2017 National Drosophila Board Meeting Agenda

Wednesday March 29, 2017, **3:00 - 6:00 PM**   **Pacific Ballroom Salon 1**
Town & Country Resort & Convention Center, San Diego, CA

1. Introduction (Laura Johnston)   **3:00-3:05**

ADRC
2. Report of the 2017 Meeting Organizing Committee (Leanne Jones)   **3:05-3:15**
3. Treasurer's Report (Michelle Arbeitman)   **3:15-3:20**
4. Report of the GSA Senior Director (Suzy Brown)   **3:20-3:30**
5. GSA and the Drosophila Board (Lynn Cooley)   **3:30-3:35**
6. Sandler Lectureship Committee (Bob Duronio)   **3:35-3:40**
7. Victoria Finnerty Undergraduate Travel Award (Alexis Nagengast)   **3:40-3:45**
8. Image Award (David Bilder) **3:45-3:50**
9. 2018 & 2019 Fly Meetings Update (Tin Tin Su)   **3:50-3:55**

Community
10. Drosophila Board Election Report (Ken Irvine)   **3:55-4:05**
11. Janelia Drosophila Research Ecosystem Meeting (David Bilder)   **4:05-4:10**
12. Alliance of Genome Resources Meeting (David Bilder) 4:10-4:15
13. Primarily Undergraduate Institutions (Alexis Nagengast)   **4:15-4:20**
14. Advocacy & Communications (Andreas Prokop (teleconference), S. Mohr) **4:20-4:30**

BREAK **4:30 - 4:50**

Resources and Projects
15. NIH Cryopreservation Workshop (Toshiyuki Takano-Shimizu)   **4:50-5:00**
16. Commercial Antibody Verification (Bing Zhang) **5:00-5:05**
17. FlyBase (Norbert Perrimon)   **5:05-5:15**
18. Bloomington Stock Center (Kevin Cook)   **5:15-5:20**
19. VDRC stock centers (Lisa Meadows)   **5:20-5:25**
20. Kyoto Stock Center (Toshiyuki Takano-Shimizu)   **5:25-5:30**
21. Species Stock Center (Patrick O'Grady)   **5:30-5:35**
22. Drosophila Gene Disruption Project (Hugo Bellen) **5:35-5:40**
23. Harvard Drosophila RNAi Screening Center (Stephanie Mohr) **5:40-5:45**
24. Harvard Transgenic RNAi Project (Jonathan Zirin)   **5:45-5:50**
25. Berkeley Drosophila Genome Project (Sue Celniker)   **5:50-5:55**
26. DGRC (Andrew Zelhoff) **5:55-6:00**
27. DIS (Jim Thompson)   **6:00-6:05**

Adjourn

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1. Introduction: Laura Johnston

2. Report of the 2017 Meeting Organizing Committee: Leanne Jones, chair, Doris Bachtrog, Claude Desplan and Amy Kiger

The 2017 Organizing Committee was assembled in 2015. Leanne Jones was invited by David Bilder and Ken Irvine in February 2015 to chair the organizing committee. Leanne invited Amy Kiger, and they recruited Claude Desplan and Doris Bachtrog for diverse expertise. The Co-Organizers communicated by email and Skype. Most decisions were made by consensus following the opportunity for input from all. Suzy Brown at GSA was involved at many stages of planning and participated in conference calls and group emails.

Interaction with the GSA Office
Suzy Brown and the GSA office were invaluable to the organization of the meeting. Suzy provided essential guidance with key timeline information, data collected from past meetings, knowledgeable suggestions and points for deliberation. Suzy made herself very responsive and helpful to our questions that arose along the way.
Timeline and Overview of Meeting Organization

Discussions were prioritized to first decide on the opening night format, Keynote speaker, and then Plenary speakers. Emphasis was focused on nominating speakers who would convey exciting science representing a diversity of topics, while maintaining gender balance and equal representation of career stages. Nominations were restricted to speakers who had not previously presented in a Plenary session at the Fly Meeting.

