to lobby their governments.

As matters stand, initiatives such as DrosAfrica or Manchester Fly Facility/droso4schools mainly preach to the converted. They have no effective means of reaching non-self-selected audiences, have no dedicated support through influential organisations or individuals that would put their weight behind them. In consequence, they are not seen as initiatives owned by, or speaking for the fly community. This makes the task of building networks close to impossible and puts any kind of engagement into question, making it a personal risk to invest valuable time that is otherwise needed to drive one's own scientific career.

I made my suggestions as to what can be done. In my view, FlyBase would provide a uniquely powerful starting point, by simply turning its front page into a community portal, which would not affect the data

base structure or cause any extra work to the team. I appreciate having been given the opportunity to speak up for this type of advocacy on Fly Board, but I understand that there is currently no hunger for this kind of innovations, and I got the impression that my views about the enormous opportunities we have appear not widely shared. I will therefore re-focus on those goals of the Manchester Fly Facility which appear achievable, including the initiatives in Croatia, Nigeria and primarily the UK - in particular bringing flies back into the national school curriculum. Such an achievement would have major impact on fly advocacy, but many hurdles will have to be taken!

Andreas

Appendix 12. FlyBase (Norbert Perrimon & Susan Russo Gelbart)

FlyBase Report to the Drosophila Board March 4, 2019

For the past twenty-six years, FlyBase has provided a centralized resource for Drosophila genetic and genomic data to enable researchers to further their research. Drosophila is one of the premier model organisms and provides cost-effective help in elucidating the etiology of human genetic diseases. 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. We will prioritize curation of data sets relevant to gene expression, cellular functions, signaling pathways, and human diseases, and display 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. As a member of The Alliance for Genomic Research (AGR), FlyBase will work closely with other Model Organism Databases (MODs) to integrate data sets and develop tools to enable cross-species analyses. This effort will have a major impact on the fly community, accelerating the development of models of human diseases.
3. To facilitate more integrative analyses and approaches, FlyBase will continue to expand its utility as a platform for integrating and displaying large-scale studies, transcriptomics and proteomics data sets. In addition, FlyBase will improve 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.

April 1, 2019 begins year 2 of our 5-year renewal with NHGRI. As anticipated, our budget was reduced with cuts over the 5-year period of up to ~25% (which normalize to 35%). Our necessary user-fee collection to supplement FlyBase funding continues. As of 04-March-2019 (nearly 1 year since fees were implemented), 283 labs have committed to pay ~\$196,443.00. We have collected \$143,643.00 of this amount. We are grateful for the strong support from our community.

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

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

OUTREACH:

Goal: *To improve the utility of FlyBase for our core community of Drosophila researchers, and to attract additional users*

FlyBase Community advisory group (FCAG) The FCAG was launched in 2014 with the aim of improving our consultation of the community about the effectiveness of current curation strategies and website features, proposed changes, and future plans. It currently comprises 554 members from 41 countries. We will continue to send out regular surveys to increase community input into upcoming changes and new features.

Video tutorials: We continue to produce video tutorials, which have had >8,000 views to help users get the most of FlyBase tools and features, and These can be found on the 'FlyBase TV' YouTube channel: <https://www.youtube.com/c/FlyBaseTV>.

GSA article mark-up: We have continued our successful collaboration with WormBase and the Genetics Society of America journals, Genetics and G3, to mark-up genetic entities and hyperlink them to FlyBase - authors approve the final links after an initial automated article mark-up and QC check by a FlyBase curator.

Presentations/Conference attendance: Staff attended and made presentations at the Annual Drosophila Research Conference in Philadelphia in April 2018, the monthly London Fly Meeting in April 2018, the Crete Fly Meeting in June 2018, the European *Drosophila* Neurobiology Conference in Krakow in September 2018, the American Society of Human Genetics meeting in San Diego in October 2018 and the Cambridge (UK) Fly Symposium in January 2019.

Twitter: We promote FlyBase using Twitter: @ FlyBaseDotrOrg <https://twitter.com/flybasedotorg?lang=en> Tweets are done regularly about new features and updates; over 2,500 followers.

FlyBase Help Desk: We maintain a project-wide help desk to provide support to users with data/web interface questions or suggestions.

CURATION:

Bibliography

Goal: *To incorporate all publications describing Drosophila research into FlyBase.* We are exploring obtaining additional Graphical Abstracts and other 'summary figures' from Cell Press and other publishers in an automated and ongoing basis.

New publications Potentially relevant publications are identified in PubMed and citations downloaded on a weekly basis. 2,319 publications were assessed in the current period; 1,968 (85%) were verified and added to FlyBase.

Edits/retrofits >6,000 PubMed IDs were added to older publications in FlyBase that previously lacked them; this also allowed incorporation of the corresponding DOIs, PubMed Central IDs, and abstract texts.

Graphical abstracts >900 graphical abstracts from papers in journals published by Cell Press were obtained and associated with references in FlyBase.

Representative publications We have been working to improve our current algorithm to better discern the most relevant publications for highly characterized genes.

First-pass curation

Goal: To prioritize research papers for full literature curation based on the presence and amount of curatable data (triaging)

Author curation We continue to use our automated email system to ask authors to triage and associate key genes to their newly published papers using our online 'Fast-Track Your Paper' tool. 690 papers have been curated by authors in the current reporting period, resulting in 4,162 new gene-to-reference associations, and representing ~65% of new curatable papers published.

Triaging using text-mining We continue to use the results of an automated Support Vector Machine (SVM) text-mining system, developed by WormBase, to triage papers not curated by authors. Data types recognized by this system include new alleles (with 72% recall/80% precision), new transgenes (82%/79%), disease models (67%/67%), and physical interactions (93%/68%).

Literature curation

Goal: *To curate new alleles and transgenic constructs, mutant phenotypes and genetic interactions, disease models, and functional information from the primary literature*

Genetic/Phenotypic curation: 535 papers have been curated for new genetic reagent information in the current period, representing 95% of new curatable papers published (which are 35% of total), based on current triaging data. 340 papers have been curated for phenotypic data in the current period, representing 90% of new curatable papers published (which are 25% of total), based on current triaging data. We aim to keep up with the number of new curatable papers published (~1,200 papers/year based on current triage and publication levels)

Gene Ontology (GO) annotation: We have focused on review and annotation of signaling pathways as part of producing a new Pathway resource in FlyBase (see below). FlyBase curators have added over 2,800 new annotations and have removed 3,000 low quality or redundant annotations from non-experimental sources or high throughput studies. We will focus on the annotation of signaling pathway members and non-coding RNAs.

Disease Ontology (DO) annotation: In this reporting period, Disease Ontology (DO) annotations have been made for phenotype-based models of 57 different diseases from 80 references. In total, 337 statements have been added, corresponding to 246 reporting disease models and 91 reporting modifiers of disease. We continue to revise and improve our current disease model annotation strategy and make it more in line with other MODs and the Alliance of Genome Resources

Neural phenotypes and datasets: As part of our collaboration with the Virtual Fly Brain (VFB) project, we have begun curation of experiments that use phenotypes to illuminate the function of neural cell types or tissues.

Neural expression: As part of our collaboration with VFB, 3,781 expression pattern statements from 120 references have been curated for neural expression. VFB priorities in the coming year include curation of drivers (especially Split-Gal4 drivers) expressed in the larvae and adult, and papers utilizing FlyLight image datasets.

Review curation: 469 reviews (published between 2011-2018) were curated, resulting in >4,500 new gene-to-reference associations. We aim to eliminate the backlog of uncurated reviews (published 2007-2011).

Physical interactions (protein-protein, protein-RNA, miRNA-RNA): 255 papers were curated; 1126 interactions curated. FlyBase curation of physical interactions is focused on the curation of low-throughput studies in which interactions are typically supported by multiple independent forms of evidence, though 11 high-throughput interaction datasets have been incorporated, as well. The vast majority of low-throughput studies are not curated by other interaction databases: only 7.6% and 5.5% of publications with FlyBase curated interactions have also been curated by BioGRID and the IMEx Consortium, respectively, making FlyBase the main source of these well-supported interactions.

The current corpus of physical interaction data comprises **42,548** interactions, **57.1%** of which are supported by low-throughput experiments. These interactions represent **28,969** distinct pairwise gene-gene interactions involving **5,817** genes, curated from **3,756** publications. Six years into this curation endeavor, **5,983** of all **9,030**

flagged papers (**66.3%**) have been reviewed, leaving a backlog of **3,047**. We have currently reviewed **100%** of the papers from 2009 to the present with user or curator flags and **87.3%** of papers identified solely by text-mining.

Our goals for the coming year are to continue curation prioritizing papers from the current year as they are flagged on a weekly basis; papers from the backlog with author/curator added flags; and papers from the backlog identified solely by text mining. We aim to complete curation of all author/curator flagged papers published from 2005-present, improve web reporting to distinguish interactions supported by high- and/or low-throughput data, and provide new linkouts from FlyBase to other interaction database resources, particularly MIST (<http://fgrtools.hms.harvard.edu/MIST/>), IntAct (<http://www.ebi.ac.uk/intact/>) and STRING (<https://string-db.org/>).

Features mapped to genome (mutational lesions): 213 features from 193 genes were curated from 87 references. We plan to keep up with curation of new papers flagged for “genome feature, and search FlyBase for null mutations that have no curated genome location data but appear to be mappable based on the “nature of allele” information that has been curated, and then curate these.

Expression data: 517 papers were curated with expression data.

GAL4 expression patterns: a table was created of the most popular GAL4 lines. Targets of GAL4 curation included: Expression pattern information accompanying BDSC GAL4 stocks (completed); and GAL4 insertions and constructs that do not have curated expression data, and are in the top 400 requested from BDSC (in progress).

Wild type expression curation: Papers with wild type expression patterns are largely identified via curator and user flags. Papers are targeted that describe 1) expression patterns for minimally characterized genes 2) postembryonic expression patterns and 3) novel sites of expression for partially curated genes. Since March, 610 papers with wt_exp flags have been reviewed.

Future plans include to work through remaining papers with GAL4 expression data; work through 1,000 papers of the backlog of (~4,000) papers flagged for wild type expression; stay up-to-date with wild-type expression curation for newly characterized genes; create a test set of papers for wild-type expression flag to help identify highest priority papers; create a table in FlyBase of most popular marker genes, insertions, and constructs; and enhance functionality of ‘GAL4 etc.’ search tab to allow additional search capabilities.

High-throughput data and metadata: Key datasets and reagent collections curated this year:

- REDfly regulatory region update
- Developmental Proteome (still in progress)
- Fly TransgeneOme (fly constructs only)
- Updates to VDRC shRNA line collections

We plan to finalize and promote Drosophila template for NCBI biosample submission, and do short-term curating of the metadata for the Oliver-lab-assessed RNASeq datasets.

Cell lines: ~ 184 cell-line-to-reference associations and 6 new cell line records were added to FlyBase. We will continue this effort in collaboration with Arthur Luhur and Chris Hemmerich at the DGRC.