Keynote Speaker. For the opening night, there was consensus against holding a panel and preference for a single Keynote Speaker. There was interest in a speaker who could present on the relationship of Drosophila studies within a broader perspective of biology, evolution and/or science education and outreach. Over 25 Keynote speaker candidates were nominated and discussed. Sean Carroll was selected by consensus, and he was invited by email and confirmed in **June 2015**.

Plenary Speakers. Over 50 candidate Plenary Speakers were nominated by **summer 2015**, and decisions were deferred until after further updates from the 2016 committee to prevent possible overlap. In **January 2016**, a short list of 12 top candidates and 3 back-ups were decided by a conference call between the four co-organizers. Plenary speakers were invited by emails sent from the different Organizers in January 2016. All invited speakers committed by **February 2016**.
The organizing committee decided to wait on platform session themes, formats, and other details until after the TAGC meeting, in order to obtain further feedback from the 2016 committee. Organizers Amy Kiger and Doris Bachtrog met with Sue Celniker and Suzy Brown at the **July 2016** TAGC for advice and to note key points of consideration for the next meeting.

Platform Sessions. In **August 2016**, the Organizers extensively revised the list of Abstract Categories and Keywords. Based on the number of submitted abstracts in each category in recent years, a final list of 19 Categories was updated to better predict the distribution of abstracts into Platform Sessions. However, it was also acknowledged (as advised by previous Organizers and the Board) that the final Platform Sessions should reflect the final distribution of submitted abstracts. New keywords were added to reflect the current research trends.

Special consideration was given to selection of co-chairs for the new format of a stand-alone "Techniques & Technology" Session, which would include invited speakers, as well as talks selected from abstracts. This format was in response to complaints that at former meetings, the

Techniques session was always "standing room only" and held at a time that conflicted with other platform sessions of interest. At the end of **August 2016**, Hugo Bellen was invited and accepted to chair this session, and he then recruited Julie Simpson as co-chair. In **September 2016,** co-chairs for the remaining 17 Platform Sessions were nominated, discussed and decided by consensus. The co-chair positions were filled by **mid-October 2016**. Co-chairs were asked to nominate a postdoc trainee to assist with the Session and poster judging.

The abstract deadline was **November 10, 2016**. 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 2, 2016. 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 13, 2016**.

Special Events. In **August-September 2016**, the Organizing Committee discussed and decided on special events for the program. Suggestions from the "2016 Meeting Rejuvenation Report" and from previous Organizers were heavily considered. The major events for the program include the following, and as discussed further below: (1) A new stand-alone "Techniques and Technology" Session for one evening. Hugo Bellen and Julie Simpson agreed to co-chair. (2) A new "PI Early Career Forum" to be held the opening day. Guy Tanentzapf was invited and accepted to chair and organize the event. (2) A new "How I Fly Science Slam" to be held one evening. Michael Eisen was invited and accepted to chair and M.C. the event. (3) A "Meet the Speakers Luncheon" as a career building opportunity for trainees, with Plenary Speakers as the mentors. (4) Workshops were open to applications due November 7, 2016, and the Organizing Committee approved 9 Workshops. (5) A special award to Dan Lindsley for the most years of contributing to and attending Fly Meetings.

Schedule of Events. The final program was decided in stages. Timing of Events was decided by **September 2016**. By **December 2016**, the final scheduling of Plenary speakers and Platforms was set.

Major changes/additions to the 2017 Meeting
The Organizing Committee carefully weighed the suggestions put forth from the 2016 Meeting Rejuvenation Committee Report with ideas on how to continue to update the conference, as well as advice provided by the 2016 Organizing Committee. The major changes introduced in the 2017 Meeting include the following and as discussed further below:
   • *Re-vamping of Session categories and keywords*
   • *Keynote Speaker rather than panel of speakers*
   • *Better timing for Workshops and better advertising of speakers/talks*
   • *"PI Early Career Forum"*
   • *Stand-alone, reformatted "Techniques & Technology" Platform Session*
   • *"How I Fly" (HIF) Science Slam*
   • *"Meet the Speakers" Careers Luncheon*
   • *Special award to Dan Lindsley for "Most Meetings Attended" (59 years!)*
   • *Some fundraising efforts by the Organizers*

Other suggestions considered but not enacted on for this year's meeting included:
   • *Enlistment of more senior trainees to serve as "big sibs" for new Meeting attendees.*
   • *More extensive fundraising by the Organizers.* This would be advantageous to support costs for invited speakers and special events but requires more pre-planning.

One suggestion discussed but rejected for this year:
   • *A scientifically-themed "doorstep" meeting.* Although there was interest in this idea, the Organizers came to the conclusion that it would be difficult to get the critical mass needed to

support a themed pre-meeting on Wednesday. In addition, the Workshops provide good opportunities for interest groups to meet. The PI Early Career Forum was decided on instead.

2017 Fly Meeting Registration and trends
Pre-registration is lower than usual with **1160 pre-registrants** as of March 5, 2017. One thought is that registration could have dropped due to that the previous year's TAGC meeting was held in July 2016 less than a year from the March 2017 conference. For historical comparison, earlier Fly Meeting pre-registrations were: 997 (2016/TAGC), 1517 (2015), 1431 (2014), 1555 (2013), 1537 (2012), 1328 (2011), 1516 (2010), 1383 (2009), 1343 (2008), 1345 (2007), 1241(2006), 1451 (2005) and1470 (2004).

This year's meeting takes place in a new political climate and following contentious travel bans. Suzy Brown and the Organizers have received only a few emails from participants, and one selected Platform speaker from Europe withdrew in protest to the US politics. One Platform Chair could not attend from India due to delays in receiving a visa.

Compensation for organizers, speakers and special awards
Free conference registration was granted to the meeting Organizers (4); the Keynote (1) and Plenary Speakers (12); invited speakers in the new "Techniques and Technology" Session who otherwise were not attending the conference (3); Dan Lindsley and his son, who will escort Dan to the meeting (2); and the Exhibitors that purchased booths. Everyone had to cover their own lodging and travel costs. There were questions about registration and travel compensation from some of the speakers and session chairs. The Larry Sandler Award Winner receives complementary airfare, registration, lodging, and GSA lifetime membership. Victoria Finnerty Memorial Fund travel grants were awarded to 7 undergraduate researchers presenting posters.

Schedule of Events
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 #DROS17 Meeting mobile app.

Opening Session and Keynote Speaker
The 2017 Meeting will follow the traditional program on the first night, with introductions, announcements from GSA, the Sandler lecture and a special science presentation. In addition, Fly Board President, Laura Johnston, requested to address the community during the opening remarks. In place of an historical panel, the Organizers decided to invite a single Keynote speaker. Over 25 Keynote speaker candidates were nominated and discussed. The Organizers liked the idea of a Keynote speaker who could reflect both the growing number of Drosophila researchers working on evolution and the growing importance of communicating the relevance of Drosophila as a system to the broader scientific community. Sean Carroll (University of Wisconsin) was selected by consensus, and he was invited by email and confirmed in June 2015. He will talk about "The Making and Unmaking of the Animal Kingdom", including highlights from Drosophila research with parallels to other animals.

Plenary Speakers
As in previous years, the criteria for choosing Plenary Speakers were scientific importance and novelty, breadth of topics, engaging speakers, and a balance in gender, career stages, and both foreign and domestic speakers. None of the speakers have presented a Plenary talk before, and only a few were noted to have given talks in or to have co-chaired Platform Sessions. From the initial list, only one invited speaker declined due to over commitments (Mala Murthy, Princeton). The confirmed Plenary speakers include 5 female and 7 male speakers with broad diversity in expertise, research topics and career stages. The Plenary Speakers listed in order of the program are Bruno Lemaitre (Lausanne), Virginie Orgogozo (IJM France), Robin Hiesinger (Berlin), Irene Miguel-Aliaga (London), Buzz Baum (UCL London), Francois Payre (Toulouse), Marcos Gonzales-Gaitan (Geneva), Julia Zeitlinger (Stowers), Marta Zlatic (Janelia Farm), Erika Bach (NYU), Nitin Phadis (Utah) and Julius Brennecke (IMBA Austria).