Human disease model integrated reports: 158 new human disease model reports (912 total)

Total: 648 specific model reports, 120 series reports, 147 cross-reference and potential reports

715 new papers associated with one or more disease models (2967 total)

Total: 2412 primary references; 526 reviews, including general reviews of the disease (170) and fly-centric reviews (356); 29 misc. (notes, editorials)

187 new genes associated with human disease model reports (853 total)

Total: 590 D. melanogaster, 237 H. sapiens, a few other species or synthetic

4 new reports for non-gene based models (chemical- or diet-induced; cell ablation) (17 total)

We plan to continue curation of major portion of the backlog for new diseases (currently ~165 papers); keep current with “disease skimming” for new papers that are flagged (addition of new references to existing disease models); and work to overhaul and subsequently retrofit our current methods for curating and storing phenotype-to-genotype associations. This work is a pre-requisite to starting curation of chemical-induced phenotypes and to improvements in our disease model annotations.

Skimming/triaging: 1905 publications skimmed and **6944 gene-to-publication links** curated. We aim to keep up to date with standard skim curation lists which will be generated regularly; apply a light-skim protocol (scan title and abstract) for papers that have been marked as ‘not likely to contain curatable data’ by the text-mining triage system; and skim-curate the newly defined “mop-up” list which will be generated yearly to catch papers that have not had any curation despite having had flags assigned.

Gene model annotation (*D. melanogaster*): For models flagged based on new data in the literature, we annotated ~40 additional stop-codon read-throughs; in several cases, added double and triple read-throughs based on FlyBase analysis. We plan to annotate new genes or exons based on RNA-Seq analyses from GRIT and Brian Oliver’s group (anticipate annotation of many additional lncRNAs); fold new TSS flags (primarily RAMPAGE and modENCODE CAGE data); polyA data into the assessment; and keep current with models flagged based on new data in the literature.

Integration/summarization

Goal: *To enhance accessibility and value to data within FlyBase*

Gene Groups We have continued to build the Gene Groups resource, in which related sets of *D. melanogaster* genes (gene families, macromolecular complexes and other functionally related gene products) are compiled and used to produce report pages. There are now a total of 998 Gene Groups, comprising 5,930 unique genes (encompassing 33% of sequence-localized genes). Notable omissions from our Gene Group resource include metabolic pathways and certain enzyme sets, but additional funding will be required to conduct that work.

Signaling Pathways We have used GO annotation as a basis to compile lists of relevant genes, and the architecture developed for Gene Groups to build Pathway Report pages. Alongside each gene, we display the number of papers used to evidence inclusion and links to these papers. We will build on this work, developing the reports to allow users to access and analyse other data associated with member genes. We will also continue to review pathways, particularly for heavily studied pathways that would benefit from a second pass curation effort.

Enzyme Commission (EC) annotations and links to metabolic databases We have developed a pipeline that takes advantage of existing GO annotations and EC cross-references within the GO so that the EC number, recommended name and the catalyzed reaction of a given enzyme is now shown near the top of relevant Gene Reports. We have also worked with the BioCyc, KEGG and Reactome databases in order to provide direct links from the ‘Pathway’ section of a FlyBase Gene Report to their databases.

Gene Snapshots We have continued to produce Gene Snapshots, the short summaries shown at the top of each *D. melanogaster* gene report designed to provide a quick overview of the function of a gene's products. There are currently 2,627 published snapshots. We aim to complete the revision of ~600 snapshots contributed by authors in our final round of email requests.

Improved categorization of transgenic alleles The data retrofit for the new 'Experimental Tool' reports has been completed. This new report type allows users to identify transgenic constructs and insertions with particular characteristics (e.g. tagged with FLAG, encoding a GAL4 driver) by linking transgenic alleles and constructs to the appropriate experimental tool(s). Entries for 398 different experimental tools have been created. These tools have been linked to 105,822 transgenic alleles to describe the components that make up the transgenic allele; 30,931 alleles are now annotated as 'encoding' a tool (e.g. GAL4, EGFP), 26,740 alleles are annotated as being tagged with a tool (e.g. a nuclear localization signal), and 21,638 alleles carry another tool (e.g. FRT, loxP). In addition, the regulatory region present (either a tool such as UAS, or a gene) has been

added to 78,037 transgenic construct alleles. We will build a search that allows users to search for constructs/insertions with particular characteristics, using the Experimental Tool information that has been recently added to the database. We will also expand the set of tools to include optogenetic tools that are used to manipulate the activity of neurons.

***D. melanogaster* non-coding RNA (ncRNA) set** All *D. melanogaster* genes producing ncRNAs now have a standardized prefix based on their class. We have worked with the RNAcentral developers to define a new data exchange format that allows direct, up-to-date and comprehensive submission of our ncRNA annotations to their database. Further, Unique RNA Sequence (URS) identifiers from RNAcentral have been added as cross-references to all relevant gene and transcript reports.

***D. melanogaster* proteome** We have continued to liaise with curators and developers at UniProt to improve the accuracy and consistency of the *D. melanogaster* proteome set produced by our two databases and will continue to do so with the aim of making our *D. melanogaster* proteome sets identical.

Ontology development

Goal: *To maintain and improve the controlled vocabularies (ontologies) which are critical for curation and the FlyBase database structure*

Fly anatomy 552 terms have been added to the fly anatomy ontology in this reporting period. Improvements have also been made to term definitions and ontology structure in several areas, including parts of the gut, imaginal tissues and many types of neuron. We will continue adding new anatomy terms and enhancing the existing terms, with a focus on new neuroanatomy terms and definitions.

Phenotypic class We will continue to review and improve the phenotypic class ontology, focusing on terms for behavioral, learning and memory phenotypes in collaboration with VFB.

Alliance of Genome Resources

FlyBase staff currently are members to several working groups within the Alliance: 'Disease and Phenotypes', 'Interactions', 'Gene Descriptions', 'Biological Function', 'Variants', 'Basic gene information', 'Orthology', Developers are involved in producing and integrating data for the Alliance website members of the Architecture working group, and setting up Redux state management. Two FlyBase members have served as Alliance Data Quartermasters (responsible for overall dataset integration / liaison between working groups and developers). Significant contributions have been made to the specification and display of basic allele and phenotype data and automated gene summaries in the Alliance database/website, orthology backend (use of specific methods), and data integrity and loading. 10 FlyBase members attended the 'all-hands' meeting in November/December 2018, and will continue to contribute to working groups within our remit and areas of expertise.

Software and website development

Goal: *To increase the efficiency, speed and accuracy of manual curation by developing/improving essential scripts*

FlyBase continues to develop the necessary curation and QA/QC tools, Chado database modules, web site features and bulk reports to accommodate new data types into FlyBase.

New Data Capture and Processing Development (Curation) include: Frequently Used GAL4 Table; Backend Ingest Redevelopment; Prototype of new Proforma parser; and Local instance (non-production) of ChEBI

Significant New Data Implementations include: Developmental Proteome "LFQ" expression; Developmental Proteome peptides; Physical Interactions MITAB file; RNAcentral JSON file; Drosophila Genome Nexus (DGN) SNP data (partial); Short-guide RNA designs

Notable Features & Enhancements to FlyBase.ORG (March 2018 to present)

The FlyBase website team rolled out the new FlyBase 2.0 website at the end of 2017. In the time since, efforts have been focused on integrating new datasets, improvements to the site, and fixing multiple bugs.

The following is a list of these features by release:

- **FB2018_02**
 - [Frequently-Used GAL4 Drivers table](#)
 - FlyBase People database restored and updated.
 - Added Dataset section to gene reports.
- **FB2018_03**
 - Updated DIOPT orthology data to 7.1
 - Implemented 15 additional RNA-Seq tracks to JBrowse using the TopoView glyph
 - Implemented Pathway reports, a subtype of the Gene group data class.
 - Implemented a species filter in HitLists
- **FB2018_04**
 - Integrated Experimental tools, a new data class for FlyBase, into the FlyBase site (search, reports, API, etc.).
 - Added ~900 graphical abstracts from Cell press.
- **FB2018_05**
 - Authored paper for the NAR Database issue.
 - Majority of tracks migrated to JBrowse.
 - RNACentral IDs added to FlyBase.
 - Various tweaks to Human Disease reports.
 - Added TRiP-OE/TRiP-KD gRNA tracks to JBrowse
- **FB2018_06**
 - Enzyme Commission.
 - Short-guide RNA (sgRNA) reagents prediction JBrowse tracks
 - Demoted species
 - New “key links” in gene report
 - Developmental profiles of protein expression
 - Experimental Tools section in gene report
- **FB2019_01**
 - Expression Summary Ribbons
 - Links to FPbase added to Tool Reports
 - New pathway reports
 - CST links added to commercially available antibodies
 - Links to metabolic pathways at BioCyc
 - Genomic tRNA database links
 - SRA aggregated RNS-Sew tracks
 - Proteomic peptides track

Other upgrades and activities:

- ID converter UI improvements (in process).
- Hitlist fixes and improvements
- Power user documentation for using Chado and our APIs (in process)
- New icons and linkouts- Positions available, iProteinDB, BioLitMine
- FlyBase Community Advisory Group (FCAG) survey

Ongoing Activities

FlyBase has maintained a normal schedule of 6 releases to flybase.org each year. There are extensive ongoing activities to maintain the website include internal and external group coordination, pipeline management and maintenance, and system administration tasks.

Development Targets For 2018-2019

For the next year, plans to support the website will be to focus development efforts on observing and listening to users to optimize the usability of the new site. Usage of the site and ideas for improvements will be captured via analytics and other existing outreach efforts. The website team provides support for development required by new FlyBase projects that are being developed. Near term projects include migration of all species and tracks from GBrowse to JBrowse, integration of developmental proteome data, integration of guide RNAs, and a revamped BLAST tool.

Future development goals:

- Complete species and track migration from GBrowse to JBrowse.
- Creation of developmental proteome graphs for gene pages.
- Integration of developmental proteome data into JBrowse.
- Integration of guide RNAs in JBrowse.
- An updated BLAST tool for the latest NCBI BLAST.
- Optimizing usability in FB 2.0 based on user feedback and observations.
- Provide support for new FlyBase curator projects.
- Continue to expand our use of cloud based services where it makes technical and financial sense.
- Evaluate open source tools for automating cloud deployment and management.
- Enhancement of public programmatic endpoints (APIs) to improve data access for external collaborations (e.g. AGR) and advanced users.
- Continue to evaluate GraphQL for use as an enhanced API endpoint and coordinate common schemas with AGR.
- Fast Track tool improvements.
- Continue to work with AGR development teams.
- Continued security improvements.