At the 2016 Board Meeting, Hugo Bellen and Board members questioned whether having 8/12 Plenary Speakers from international institutions was in conflict with the mission of the conference. While the Organizers did note this by-chance representation in finalizing the list of invitees, they also did not heavily weigh host country of the invited speakers over priority consideration of the quality of the individual speakers, having diverse representation of topics, and never having presented a Plenary talk in previous meetings. The Organizing Committee in their experiences has found the Annual Meeting to be the best and broadest representation of the Drosophila research community. If nationality of research programs is a concern, the Organizers would like to suggest that the Board consider discussing whether the Fly Meeting Organizing Committee has a mandate or not regarding representation of invited speakers and session co-chairs and that this decision be communicated early on to the Organizers.

Abstract Categories and Keywords
The 2017 Organizers used data from previous meetings provided by GSA in order to merge or expand categories for a total of 19 final abstract categories (versus 17 categories in 2016). Specific changes include renaming and broadening categories, merging categories with lower number of abstracts in recent years, and expanding new categories in areas with higher numbers of abstracts in recent years. For example, "Cell cycle" was removed as a separate category heading and added as a keyword and its associated keywords to the relevant "Cell Division and Growth Control" category. Conversely, the growing popularity of the "Models of Human Disease" category was split into two new categories representing "Neurodegeneration and Neurological Disorders" and "Developmental and Physiological Disorders."
Keywords were reviewed, and mostly additions were made within many categories. It was decided that keyword reuse across categories was important in order to better convey the context and details of individual research. As one example, the keyword "autophagy" was added to "Intracelluar Dynamics: Cytoskeleton, Organelles & Trafficking", "Cell Division and Growth Control", "Cell Death and Immunity", and "Physiology, Metabolism and Aging."

The **2017 Abstract Categories** and notes on the major revisions, additions and deletions are listed in **Table 1**.

The same 19 categories are being used for poster sessions. Heeding advice from the previous Organizing Committee and the Board, we waited to make final decisions on the Platform Sessions after the number and distribution of submitted abstracts were known. Following abstract submission, the categories were re-organized into 17 Platform Sessions. Five categories that had the most abstracts were given two split sessions (I & II, for a total of 14 talks). Ten categories were assigned a single session (7-8 talks). Two categories were merged into one session ("RNA Biology" and "Evolution in development, other species" with 4 talks each). With these changes, the pre-assigned co-chairs were also combined on the final program. "Techniques & Technology" has 9 talks, with both invited talks (7) and selected talks from abstracts (2). "Educational Initiatives" has no talks and only a poster session.

The **2017 Abstracts Submitted and Allocated Platform Talks** are listed in **Table 2 (A & B)**.

Platform Co-chairs
The 2017 Organizing Committee followed the approach of the previous meetings and designated two co-chairs to each session with the potential for one established/"heavy hitter" in the field and one more junior investigator. The "social engineering" goal of including the "heavy hitter" is to get more of the senior researchers to attend the fly meeting, which they otherwise might not do, and thus make the meeting better for all attendees who would then have a chance to interact with, or at least hear from, senior researchers in the fields. The goal for the junior researchers is to give them exposure. This worked well for the 2015 and 2016 meetings. Co-chairs were chosen for the scientific excellence but also to ensure diversity across many dimensions including gender, geography and institution type. The acceptance rate varied, and additional invitations were required to fill the co-chair positions for 11 of the Platform Sessions.

In addition, co-chairs were asked to invite a Postdoctoral trainee for each session. In some cases, the Organizers helped to identify and invite trainees.

The 2017 **Platform Session co-chairs** who selected abstracts for Platform presentations are listed with affiliation by session in **Table 3**. The 2017 **Platform Session Trainees** are listed in **Table 4.**

Abstract deadline
The abstract deadline was **November 10, 2016**. Abstracts selected for talks were decided by December 13, 2016.

Submitted abstracts
A total of **716 abstracts** were submitted under **19 categories** and associated with keywords. Totals in recent years were 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).

Abstracts could select a primary and secondary category for talk consideration. There were **392 requests** in the primary category (and 784 requests across primary and secondary categories) for **156 Platform talks**, which resulted in a **39.8% success rate.** This was slightly lower than the 43% success rate (361 requests for 157 talks) in 2016. The number of total abstracts varied across sessions (see **Table 2A-2B**).

The highest number of abstracts was submitted in "Gene Regulation", with 65 abstracts as a primary choice and a total of 175 abstracts as primary or secondary choice. The lowest number of abstracts was in "RNA Biology", with 14 abstracts as a primary topic and 36 as a primary or secondary topic. In 2016, the range was from 102 abstracts in "Drosophila Models of Human Disease" to 16 abstracts in "Immunity and Pathogenesis". The number of abstracts submitted in specific categories was consistent with recent trends, although the revised categories and allocations did balance out some of the previous extremes. This year, "Drosophila Models of Human Disease" was split into two new sub-categories, which had a combined 79 abstracts as primary choice and 135 abstracts as primary or secondary choice across both "Neurodegeneration and Neurological Disorders" and "Developmental and Physiological Disorders." Given the continually high numbers of abstracts submitted every year in "Regulation of Gene Expression," future meeting Organizers may want to consider similarly stratifying the submitted abstracts into two more specific categories that best reflect the gene expression field. On the other extreme, this year, "Immunity" was merged into "Cell Death and Immunity," which fared better than previous years as a stand-alone session with a total of 31 abstracts as primary choice and 46 abstracts as primary or secondary choice in this new category. Similarly, "RNA Biology" has had low abstract numbers over the years, and the lowest number of any category this year, so it may be a good candidate for a new merged category to ensure more even abstract submission across all categories (perhaps within a new Gene Expression category?). The fraction of abstracts in a given category that requested talks also ranged widely, from 72% in "Cell Division and Growth Control" to 33% in "Gametogenesis" (In 2016, the range was from 76% in "RNA Biology" to 37% in "Neural Development"). This disparity creates an interesting problem in deciding how to allocate the number of talks to a particular category (see below).

Platform Session organization
The Organizers determined the number of allocated talks to each Platform Session based on the number of submitted abstracts (see **Table 2**). Co-chairs were asked to generate a ranked list for selected talks with a target number of several more abstracts than the allocated number of talks for that session. Co-chairs were given 2.5 weeks to review and submit their ranked lists of selected abstracts for Platform talks to the Co-Organizers by December 2, 2016. The Organizers reviewed and selected final talks by December 13, 2016. Since co-chairs reviewed abstracts submitted as primary or secondary choices, there were multiple examples of overlap between rankings across Sessions, and preference was given to the primary choice category. The

Organizers identified and removed duplicates, and moved up talks from further down the rankings as needed. The Organizers also ensured that there was a balance in gender and career stages of the selected abstract speakers within a session. To avoid over-representation of any individual laboratory at the Meeting, the Organizers allowed up to two selected talks from the same laboratory in different Platform Sessions, or at most three talks, counting the PI as a Plenary Speaker. Co-chairs were permitted to select talks from their own laboratory if there was consensus from the other co-chair and by final review from the Organizers. Having the ranked list of abstracts was critical for replacing any conflicted talks, for balancing talks among laboratories to assure representation in the field, and for replacing several talks when speakers withdrew abstracts after notification of platform talk assignment.