Figures:

Export TSV

Allele	Insertions / Constructs	Assoc. gene	Common terms	Major tissue	Major stage	Description	# Stocks	# Refs
Scer ^{GAL4} ^{104Y}	P(GawB)104y P(GawB)		ventral body, VBO	lateral accessory lobe fan-shaped body lateral fan-shaped neuron ExF12 lateral fan-shaped neuron ExF11	adult stage	Drives expression in several central brain structures, most prominently in the dorsal and fan-shaped body, including dorsal layers 6-8 and ventral layers 1-2; also drives expression in the lateral accessory lobe (VBO)	0	22
Scer ^{GAL4} ¹⁰⁹⁽²⁾⁸⁰	P(GawB)109(2)80 P(GawB)		da neuron, md neuron	abdominal dorsal multidendritic neuron dendritic arborizing neuron	larval stage adult stage P-stage embryonic stage	Drives expression in multidendritic and dendritic arborizing neurons.	2	85
Scer ^{GAL4} ¹¹⁵¹	P(GAL4)1151 P(GAL4)			adult somatic muscle adeipithelial cell	larval stage adult stage P-stage	Drives expression in larval adeipithelial cells, and in adult somatic muscles and their pupal precursors.	0	31

Figure 1 – Frequently Used GAL4 Drivers Table

Datasets (2)			
Study focus (2)			
Experimental Role	Project	Project Type	Title
bait_protein	BDTNP_TFBS	genome binding	ChIP characterization of transcription factor genome binding, Berkeley Drosophila Transcription Factor Network Project.
bait_protein	modENCODE_regulation_TFs	genome binding	Genome-wide localization of transcription factors by ChIP-chip and ChIP-Seq.

Figure 2 – Dataset section in gene report.

Model Organism Orthologs (via DIOPT v7.1)						
Mus musculus (laboratory mouse) (7)						
Species\Gene Symbol	Score	Best Score	Best Reverse Score	Source	Alignment	Complementation? Transgene?
Mmus\Bcl6b	2 of 15	Yes	Yes	Compara, eggNOG, Inparanoid, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp, TreeFam, ZFIN		
Mmus\Bcl6	1 of 15	No	Yes	Compara, eggNOG, Inparanoid, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp, TreeFam, ZFIN		
Mmus\Osr1	1 of 15	No	No	Compara, eggNOG, Inparanoid, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp, TreeFam, ZFIN		
Mmus\Osr2	1 of 15	No	No	Compara, eggNOG, Inparanoid, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp, TreeFam, ZFIN		
Mmus\Sp5	1 of 15	No	No	Compara, eggNOG, Inparanoid, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp, TreeFam, ZFIN		
Mmus\Zfp362	1 of 15	No	No	Compara, eggNOG, Inparanoid, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp, TreeFam, ZFIN		
Mmus\Zfp524	1 of 15	No	Yes	Compara, eggNOG, Inparanoid, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp, TreeFam, ZFIN		

Figure 3 – Gene report orthology section with DIOPT 7.1 data

Input: Enter gene symbol(s) or ID(s), separated by spaces Search

Species: *D. melanogaster* Gene(s): e.g. Cdk1, CG5363, FBgn0004106, 34411

Output: HUMAN AND MODEL ORGANISMS (via DIOPT)

- H. sapiens* (Human)
- R. norvegicus* (Norway rat)
- M. musculus* (Laboratory mouse)
- X. tropicalis* (Western clawed frog)
- D. rerio* (Zebrafish)
- D. melanogaster* (Fruit fly)
- C. elegans* (Nematode, roundworm)
- A. thaliana* (Thale cress)
- S. cerevisiae* (Brewer's yeast)
- S. pombe* (Fission yeast)

un/check all: instead search *Drosophila* species, insects etc.

Figure 4 – The Orthology search tool.

Search Term: dpp Species: <i>Drosophila melanogaster</i> (Fruit fly) Gene: dpp Reports: NCBI FlyBase							
Ortholog Gene	Ortholog Gene Reports	Via DIOPT (v7.1)					
		Score	Best Score	Best Rev Score	Source	Align	Transgene in Fly
<i>Homo sapiens</i> (Human)							
BMP2	NCBI Ensembl OMIM HGNC	8 of 15	Yes	Yes (+)	Compara, eggNOG, Homologene, Inparanoid, Isobase, Panther, Phylome, RoundUp	(+)	
BMP4	NCBI Ensembl OMIM HGNC	7 of 15	No	Yes (+)	Compara, eggNOG, Inparanoid, orthoMCL, Panther, Phylome, RoundUp	(+)	Yes
GDF1	NCBI OMIM HGNC	3 of 15	No	Yes (+)	eggNOG, Panther, TreeFam	(+)	
GDF3	NCBI OMIM HGNC	3 of 15	No	Yes (+)	eggNOG, Panther, TreeFam	(+)	
BMP10	NCBI OMIM HGNC	2 of 15	No	Yes (+)	eggNOG, Panther	(+)	
BMP15	NCBI OMIM HGNC	2 of 15	No	No (+)	eggNOG, Panther	(+)	
BMP3	NCBI OMIM HGNC	2 of 15	No	Yes (+)	eggNOG, Panther	(+)	
GDF10	NCBI OMIM HGNC	2 of 15	No	Yes (+)	eggNOG, Panther	(+)	
GDF15	NCBI OMIM HGNC	2 of 15	No	No (+)	eggNOG, Panther	(+)	

Figure 5 - Orthology search results.

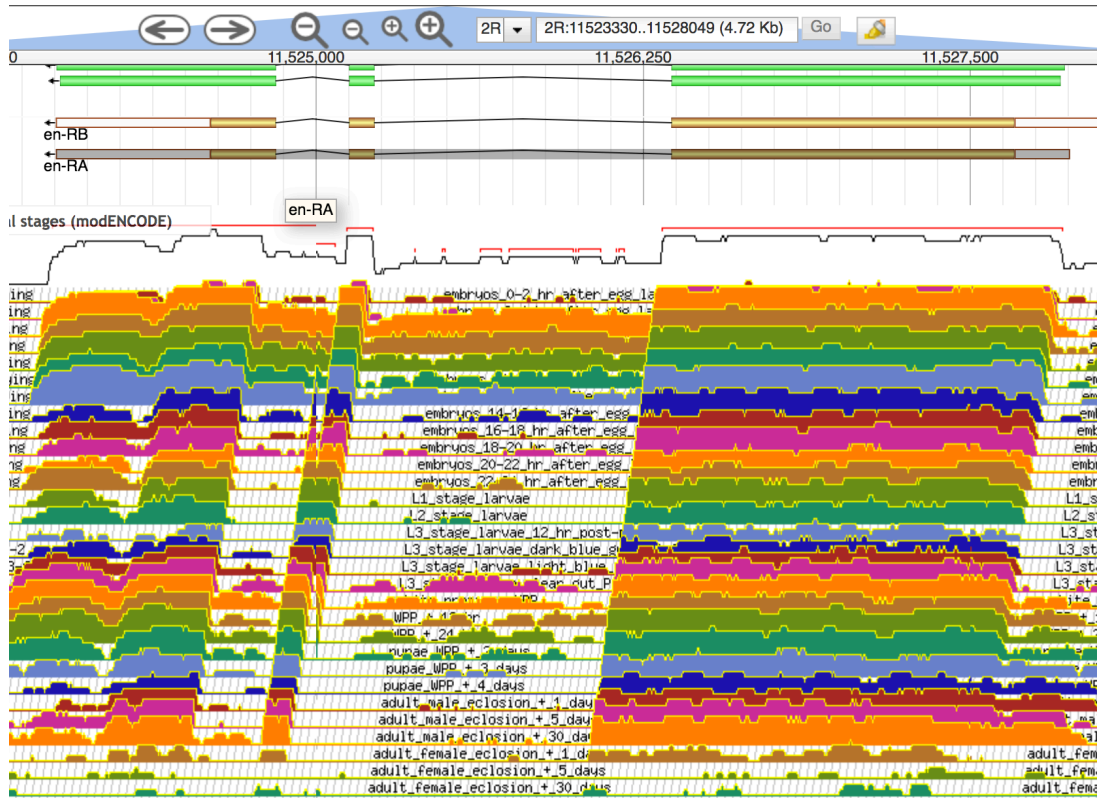


Figure 6 – Dmel RNA-Seq tracks in JBrowse

General Information				
Name	Sevenless Signaling Pathway	Species	<i>D. melanogaster</i>	
Symbol	SEVL	FlyBase ID	FBgg0000941	
Date last reviewed	2018-06-10	Number of members	27	
Description				
Description	The specification of the R7 photoreceptor cell in each ommatidium of the developing <i>Drosophila</i> eye is dependent on activation of Sevenless receptor tyrosine kinase (<i>sev</i>), which acts via the canonical Ras/Raf/MAP kinase cascade to promote the expression of <i>lz</i> and <i>pros. sev</i> , expressed in presumptive R7 cells, is activated by binding to Bride of Sevenless (<i>boss</i>), a seven-transmembrane protein expressed in R8 cells. (Adapted from FBrf0127283 and FBrf0221727).			
Notes and selected reviews	Selected publications for background information: Signal transduction and the fate of the R7 photoreceptor in <i>Drosophila</i> (FBrf0055173), The Sevenless signaling pathway: variations of a common theme (FBrf0127283), The fly eye: Through the looking glass (FBrf0237528), The little R cell that could (FBrf0180351), Parsimony and complexity: Cell fate assignment in the developing <i>Drosophila</i> eye (FBrf0236340), Receptor tyrosine kinases in <i>Drosophila</i> development (FBrf0221727). Note: Pathway Pages in FlyBase are under development. The pathway gene tables display genes that have been experimentally shown to act within the pathway or modify pathway activity. We welcome any feedback to help improve the usefulness and accuracy of these gene lists.			
Biological Process Gene Ontology (GO) term(s)				
Related Gene Groups				
Component group(s)	Effectors Negatively Regulated by Sevenless Signaling Pathway Negative Regulators of Sevenless Signaling Pathway Positive Regulators of Sevenless Signaling Pathway Sevenless Signaling Pathway Core Components			
Members (27)				
For all members:	View Orthologs	Export to HitList	Export to Batch Download	
Effectors Negatively Regulated by Sevenless Signaling Pathway				
Gene Symbol	Gene Name	Gene Group Membership	GO Molecular Function (Experimental)	# Refs

Figure 7 – Pathway report for Sevenless Signaling Pathway

dpp

Filter by species

- D. melanogaster* (5751)
- H. sapiens* (transgenes in flies) (5)
- other *Drosophila* species (69)
 - D. simulans* (11)
 - D. sechellia* (2)
 - D. yakuba* (7)
 - D. erecta* (8)
 - D. ananassae* (3)
 - D. pseudoobscura* (14)
 - D. persimilis* (3)
 - D. willistoni* (2)
 - D. mojavensis* (2)
 - D. virilis* (9)
 - D. grimshawi* (1)
 - Others (7)
- Other species (389)

6145 selected

dpp decapentaplegic (CG9885, F

Feature type: protein c

Sequence Location: 2L:2,428,

Gene Snapshot >

Mad Mothers against dpp (CG12

Feature type: protein c

Sequence Location: 2L:3,146,

Gene Snapshot >

Dad Daughters against dpp (CG5

Feature type: protein c

Sequence Location: 3R:17,05

Figure 8 – HitList species filter (highlighted in red)

Langen et al. (2015) (FBrf0228855)

Title: The Developmental Rules of Neural Superposition in *Drosophila*.