Considerations for Platform Sessions and Talk allocations
Previous Meeting Organizers have detailed the notable challenges in organizing the Platform Sessions. Briefly, fairness in selecting Platform Talks is confounded by several dynamic factors: (1) the number of abstracts submitted per category migrates over time (up or down); (2) the number of abstracts requesting talks varies across categories; (3) the chance of getting a talk selected varies across sessions; and (4) categories and co-chairs must be pre-assigned in order to review abstracts, however, before knowing what number of abstracts that will be submitted per category or the number of talks allocated.
The 2017 Organizers took several measures to both help predict and adapt to the number abstracts submitted by category:

The Organizers reviewed the trends for abstract submissions by Categories from the 2014, 2015 and 2016 Meetings and, from this, reassigned some topics either as merged or separated Categories (see **Table 1**). The new Categories seem to have fairly well predicted the 2017 submitted abstracts. One update to the Categories that may need to be re-evaluated is how to best represent the growing number of abstracts in Evolution related sessions. While "Evolution and Population Genetics" had 60 primary abstracts, "Evolution in Development, other species" had only 19 abstracts. Trends continued for unchanged Categories that could be addressed in future meetings, e.g., merge "RNA Biology" that has low numbers of abstracts with another category, and split "Regulation of Gene Expression" that has high number of abstracts into two more specific topics.

Co-chairs were invited for all Categories, with the exception of one chair for "RNA Biology" that has seen lower abstract numbers in recent years. A single chair turned out to be appropriate for the low number of abstracts and the final decision to merge "RNA Biology" with "Evolution in Development" in a shared Platform Session.

The Organizers did not make final decisions on the distribution of talks or even categories into official Platform Sessions until after the abstracts were submitted. With "Techniques & Technology" moved to a stand-alone time slot, there were 17 Categories with opportunities for talks to fill 21 sessions. From the submitted abstracts, five categories were assigned to split sessions (I & II) with the opportunity for more talks, two categories were merged to share a single session (4 talks each, and both listed in session title), and ten categories with a standard session (7-8 talks). Some categories were predicted to need split sessions, such as "Regulation of Gene Expression." However, it was not predicted for certain new categories, such as "Patterning, Morphogenesis and Organogenesis." We agree with previous Organizers that these sorts of adjustments to either merge or split sessions are not necessarily problems or even avoidable. However, it may help for fairness in talk selections and the amount of work for co-chairs if the most popular categories over many years are eventually stratified at some point to better reflect sub-fields in future categories and sessions.

As detailed further above, speakers for the Platform Sessions were ranked by the co-chairs and determined by the four Organizers.

Poster Sessions

There are currently **622 abstracts** scheduled to be presented as posters. There were 787 abstracts submitted in total, including the 156 abstracts selected for Platform talks and 66 late abstracts. The breakdown of posters by category for the regular abstracts is shown in the **Table 2A.**

Poster Awards
A total of up to six poster awards are slated to be given to the top three Graduate student posters (1st, 2nd and 3rd) and the top three Undergraduate posters (1st, 2nd and 3rd). There is no longer a category for postdoctoral poster awards, as many of the judges are the Postdoc trainees functioning as Platform Session co-chairs. Awards will be given based on merit only, 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, posters will be judged initially by the Session co-chairs and/or Postdoctoral trainees 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 co-chairs/trainees will communicate the recommended posters for each Session to Organizer Amy Kiger by Friday. All four Co-Organizers will meet Friday night to determine the poster award winners. Ribbons will be pinned on the wining posters so that attendees can examine the winning posters. The winners will be recognized during the final Plenary Session on Sunday and their posters displayed outside the room.

Workshops
Workshop applications and selection criteria were similar to past meetings. Nine applications were received, reviewed and approved. In addition, GSA will present a career-oriented Workshop for a total of ten listed Workshops. Based on feedback from attendees at previous Meetings, the Organizers tried to schedule Workshops at times in the program that are more conducive to participation, i.e., not too late into the evening and to avoid parallel Workshops covering overlapping interests. The two major Workshop Sessions will be Thursday night 7:45-9:45 PM and Friday afternoon 1:45- 3:45 PM. One exception is the historical Ecdysone Workshop, which had already planned to take place at the pre-meeting time on Wednesday 12:00-6:00 PM. The Organizers suggest that in future years, all Workshops be held to similar treatment and scheduling constraints. This would also give Meeting Organizers more flexibility for pre-meeting programming. This year, the Organizers insisted that all Workshop speakers and a schedule must be provided for the Conference website in order to help better inform Meeting attendees and manage attendance across different parallel Workshops. The Workshop Organizers have responded with varying degrees of information, but all include speaker information online at this time.

Workshops listed in order of the program: (1) Ecdysone Workshop (Wednesday); (2) Integrating Research and Teaching at PUIs using Drosophila melanogaster as a Model Organism (Thursday); (3) Wound Healing and Regeneration (Thursday); (4) Feeding Behavior, Nutrition and Metabolism (Thursday); (5) Everything You Ever Wanted to Know About Sex (Thursday); (6) Spotlight on Undergraduate Research (Friday); (7) Drosophila Microbiome (Friday); (8) Developmental Mechanics (Friday); (9) Biogenic Amines and Behaviors (Friday); (10) Navigating the Career Decision Making Process (Friday).

"PI Early Career Forum"
This new event was created to provide more career building, networking and socializing opportunities for early career PIs (less than five years heading their own laboratory) and, potentially, to generate a stronger sense of community between all Fly PIs. The Fly Meeting Rejuvenation Committee Report and the Drosophila Board raised concerns about bringing in and retaining the younger generation of Fly researchers. It was noted 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 was created as an effort to help build deeper ties and sense of community amongst Drosophila researchers, as well as to provide meaningful ways to help give a leg-up to early career PIs. The Organizers decided on this event for the pre-meeting time slot on Wednesday after ruling out support for sustainable participation in a scientifically-themed "doorstep" meeting due to redundancy with Workshop opportunities.

The Organizers came up with a short-list of candidate organizers for the Early Career Forum. Guy Tanentzapf, who has a record of supporting early career PIs, was asked and accepted to chair. Amy Bejsovec agreed to co-chair. The Meeting Organizers conveyed general ideas on how the event may take shape, including scientific talks from early career PIs, career panel discussions, and social events. However, the Early Career Forum chairs were given autonomy in deciding on the final format and Forum abstract selection process.

A report from Guy Tanentzapf on organization of the Forum is below. The final program runs all day from Wednesday 9:00am – 6:00pm (see **Appendix A**). The program includes 16 talks by early career PIs selected from abstracts, lunch with the Fly Board, a panel discussion with Associate Professors Melissa Harrison, Judith Leatherman, Blake Riggs and Tina Tootle, and concludes with a PI- only reception (open to all PIs who are attending the annual meeting). Information about the Early Career Forum was included at the time the Fly Meeting Abstract Submission and Registration website opened. It was decided that it would be restricted to limited attendance in order to accommodate the available conference space on Wednesday. Although registration and participation were open to anyone, priority was given to early career PIs (less than five years out), then other PIs, postdocs and students in order to keep the meeting more focused on early career PI attendees and interests. A fee of $50 per ticket was charged to ensure attendance and better plan for provided meals and refreshments during the breaks. A total of **49 participants are registered.** [It will be helpful to get and review information on the final registrants and who actually shows up, *e.g.,* career stage, gender, research fields.] Although the guidelines for talks at the early career forum specified that the goal is to introduced "yourself and your lab to the community", it was decided that there should be little, if any, overlap between talks at the Forum and talks in Platform Sessions, in order to provide more opportunities for talks overall. At the Meeting abstract submission website, a check box was provided to allow participants to self choose their preference for a Platform or Forum talk, in the case of duplicate selections. There were 58 abstracts submitted, with submissions from 40 PIs (career stage unknown!), 2 staff scientists, 8 postdocs, 2 graduate students and 6 undergraduates.

Guy Tanentzapf made the talk selections with criteria for "a broad representation of the research in the fly community (neuroscience, ecology and evolution, cell biology, stem cell biology, molecular biology, immunity, etc.), gender balance, and diversity in terms of institutions (PUIs, State schools, major private research universities) and to a lesser extent geography. It would have been very helpful if URM information were available." Abstracts that were selected for Platform Talks and had noted a preference for Platform Talks were removed from consideration. The 16 selected speakers include 11 women and 5 men all within the first five years of running their laboratory. Four speakers are from primarily undergraduate institutions (PUIs), and three speakers are from outside the USA (Austria, Canada, UK).