Citation: Cell. 2015;162:120--133 **Publication type:** paper

Abstract >

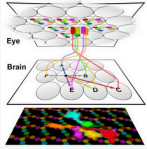


Figure 9 – Graphical abstract in a Hitlist

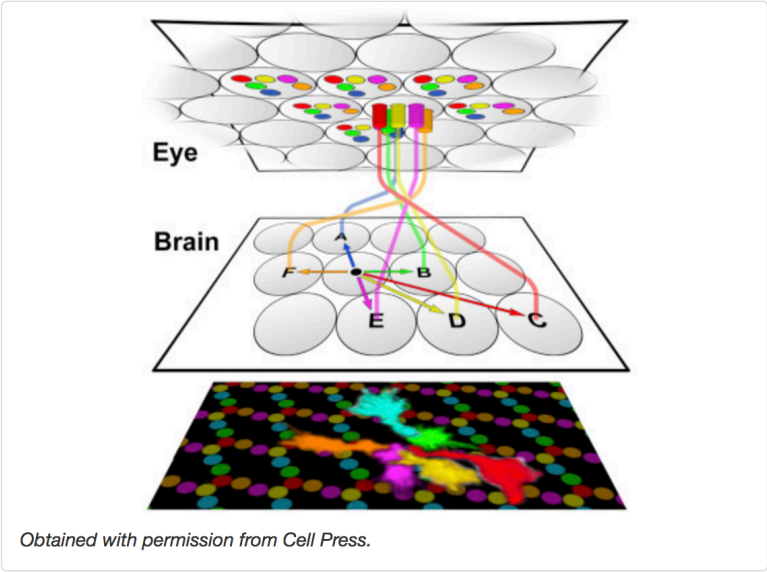
Graphical Abstract	 <p>Obtained with permission from Cell Press.</p>
PubMed ID	26119341
PubMed Central ID	PMC4646663 (PMC) (EuropePMC)
DOI	10.1016/j.cell.2015.05.055

Figure 10 – Graphical abstract in Reference report.

General Information			
Symbol	mCherry	FlyBase ID	FBto0000118
Name	monomeric Cherry fluorescent protein		
Description			
Description	mCherry is a monomeric red fluorescent protein with an excitation peak of 587nm and an emission peak of 610nm in vitro. It is an artificial derivative of the naturally occurring fluorescent protein encoded by the Discosoma drFP583 gene (GenBank:AF168419; AAF03369) (PMID:15558047).		
Uses	red fluorescent protein		
External Crossreferences and Linkouts	GenBank Nucleotide - A collection of sequences from several sources, including GenBank, RefSeq, TPA, and PDB. AY678264		
Related experimental tools			
Common gene of origin (18)	Tool	Uses	
	C-mCh	split fluorescent protein	
	DsRed1	red fluorescent protein	
	DsRed2	red fluorescent protein	
	DsRed(E5)	fluorescent timer protein	
	DsRed(M1)	red fluorescent protein	
	DsRed(S197Y)	red fluorescent protein	
	DsRed(T1)	red fluorescent protein	
	DsRed(T4)	red fluorescent protein	
	DsRed(Unk)	red fluorescent protein	
	E2-Orange	orange fluorescent protein	
	mOrange	orange fluorescent protein	
	mRFP1	red fluorescent protein	
	mRFP(Unk)	red fluorescent protein	
	mRFPPruby	red fluorescent protein	

Figure 11 – Experimental tool report

2018 FlyBase Web Usage

The following are web statistics from the FlyBase website as captured by Google Analytics. Unless otherwise stated, all usage statistics in this document cover the period of Jan-Dec for the years 2015-2017 and Jan-Nov for 2018. In summary, the usage statistics, when compared to the previous year period, indicate that our overall usage, user activity, and number of users has decreased. In addition, data class report and tool usage has not significantly changed from previously observed and well-established patterns.

One cause for the decrease in usage is a technical issue with our analytics tracking in the new site that resulted in a partial loss of data from several of our tools during Jan and Feb of 2018. However, this does not explain decreases in the other months since this issue was fixed (Mar-Nov). Other possible reasons include technical differences between the FlyBase 2.0 site and our previous site that is affecting the analytics data, an actual drop in usage, or some other anomaly on the Google Analytics side. Once more data is collected, we plan further analyses to try to determine the underlying cause.

Figure 1 shows FlyBase pageviews for the previously mentioned time periods. 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 for 2018 thus far is 826k, with a high of 968k and a low of 696k. The periodic dips in this plot all correlate with expected holiday patterns. Compared to Jan-Nov of 2017, pageviews are down 18%.

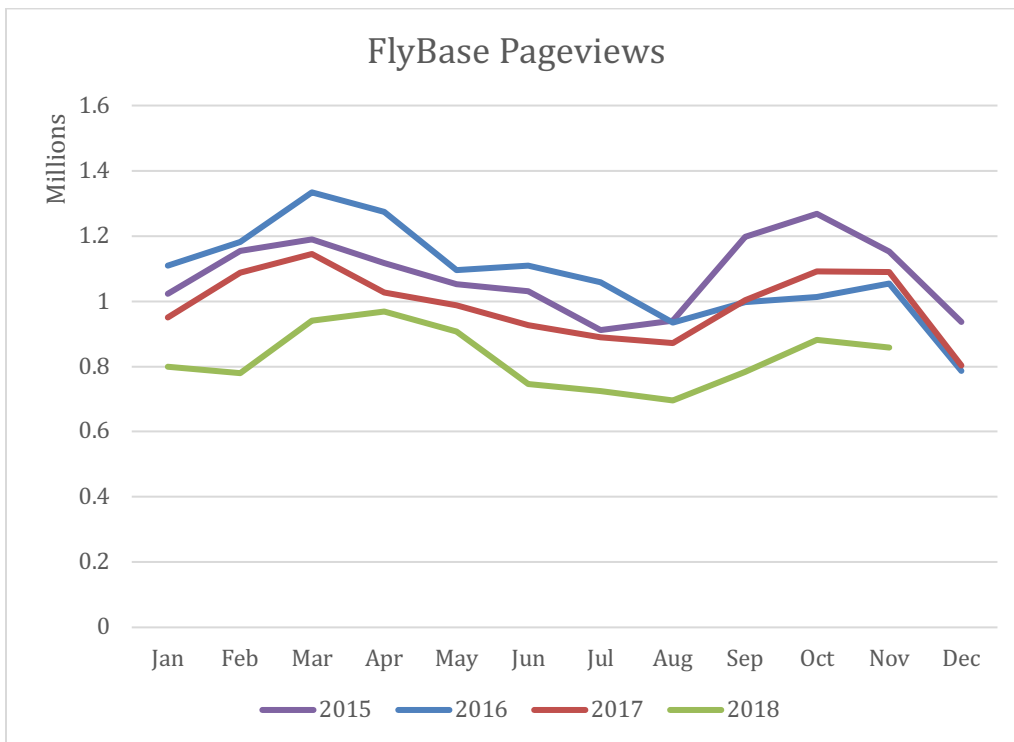


Figure 1 – FlyBase Pageviews

Figure 2 shows FlyBase sessions (visits) for the same period as pageviews. 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 for 2018 thus far is 122k, with a high of 140k and a low of 101k. Compared to Jan-Nov of 2017, sessions are down 16%.

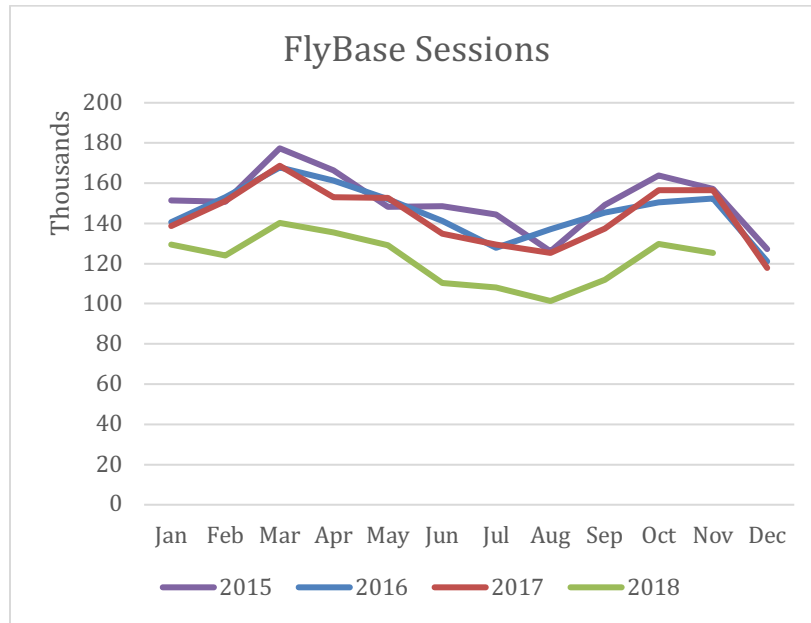


Figure 2 – FlyBase sessions for Jan 2015 – Nov 2018

Figure 3 shows FlyBase users for the same period as pageviews. 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 for 2018 thus far is 44k/month, with a high of 51k and a low of 35k. Compared to Jan-Nov of 2017, the number of FlyBase Users are down 10%.

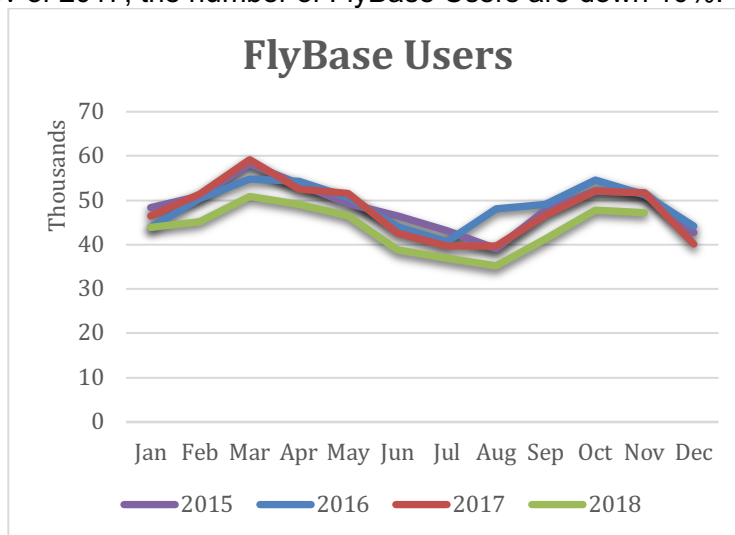


Figure 3 – FlyBase users for Jan 2015-Nov 2018.

Figure 4, “FlyBase Data Class Usage by Pageviews”, shows the total pageviews for FlyBase data class reports for Jan-Nov 2018. The top 5 data class reports are Genes, References, Insertions, Alleles, and Stocks. This is relatively unchanged over previous years aside from Stocks slipping from the second position to fifth.

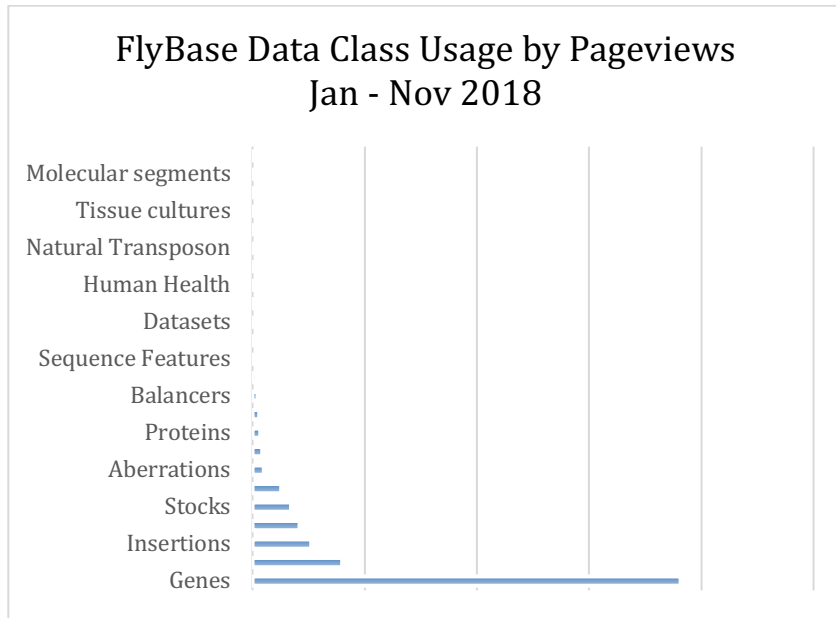


Figure 4 – Pageviews by FlyBase Data Class. * Experimental Tools were first introduced on Aug 23, 2018.

Figure 5, “FlyBase Tool Usage”, shows that our top 5 tools are BLAST, Simple Search, Jump to Gene, GBrowse, and Sequence Downloader.

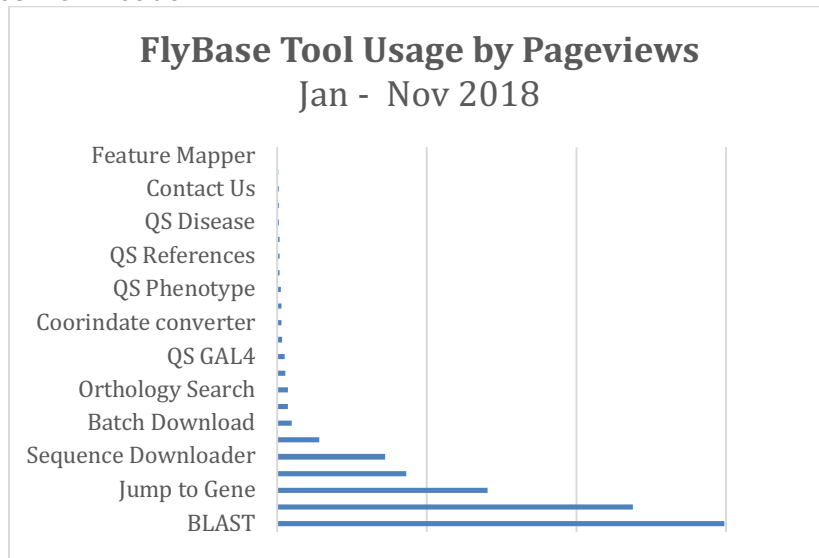


Figure 5 – FlyBase Tool Usage.

Appendix 13. Bloomington Drosophila Stock Center (Kevin Cook)

BLOOMINGTON STOCK CENTER

New facility After several years of planning, we are moving the back-up stock copies and the staff who care for them to a newly renovated facility across campus. Splitting our operation will help with disaster preparedness.

Stock Holdings as of March 4, 2019

- 71,407 stocks with 74,536 unique genetic components
- 17,459 annotated genes are associated with alleles, constructs or deficiencies in the collection
- 12,199 annotated *D. melanogaster* genes are associated with alleles or constructs in the collection

2018 Use Statistics

- 222,975 samples shipped in 13,173 shipments
- 3.2 orders per stock on average with a range of 0 to 153; 63% of stocks ordered at least once, 18% ordered 6 or more times, 9 stocks ordered >100 times, the most popular stock was elav-GAL4 (#8760)
- 3,751 registered user groups, 1,976 of which ordered stocks in 2018
- 8,029 registered users, 2,807 of whom ordered stocks under their own name in 2018

Growth 3,432 stocks were accessioned in 2018:

- 1,025 guide RNA stocks for gene overexpression from TRiP
- 519 UAS-human-gene stocks from Hugo Bellen, Sue Celniker and others
- 356 guide RNA stocks for gene knockout from TRiP
- 303 short hairpin RNA stocks for RNAi from the TRiP
- 279 GAL4 'CRIMIC' stocks made via CRISPR/Cas9 from Hugo Bellen, Norbert Perrimon and colleagues
- 183 GAL4 enhancer trap stocks from the InSITE project
- 177 GAL4 swaps into *Mi{MIC}* insertions from Hugo Bellen and colleagues
- 55 stocks for detecting or manipulating neuronal activity from various labs
- 29 *Mi{MIC}* swaps to make fluorescent protein or gene traps from Hugo Bellen and colleagues
- 19 split-GAL4 HACK donor stocks from Chris Potter
- 487 stocks from other donors

Staff 60 stockkeepers (25.2 full-time equivalents), 8 managers/scientists and 1 research associate.

Grant Funding We are in year 5 of a 5 year grant from NIH with \$440,923 direct costs. We submitted the renewal proposal in September and received good reviews and a perfect score (10). We should hear about funding in early May.

New Stocks We expect to add ~3,540 new stocks in 2019:

- 2,150 TRiP guide RNA and RNAi stocks
- 800 CRIMIC stocks from the Norbert Perrimon, Hugo Bellen and colleagues
- 400 UAS-human-cDNA stocks from Hugo Bellen, Sue Celniker and colleagues
- 90 lexA enhancer trap stocks from the StanEx project
- 50 stocks expressing tagged transcription factors from the modERN project
- 500 assorted stocks from the community at large

Pruning We did not undertake systematic culling in 2018, but we lost or discarded 106 assorted 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

Appendix 14. Vienna Drosophila RNAi Center (Lisa Meadows)

Vienna Drosophila Resource Center (VDRC), Vienna, Austria

The VDRC (www.vdrc.at) is a **non-profit** research infrastructure. Its mandate is to maintain and distribute transgenic RNAi lines and other resources to Drosophila researchers, both locally and 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. Current funding will continue until June 2020.

Key changes during 2018

- More shRNA lines added.
- Average delivery time reduced further to less than 5 days.

Usage Statistics 2018

- **45,226** stocks delivered to **608** user groups in **1,515** separate orders.

Resources as of Mar 2019

Total stocks currently available to the community: **29,502**

- 27,310 RNAi lines (16,763 in GD, 9,822 in KK and 725 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.
- 895 Tagged FlyFos TransgeneOme (fTRG) lines.
- A small, but growing number of plasmids and stocks made available to the community from Private Stock Collections, including include mutant alleles, tagged constructs and reporters.
- 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 continuing to create 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.

Appendix 15. Kyoto Stock Center (Shinya Yamamoto for Toshiyuki Takano-Shimizu)

PGC cryopreservation at KYOTO Stock Center

Despite the pressing need to develop a viable long-term storage method to safeguard *Drosophila melanogaster* strains from genetic drifts, previous attempts to cryopreserve *Drosophila* embryos had limited success and are not in use. Using a novel cryopreservation and transplantation method for Primordial Germ Cells (PGCs, a.k.a. pole cells) developed in the Kobayashi lab at the University of Tsukuba and the Tanaka group at the National Agriculture and Food Research Organization of Japan, the KYOTO Stock Center has been working on a collaborative project to cryopreserve a subset of its stocks collection.

- 1) Members involved & Collaborators: Kobayashi, S.; Asaoka, M. & Sakamaki, Y. at University of Tsukuba; Tanaka, D. & Fukumo, T. at National Agriculture and Food Research Organization of Japan; & Nishimura, K.; Miyai, M.; Yamamoto, S.; Sanuki, R.; Tomaru, M. & Takano-Shimizu, T. at Kyoto Institute of Technology.
- 2) Outline of the Protocol: i) Repeatedly remove by suction PGCs from 20~30 embryos using a fine polished single glass needle, ii) Treat the PGCs with cryoprotectant, clean the PGCs and place it back into the needle, cryopreserve the PGCs by deep freezing the needle in liquid nitrogen, iii) Remove the needle from liquid nitrogen storage and defrost in a 30°C silicone-oil bath, & iv) transplant PGCs into 10~20 host embryos.
- 3) Success rate: The probability of obtaining one or more progeny from donor/injected embryo is about 10~20 % (this number is somewhat low since the sex of the donor PGC must match with the sex of the host embryo, and the donor PGC needs to enter the germline stem cell fate in the ovary or testis). We are continuing to improve this technique to increase the efficiency, but even with the current success rate, the probability of obtaining one or more progeny from a single needle (injected into multiple embryos in parallel) is 40~60 %, indicating that 5 needles or so per stock are enough to reliably preserve and recover a single strain of interest.
- 4) Examples of strains that have been cryopreserved at KYOTO stock center: phiC31 docking sites (e.g. attP40, VK00033 & VK00037) stocks, vas-EGFP line, balancer stocks.

We would be happy to get recommendations from the *Drosophila* Board and the fly community regarding which (or what type of) stocks should be prioritized for cryopreservation.

Appendix 16. Species Stock Center (Patrick O'Grady)

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 stock center has been running at Cornell University for the past year and is currently supported by an NSF RAPID grant. We will be reapplying for regular funding from NSF during the late spring. Highlights of the years activity include:

- (1) We have shipped a total of 797 stocks (82 species) to over 150 labs this year.
- (2) We have developed a new website to replace the temporary Cornell blog site we have been using since fall 2017. This site include an integrated ordering system, images and natural history information for the species we maintain. This site will debut in April 2019.
- (3) We have added 55 new stocks this year, representing 23 different species.

Appendix 17: Gene Disruption Project (Hugo Bellen)

Update of the GDP (Bellen, Perrimon, Spradling)

MiMICs constitute the most versatile tools for gene annotation. A MiMIC in a coding intron of a gene can be converted into a GFP protein trap, facilitating detection of the gene product, affinity purification of protein complexes that include the targeted protein and conditional knock-down of the targeted gene¹. Alternatively, MiMICs can be converted into T2A-GAL4 gene traps that generate a strong loss of function allele that expresses GAL4 in the spatial-temporal pattern of the targeted gene². The GAL4 can be used to detect the expression domain of the targeted gene and facilitates rescue of the GAL4-disrupted gene with UAS-cDNAs. Using UAS-cDNA of human orthologs of the gene allows us to assess whether potential human variants are pathogenic and conduct a systematic structure-function analysis of proteins³⁻⁵.

One of the main goals of the GDP is to have a comprehensive set of MiMICs and MiMIC-like cassettes in every conserved *Drosophila* gene. After generating 17,000 MiMIC insertions and tagging 1,700 genes with intronic MiMICs by transposition^{1,6} the GDP (currently a collaboration with Norbert Perrimon and Allan Spradling) started to use targeted integration of MiMIC-like cassettes through CRISPR/Cas9 mediated homologous recombination (CRIMIC) to tag the remaining conserved genes⁷. We have currently generated approximately 2,250 SA-GFP-SD or T2A-GAL4 insertions based on MiMIC conversions^{6,7} or CRIMIC insertions⁷. These stocks are highly popular and heavily used. However, we do not know if the GDP will continue as we are still awaiting the outcome of the funding decision of NIGMS. Council met more than 2 months ago. We obtained a Study Section percentile ranking of 14. This is a much higher percentile than past renewal applications have received, probably because one of the three primary reviewers objected to additional support for *Drosophila* research as it was not the best model organism. There were essentially no scientific criticisms or issues with productivity or use of the collection.

The CRIMIC pipeline requires cloning of a homology donor, consisting of a MiMIC-like cassette placed between ~1000 bp homology arms to each side of the Cas9 cut site for each targeted gene. After substantial troubleshooting, the GDP has reached an 80% success rate for cloning the donor constructs. Nevertheless, cloning of the homology constructs constitutes a bottleneck for the pipeline, since each construct needs to be quality controlled and prepped. In order to streamline the production of homology donors, we tested two main cloning-free methods. The first method makes use of single stranded DNA (ssDNA) donors. ssDNA donors require shorter homology arms (~100 bases) for successful homologous recombination. The 100 bases of homology can be easily added to the MiMIC-like cassette through PCR primers. We generated multiple PCR templates that contain a middle cassette flanked by 25 base pairs of primer binding sites. 125 base primers (100 bases for homology and 25 bases for priming) can be produced as ultramers. The PCR product can be made into a single stranded homology donor by modifying one of ultramers by 5' phosphorylation and digesting the PCR product with λ -exonuclease, which has a preference to digest 5' phosphorylated DNA. Therefore, the strand that is not 5' phosphorylated remains as undigested ssDNA homology donor. We optimized PCR and the subsequent digestion step to produce ssDNA homology donors of <2kb in size. Since the template binding region of primers is the same for different genes, conditions that are optimized for one gene work for all other genes. The other approach we tested was to minimize the size of the homology donors to the limit that it became feasible to synthesize the donors directly. For this end we designed new cassettes containing minimal elements. The first cassette that we tested was attP-SA-STOP-polyA-U6::gRNA1-attP flanked by 100 bp of gene-specific homology arms. This cassette was synthesized as dsDNA in a plasmid by a company. We included gRNA1 target sites next to the homology arms so that in vivo when the gRNA1 starts to get expressed, the

homology donor cassette gets excised from the plasmid, boosting the homologous recombination rate. In addition, gRNA1 can serve as a dominant marker in combination with a reporter construct that was designed in Tzumin Lee's laboratory. This construct reconstitutes a ubiquitously expressed fluorescent protein when Cas9 and gRNA1 are present. Additionally, we decreased the size of T2A-GAL4 by generating T2A-miniGAL4, which is half the size of GAL4 with about half the transcriptional activity. We designed the attP-SA-T2A-miniGAL4-polyA-U6::gRNA1-attP cassette to synthesize homology donor constructs.

In order to test the transgenesis efficacy of each of these methods and compare them with our published CRIMIC method, we selected 10 genes in the production pipeline of CRIMIC and injected different homology donors using exactly the same integration site and gRNAs. Out of these 10 genes, the CRIMIC pipeline successfully tagged five. Three constructs could not be cloned, and two constructs did not result in transgenics following injection. Two ssDNA homology donor constructs, attP-3XP3GFP-attP and attP-SA-T2AminiGAL4-polyA-U6::gRNA1_attP were similar in efficiency and successfully tagged four genes. In comparison dsDNA with attP-SA-STOP-polyA-U6::gRNA1-attP (700 nt) or attP-SA-T2AminiGAL4-polyA-U6::gRNA1-attP (2000 nt) homology donor constructs gave positives for 10 out of 10 targeted genes. We are currently confirming the tagging success rate of dsDNA constructs and molecularly testing the mutagenic potential of the cassettes. Note that the cost of synthesizing these constructs is lower than the current cost of CRIMIC homology donor construction. We believe that the ease and speed of this technology will propel *Drosophila* to further heights.

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Appendix 18: Human cDNA Project (Hugo Bellen)

Update of the Human cDNA project (Bellen, Celniker, Yamamoto, Wangler, Takano-Shimizu, Warr, Johnson)

Transgenic flies that allow expression of human proteins are useful in the study of both rare and common human diseases. Humanization of fly genes by rescuing the fly LOF mutation with a human ortholog using T2A-GAL4 or ubiquitous/tissue specific GAL4 can provide evidence that the function of the two genes are evolutionarily conserved. Even if a human ortholog cannot functionally replace the fly gene or in cases in which the fly lacks a direct ortholog of the human gene of interest (e.g. α -Synuclein), ectopic over-expression experiments in a wild-type fly can provide molecular insights into gene and variant function. The current limiting step is the lack of a large high-quality human cDNA library that is easily accessible to the fly community. To overcome this hurdle, we formed a collaborative team of investigators in the US, Japan and Australia to generate a large collection of a Gateway® compatible high-quality full length human cDNAs that are subcloned into ϕ c31 transgenesis vectors (pUASg.HA-attB, pGW.HA-attB). We are generating transgenic lines [mostly in VK37(2nd) and VK33(3rd) docking sites] that corresponds to reference (wild-type) human alleles. We are depositing the plasmids into the VDRC and transgenic lines to BDSC and Kyoto Stock Centers. The project in the US is supported by a R24 grant from ORIP and we proposed to generate a collection of 8,000 fly transgenic vectors and 1,500 transgenic lines between 2016-2020. Furthermore, we obtained a one year administrative supplement (2018-2019) to prioritize the generation of Alzheimer's disease associated genes from the NIA, including some human genes that do not have an obvious ortholog in *Drosophila*.

In the initial phase of the project, three groups were manually generating human cDNA transgenic vectors and flies related to their genes interest. Coral Warr (now in Tasmania) and Travis Johnson at Monash University in Australia generated ~400 human cDNA vectors and transgenic lines to assess the effect of ectopic expression of human cDNAs in flies in vivo. In the Bellen, Yamamoto and Wangler labs at Baylor College of Medicine (BCM), we generated ~250 human cDNAs and vectors and transgenic lines that correspond to genes that were identified as disease causing/associated in the Undiagnosed Diseases Network (UDN), Baylor-Hopkins Centers for Mendelian Genomics (CMG) and the Simons Foundation Autism Research Initiative (SFARI) to perform functional studies of disease associated variants. In the Takano-Shimizu lab at Kyoto Institute of Technology in Japan, they generated ~100 human cDNA vectors and transgenic lines based on requests from Japanese fly researchers as part of their "Humanized Fly Project".

In the second phase of the project, the Celniker lab at Lawrence Berkeley National Laboratory (LBNL) started to perform large scale subcloning of human cDNAs with the aid of robotics and they have been systematically generating full length human cDNA clones that correspond to genes conserved between *Drosophila* and Human. Her group has obtained a high-quality human ORFeome collection (human ORFeome 8.1) from Marc Vidal's group at Harvard. Currently ~4,200 clones have been put into the pipeline, ~3,000 of which have been completed and sequence verified. These completed clones are being injected in Bellen/Yamamoto labs, Takano-Shimizu's labs and Celniker's labs. ~50% of these clones have been injected or are in the process of being injected at these three locations and are or will be publicly distributed via BDSC and Kyoto. To cover the genes that were not present in the Vidal collection, we have obtained a second large collection of human cDNAs that was assembled by the late Kenneth Scott at BCM (33,000 full length clones). This collection, which corresponds to the "Ultimate ORF clones" assembled by Invitrogen (now Thermo Fisher) is maintained at BCM and is being shipped to LBNL to be re-arrayed and subcloned by the Celniker lab.

The stocks that have been shipped to BDSC are searchable through the following website. Currently, transgenic lines that correspond to ~1,100 human genes are available from BDSC. We anticipate that this number will reach 3,000 by the end of this project.

<http://flybase.org/reports/FBBrf0237477.html>

A specific page on the DGRC website to search for human cDNA clones is under construction in the "Collections" page.

<https://dgrc.bio.indiana.edu/clones/Catalog#>

Appendix 19. Harvard Transgenic RNAi Project; TRiP (Jonathan Zirin)

Transgenic RNAi Project (TRiP) at Harvard Medical School

Prepared by Jonathan Zirin, PhD, Assistant Director DRSC/TRiP (March, 2019)

The Transgenic RNAi Project (the TRiP) has entered its third 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 ~**14,539** Fly RNAi stocks, with ~**120** in production. These completed stocks, in production and nominated represent ~**10,580** unique FBgns which we calculate covers over **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	9331	soma, germline	19
	VALIUM21	shRNA	96	soma, germline	19
	VALIUM22	shRNA	1628	soma, germline	19

We produce 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, then 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 vermilion 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 shRNA UAS-RNAi lines (<https://stockcenter.vdrc.at/control/main>)

◆ 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 produce 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:

Collection	Function	Vectors	Cross to	Notes	Stocks
<u>TRiP-OE</u>	<u>VPR</u>	Gene Activation pCFD4	Gal4+dCas9-VPR	Use with TRiP-CRISPR Toolbox	2,128
	<u>flySAM</u>	Gene Activation U6B-sgRNA2.0	Gal4+flySAM	Use with TRiP-CRISPR Toolbox	216
	<u>flySAM.dCas9</u>	Gene Activation flySAM2.0	Gal4	flySAM2.0 lines contain both sgRNA and dCas9-activator	262
<u>TRiP-KO</u>	Gene Cutting	pCFD3 pCFD4 pCFD6	Gal4+Cas9	Use with TRiP-CRISPR Toolbox	2,145

1) TRiP-CRISPR

Cross to Gal4>Cas9 to knockout gene expression in somatic cells

TRiP-KO

Cross to germline-Cas9 to generate knockout animal

FOR SOMATIC TISSUE-SPECIFIC MUTATIONS

FOR GERMLINE MUTATIONS

TRiP-OE VPR

TARGET GENE OVEREXPRESSION

1st generation TRiP-OE collection in PCFD4 vector

TRiP Toolbox of Gal4>dCas9-VPR stocks, available at BDSC

Cross to Gal4>dCas9-VPR to activate gene expression

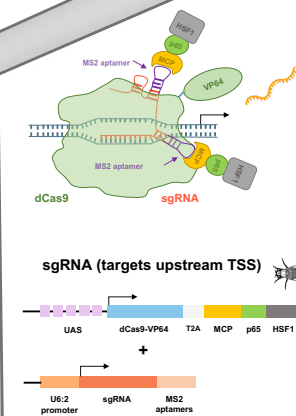
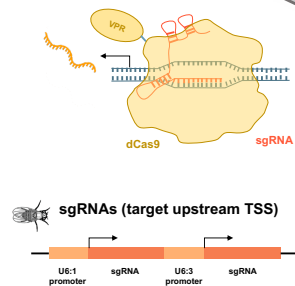
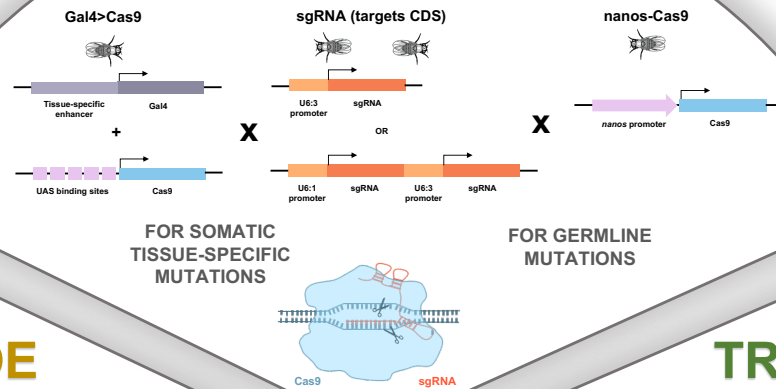
TRiP-OE flySAM

TARGET GENE OVEREXPRESSION

2nd generation TRiP-OE collection in flySAM2.0 vector

Induces stronger gene expression

Cross to any Gal4 to activate gene expression



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) (Lin et al., 2015; Chavez et al., 2015; Konnerman et al., 2015, Jia et al., 2018). TRiP-OE stocks are now being made exclusively with the **flySAM.dCas9 method**. 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 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

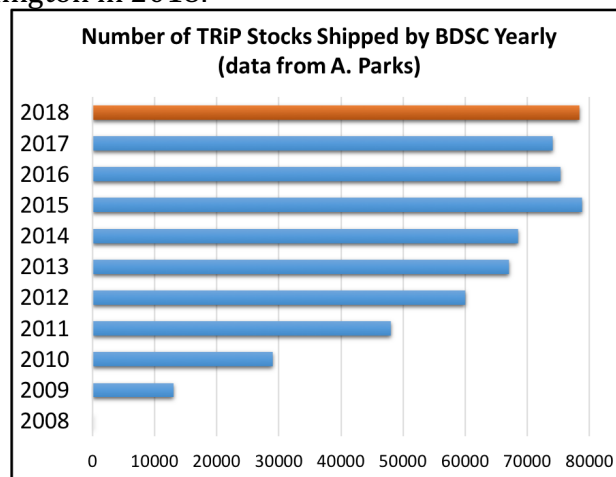
benefit of the research community, production of TRiP-KO stocks is coordinated with similar efforts headed by Drs. Phillip Port and Michael Boutros at the German Cancer Research Center (<http://www.crisprflydesign.org/>) and Drs. Shu Kondo and Ryu Ueda at The NIG, Japan (<https://shigen.nig.ac.jp/fly/nigfly/cas9/>).

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. 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.

◆ TRiP stock distribution

To date the TRiP has produced **~4500** 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 guideRNAs page (https://bdsc.indiana.edu/stocks/genome_editing/sgrna.html). Select stocks are also available from the THFC. In 2018 the BDSC sent **78,370** subcultures of TRiP stocks to **1406** different user groups in **47** countries. **75,323** of these were RNAi, **1,382** were from the new TRiP-CRISPR library of sgRNA stocks, **1409** were Toolbox, **256** of these were UAS-LUC-mir stocks. The TRiP expects to send **150 RNAi and 2000 sgRNA** stocks to Bloomington in 2018.



◆ Validation of the TRiP lines

In the past year we expanded the **RNAi Stock Validation and Phenotypes Project (RSVP)** database (new name: **RSVP Plus**) to track the phenotype data for CRISPR lines as well as modified the UI for users to access and upload new data for CRISPR stocks (<http://fgr.hms.harvard.edu/rsvp>). RSVP Plus allows users to search and view information about knockdown/knockout/overexpression efficiency (qPCR data) and phenotypes (text and when available, images) for specific RNAi and sgRNA fly stock/Gal4 driver combinations (supported by the TRiP's NIH grant as well as a grant from the NCR/ORIP). RSVP includes results curated by FlyBase for other major stock collections, such as phenotypes associated with VDRC fly stocks. Currently on RSVP Plus there are **>11,000** 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.

◆ 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.

The image shows two side-by-side screenshots of a web application. The left screenshot is the main database interface, and the right is the nomination form.

DRSC/TRiP sgRNA Fly Stock Database

Search for **TRiP-CRISPR Overexpression (TRiP-OE)** and **TRiP-CRISPR Knockout (TRiP-KO)** fly stocks by gene or stock ID to obtain detailed information on sgRNA sequence, vector, and availability.

» Search stocks by:

- Gene Identifiers (CG, FBgn, gene name, gene symbol)
- GP or GS number

Enter Search Terms:

» [Nominate genes](#) for TRiP-OE or TRiP-KO production

» [Download](#) list of all finished stocks (Last updated: 2017-02-26)

» Other links:

- [Vector maps and cloning protocols](#) to build your own constructs and files for custom applications, time-sensitive studies, or isoform-specific targets
- [Quick link to CRISPR sgRNA design tool](#)
- [Internal tracking site](#) (login required)

Nominate Genes

1) Download the appropriate template and fill in the information:

- File to fill in only gene information (sgRNA will be designed by Claire): [Gene Info template](#)
- File to fill in gene and sgRNA information (primer sequences will automatically be generated by the system): [Gene and sgRNA Info template](#)
- File to fill in gene, sgRNA and primer information: [Gene, sgRNA, and Primer Info template](#)

2) Enter Project Information:

Scientist:

Project:

Email:

Designed By:

Comment:

Initial Motivation:

Type:

Vector (?):

Target:

Experiment Type:

Injection Site:

3) Upload Template File (use templates above)

No file chosen

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Appendix 20. Harvard Drosophila RNAi Screening Center; DRSC (Stephanie Mohr)

Drosophila RNAi Screening Center (DRSC) at Harvard Medical School

Prepared by Stephanie Mohr, Director of [DRSC/TRiP Functional Genomics Resources](#), March 2019

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 generating knockout cell lines, with a specific focus on knockout of tumor suppressor genes, as funded by R24 OD024984.
 - We have thus far generated ~30 knockout cell lines and already provided about one-third of these to the [DGRC](#) (Indiana) for distribution to the community
- **CRISPR knock-ins.** We are partnering with the Bellen lab (O. Kanca) to test and use various cell knock-in technologies, working towards a goal set out in our funded R24 OD024984 to build cells tagged in specific sub-cellular organelles and compartments.
 - Table 1 shows GFP-tagged cell lines that we have engineered and verified
 - Additional candidate GFP-tagged cell lines are in various stages of production
 - Additional verified cell lines will be sent to DGRC
 - More info at **Platform Talk 154** and **Poster 805** (see also **Poster 808**)

Table 1: Verified lines created using CRISPR Cas9-mediated to knock-in GFP.

Organelle or Compartment	Fly protein	Clones ¹	Clones imaged	insertion sequence verified	Ab for co-localization	Ab co-localizes	Sent to DGRC
Endoplasmic reticulum (ER)	Calnexin99A	16	✓	Yes	α-Cnx	Yes	clone #4
Golgi (cis-Golgi)	Gmap	10	✓	Yes	α-GMAP	Yes	clone #4 , clone #7
Golgi (trans-Golgi)	Golgin-245	1	✓	Yes	α-Golgin-245	Yes	clone #1
Kinetochores	Polo	2	✓	Yes	α-aTub	Yes	clone #2
Lysosomes	Arl8	9	✓	Yes	α-Arl8	Yes	
Nuclear membrane, inner	Lamin	53	✓	Yes	α-Lamin	Yes	
Nucleolus	Fibrillarin	14	✓	Yes	α-Fib	Yes	clone #11 , clone #12
ER, transitional	Sec23	30	✓	Yes	α-Sec16	?	
Endosomes, recycling	Rab11	23	✓	Yes	--	--	clone #14
Lysosomes	spin	2	✓	Yes	--	--	

¹ Number of unique GFP+ single-cell clones growing after transfection and FACS.

II. *Drosophila* cell screening at the DRSC. High-throughput screening, funded by R01 GM067761, continues to be a key technology supported by our group (both on-site and off-site). We offer the following.

- **CRISPR pooled screening—knockouts.** We partnered with the Perrimon lab on pooled-format knockout CRISPR screens (Viswanatha et al. 2018; Okamoto et al. 2018).
 - Collaboration ongoing, multiple parallel and complementary screens, see **Poster 782**
 - Seeking additional collaborations, see **Poster 805**
- **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. A pilot screen has been completed. We seek collaborations.
- **CRISPR arrayed format screens.** We are actively testing arrayed CRISPR approaches for follow-up studies or small-scale screens. We have done a pilot test. Both plasmid-based and synthetic sgRNAs were effective generating phenotypes visible by fluorescence microscopy. We seek collaborations.

- **RNAi arrayed screens—still going strong.** We are currently 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). See **Poster 805**
- **Transfer of plasmid-based shRNAs to DGRC.** We have used liquid handling automation to copy a set of ~100 96-well plates of TRiP VALIUM shRNA plasmids and provided these to the Drosophila Genome Resource Center (DGRC) for community distribution. These can be used with a plasmid providing Gal4 in cell-based studies and are useful for making new shRNA fly stocks.

III. Bioinformatics at the DRSC (see Poster 814). 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. iProteinDB and BioLitMine, as well as at FlyBase, Alliance for Genome Resources, and MARRVEL. We get ~38,000 visits per month of our website and tools. Recently we:

- **Developed and launched [iProteinDB](#)** (Hu et al. 2019), an integrated database of information about post-translational modifications of proteins. See **Poster 818**
- **Developed and launched [BioLitMine](#),** a database for literature mining, including based on genes, pathways, and medical subject headings, for identifying publications and PIs based on PubMed data
- **Developed and launched a [single-cell RNAseq data portal](#)** for display and navigation of data generated by the Perrimon lab (Hung et al. 2019)
- **Expanded [RSVP](#) to include CRISPR data.** The RNAi + Gal4 structure was modified to accommodate sgRNA + Cas9 type + Gal4, so that community data from *in vivo* CRISPR studies can be added.
- **Improvements to our [Find CRISPR](#) resource:**
 - **Developed a machine learning algorithm for CRISPR sgRNA design** based on large-scale CRISPR pooled format screen data (Viswanatha, Merckaert, Hu, et al. unpublished)
 - **Used the ML approach to annotate an ‘efficiency score’** for sgRNA designs
 - **Annotated SNPs** in the injection stock used for sgRNA fly stock production
 - **Added a batch query option** for identification of sgRNA sequences
 - **Improved the results interface** to show genome browser and a summary table
- **Performed routine maintenance and updates** to existing tools for reagent design and ortholog mapping (e.g. DIOPT), reagent identification (e.g. UP-TORR), data view tools, the website, etc.
- **Published online [a PDF with links to tools](#)** based on a biological study workflow that should help researchers identify and navigate our various resources.

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 (est. release fall 2019).

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 informational websites that contribute to knowledge sharing and outreach within and outside the fly community.

A. Increasing community awareness of DRSC/TRiP resources

- **Posters at the ADRC:** 782 and 805 (cells), 809 (*in vivo*), 814 and 818 (bioinformatics)
- **Presentations to local groups of fly labs.** In 2018, we expanded efforts to present to local fly groups. We found this to be an excellent way to reach more people and get feedback. We seek opportunities that would help us reach audiences in regions not covered last year.
 - Flies on the Beach annual meeting of Florida-area fly researchers (FL)
 - Fly Club monthly meeting of fly researchers at Brown University (RI)
 - University of Arizona regional meeting of fly researchers (AZ)
 - University of Massachusetts Worcester regional meeting of fly researchers (MA)
 - Boston Area Drosophila annual meeting of fly researchers (MA)

- Seattle-area monthly meeting of fly researchers (WA)
- Flyrnai.blogspot.com. New and past content related to fly RNAi technologies.
- [News and events](#) regularly posted on our DRSC/TRiP-Functional Genomics Resources webpage
- [Twitter @DRSC_TRiP](#)

B. Broader community outreach

- [Drosophila protocols portal](#). We maintain a searchable database of protocols distributed across different platforms (publications, websites, YouTube, etc.). Update is needed.
- [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](#).
- [Flydiseasemodels.blogspot.com](#). We regularly post new content related to use of *Drosophila* in human disease-focused studies, especially reports of new fly disease models. Added value generated by the keyword tagging strategy (posts are always and only tagged with disease terms).

VI. Recent publications from our group or using our resources:

- Grobler Y, Yun CY, Kahler DJ, Bergman CM, Lee H, Oliver B, Lehmann R. **Whole genome screen reveals a novel relationship between Wolbachia levels and Drosophila host translation.** PLoS Pathog. 2018 Nov 13;14(11):e1007445. PMID: 30422992. (*Used the DRSC genome-wide RNAi library*)
- Hodgson JJ, Buchon N, Blissard GW. **Identification of insect genes involved in baculovirus AcMNPV entry into insect cells.** Virology. 2019 Jan 15;527:1-11. PMID: 30445201. (*Used a DRSC custom-made RNAi library*)
- Hu Y, Sopko R, Chung V, Foos M, Studer RA, Landry SD, Liu D, Rabinow L, Gnad F, Beltrao P, Perrimon N. **iProteinDB: An Integrative Database of Drosophila Post-translational Modifications.** G3 (Bethesda). 2019 Jan 9;9(1):1-11. PMID: 30397019. (*From the DRSC bioinformatics group*)
- Hung R, Hu Y, Kirchner R, Li F, Xu C, Comjean A, Tattikota SG, Song WR, Ho Sui S, Perrimon N. **A cell atlas of the Drosophila midgut.** BioRxiv: <https://www.biorxiv.org/content/10.1101/410423v1> (*DRSC provided bioinformatics support and created a data portal, <https://www.flymai.org/scRNA/>*)
- Okamoto N, Viswanatha R, Bittar R, Li Z, Haga-Yamanaka S, Perrimon N, Yamanaka N. **A Membrane Transporter Is Required for Steroid Hormone Uptake in Drosophila.** Dev Cell. 2018 Nov 5;47(3):294-305.e7. PMID: 30293839. (*Second example, successful pooled-format CRISPR screen*)
- Viswanatha R, Li Z, Hu Y, Perrimon N. **Pooled genome-wide CRISPR screening for basal and context-specific fitness gene essentiality in Drosophila cells.** Elife. 2018 Jul 27;7. pii: e36333. PMID: 30051818. (*First example, successful pooled-format CRISPR screen in fly cells*)
- Wang L, Xia J, Li J, Hagemann TL, Jones JR, Fraenkel E, Weitz DA, Zhang SC, Messing A, Feany MB. **Tissue and cellular rigidity and mechanosensitive signaling activation in Alexander disease.** Nat Commun. 2018 May 15;9(1):1899. PMID: 29765022. (*DIOPT incorporated in workflow [Fig. 1]*)

Appendix 21. Berkeley Drosophila Genome Project; BDGP (Sue Celniker)

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. We are continuing our microbiome studies and hope to have papers soon that describe the genomes of *B. flexus*, *L. brevis*, *L. mesenteroides*, *L. plantarum* and *P. taichungensis*. We continue to characterize the transcriptome (smORFs). We are also continuing the modENCODE project rebranded as modERN to map transcription factor binding sites and transcription factor knock-downs using RNAi following by RNA-seq. The data will be available from the ENCODE DCC. Finally 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 with improvements to the heterochromatin and the Y chromosome. 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*. The five published genomes are available at GenBank and would be valuable to consider having them at FlyBase.

D. cDNA Clone Resources

We maintain our clone resources which have not substantially changed from the 2018 report as a collection available for DGRC to request if they need back-ups and occasional fill requests for clones not yet available from the DGRC. The exception is the production of a human ORF collection for expression in flies. We are working with Dr. Hugo Bellen's group on this resource.

Table 1. Summary of Human Expression Clones.

Collection	Vector	Promoter	N-term Tag	C-term Tag	ORF Stop Codon?	System	Past year (3/2018-3/2019)	Total
hGUHO	pUASg-HA.attB	UAS	--	3xHA	No	Gal4-UAS	0	153
hGUHO	pGW-HA.attB	UAS	--	3xHA	No	Gal4-UAS	1296	2367

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 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. Our improved gene reports 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 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 was published last year in April in iScience Booth et al., “OpenHiCamm: High-Content Screening Software for Complex Microscope Imaging Workflows”. To date annotated experiments for ~8500 genes and hundreds of CRMs documented with over 180,194 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 351 transgenic GFP tagged-TF fly lines. They are deposited at the Bloomington Stock Center. The White Lab has performed ChiP-Seq for 480 lines. The data is being processed through the ENCODE pipeline and is being distributed through the ENCODE DCC. The first data resource paper came out last year in March in Genetics, Kudron et al., “The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of *Drosophila* and *Caenorhabditis elegans* Transcription Factors”. In addition we produced TF knock down RNAi followed by RNA-seq experiments for a number of TFs [~40 sequenced (~1000 RNA samples)]. The validated RNA-seq files have been submitted to the ENCODE DCC and are in their process to be made available to the community. 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 and is being considered for a renewal by May Council. A 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 the University of Washington (R. Waterston, PI, Celniker and White, co-PIs) to participate in a consortium performing ChIP-seq analysis of transcription factors and RNAi knockdown in embryonic development and from Baylor College of Medicine (Bellen, PI, Celniker, co-PI) to construct human ORF clones for expression in flies.

Appendix 22. Drosophila Genomic Resources Center; DGRC (Andrew Zelhof)

Drosophila Genomics Resource Center (DGRC): Booth #321

Key Changes to Report:

1. Personnel
2. Funding
3. New Member of the Scientific Advisory Board

Personnel:

Andrew Zelhof Ph.D., Director
Arthur Luhur Ph.D., Associate Director of Cell Resources
Kris Klueg Ph.D., Associate Director of DNA Resources
Daniel Mariyappa Ph.D., Associate Director of Development
Chris Hemmerich, Database Specialist
Johnny Roberts, Project Scientist
Danielle Pickens, Project Scientist

Funding: NIH P40OD010949 - The DGRC has received NIH funding for another five years, April 1st, 2018 to March 31st, 2023. There was no increase or decrease in the NIH budget. The award amount has remained the same as the past six years.

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 2018, demand for our “products” (cDNA clones, vectors, and cell lines) remains strong; we shipped 3039 individual items at a value of \$173,909 in 2018.

Year	Vectors/cDNAs Shipped	Cell Lines Shipped	Products Shipped ¹	Total Value Shipped ²
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
2018	2357	250	3039	\$173,909.00

Table 1: Summary of items shipped over the last five 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. As we discussed, with our Advisory Board in September 2018, the major difference between items ordered in 2018 as compared to previous years is that the demand for bulk collections has dropped precipitously. We will continue to monitor this difference to determine if this was a one-year difference or a shift in the ordering preferences of our users.

New Collections:**Cell Lines added in the past year:**

Number	Cell line	DRSC cell line ID	Associated NIH grant
1	S2R+-CG8786-KO	CG8786-6	R24OD019847
2	S2R+-Tnks-KO	Tnks-91	R24OD019847
3	S2R+-Apc-KO-E5	Apc-E5	R24OD019847
4	S2R+-Apc-KO-C2	Apc-C2	R24OD019847
5	S2R+-Apc2-KO	Apc2-C11	R24OD019847
6	S2R+ MT::Cas9		R01GM067761 5T32GM007748
7	S2R+-ZnT53C-KO	ZnT53C	R01GM067761 R21 ES-025615 5 P30 CA-06516 R01 GM 067761 R21 ES-025615 5 P30 CA-06516
8	S2R+-IA2-KO	IA2	5 P30 CA-06516
9	Cnx99a-GFP-4/Cas9	Cnx99a-GFP-4/Cas9	R24OD019847
10	Fib-GFP-11/Cas9	Fib-GFP-11/Cas9	R24OD019847
11	Fib-GFP-11/Cas9	Fib-GFP-11/Cas9	R24OD019847
12	Gmap-GFP-4/Cas9	Gmap-GFP-4/Cas9	R24OD019847
13	Gmap-GFP-7/Cas9	Gmap-GFP-7/Cas9	R24OD019847
14	Rab11-GFP-14/Cas9	Rab11-GFP-14/Cas9	R24OD019847
15	polo-GFP-2/Cas9	polo-GFP-2/Cas9	R24OD019847
16	Golgin245-GFP-1/Cas9	Golgin245-GFP-1/Cas9	R24OD019847

Vector and Clones added in the past year:

Common Vectors

1. Three FLIP-FLOP vectors from Dr. Hugo Bellen (*Nagarkar-Jaiswal et al., eLife 2017*)
2. Three CRISPR plasmids from Dr. Simon Bullock (*Port et al., Proc Natl Acad Sci U S A. 2014*)
3. Eleven plasmids for RMCE with MIMIC/CRIMIC inserts from Dr. Hugo Bellen (*Li-Kroeger et al., eLIFE 2018, PMID: 30091705*).
4. Eight plasmids from Dr. Christopher Potter - varying publications and uses. (*Lin and Potter; Genetics. 2016; Riabinina et al Nat Methods. 2015, and unpublished*)

Human cDNA collection (in Drosophila transformation vectors) – all unpublished and are the product of **NIH R24OD022005**.

1. Dr. Hugo Bellen: 146 clones
2. Berkely Drosophila Genome Project - 1248 clones (with 100-200 more coming)

Scientific Advisory Board:

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

Appendix 23: Drosophila Information Service; DIS (Jim Thompson)

DIS Report (Jim Thompson)

Drosophila Information Service volume 101 was published in early January with a large number of reports submitted in calendar year 2018. Since first being published in 1934, we welcome research reports, new mutants, teaching exercises, large data archive records, and other reports annually. DIS (cited in bibliographies as Dros. Inf. Serv.) is freely available at www.ou.edu/journals/dis. Although we publish one annual issue at the end of each calendar year, submissions are accepted at any time. The firm submission 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.

Appendix 24. List of all national *Drosophila* meetings to date (from Thom Kaufman)

2019: Dallas , TX	1998: Washington, DC	1978: <i>Coal Strike, Cancelled</i>
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: <i>Skipped due to change from fall to spring</i>
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