Guy made several important notes about the organization to keep in mind for future Forums:

1. Talk selection was a difficult process given the limited information provided with the abstracts. He had to do a lot of online research and "googling," which has its limits.
2. Although information on this new event was on the meeting website at the time of abstract submission, one key obstacle was in reaching all the new fly PIs to encourage registration. A couple of people wrote to him afterwards and expressed disappointment that they didn't find out about it until too late. He suggested a need that has been

discussed at previous Board meetings for some sort of database to identify/register new fly labs (while registering a BUN number at Bloomington?).
3. This is certainly a job for two people. Guy is happy to help again next year in order to provide continuity and relay information that he learned this time around.
4. This is a pilot Forum that has already demonstrated a reasonable amount of interest. He notes, "we might have to run through a couple of iterations before it has the right format, tinker after seeing what aspects work and which ones don't, and keep an open mind."

Stand-alone and reformatted "Techniques & Technology" Session
Based on feedback and observations from previous years, the Organizers decided to hold a new format for the "Techniques & Technology" Session. Since this topic cuts across all Drosophila research, it was decided that it would do well as a stand-alone session. Given the cutting edge nature of technology advancements, it was also decided that it should include the possibility for invited speakers as well as selected speakers from abstracts. In this regard, it would be a hybrid between a Platform Session and a Workshop. The Organizers identified a time slot on Saturday night for the stand-alone session (7:30-10:00 pm).

Special consideration was given to selection of "Techniques & Technology" co-chairs, who would have the autonomy to organize a mini-program with the broadest relevance to the Drosophila research community. Hugo Bellen was invited and, fortunately, accepted this position the end of August 2016. He then recruited Julie Simpson as co-chair. The co-chairs were asked to consider and submit a list of invited speakers within the next couple of months. The co-chairs decided on and extended speaker invitations by November 2016, with a total of nine speakers (7 invited, 2 from abstracts). We expect that the breadth and interest in topics as well as speakers in this session will make this a well-attended session.

Several notes of consideration and lessons learned for this format at future Meetings:
1. Given the timing needed to ensure availability of invited speakers, the Organizers suggest that more lead-time be given to identify the co-chairs/organizers so that they have the sufficient time needed to deliberate on and invite speakers.
2. In contrast to the lead-time needed for invited speakers, the abstract submission deadline isn't until November. A defined number of slots should be reserved for possible selections from submitted abstracts. Given the relatively low number of submitted abstracts in this category, however, it can be a limited number (this year, 2 abstracts were selected from 7 requested talks in this session on par with acceptance rate in other sessions).
3. Ideally, the list of suggested invited speakers should be reviewed by the Organizing Committee before invitations are extended. This would help ensure representation and balance in the speakers and avoid possible redundancies within the program. This did not happen this year, and the session is unintentionally but noticeably male dominated.
More logistical information and/or contacts need to given to the co-chairs/organizers to relay to the invited speakers. Specifically, it would be helpful to have prepared information on a work flow for how invited speakers will submit abstracts to the GSA website for the program, and whether invited speakers will be offered any compensation or not for registration. It was decided this year that invited speakers could receive free registration, similar to the compensation given to invited plenary speakers.

"How I Fly (HIF)" Science Slam
The Organizers included the "How I Fly (HIF)" Science Slam as a new open event that will take place as a stand-alone event on Friday night (7:30-9:00 pm). Michael Eisen agreed to organize and M.C. the event. The format will be for volunteers to share a few minute "story" on their research presented for a general audience. The intent is to provide a fun, social event to share exciting advances made through Drosophila research while also encouraging researchers, especially trainees, to hone their skills pitching their work to a general audience. Similar events have been running with success at other conferences and research institutions.

Special Award to Dan Lindsley

Dan Lindsley will be given a special award during the first Plenary Session, "In recognition of attendance at and contributions to a record **59 years** of Annual Drosophila Research Conferences." He will receive a framed print of a hand-drawn fly with this inscription.

Planned assistance to the 2018 Drosophila Conference Organizing Committee
All of the worksheet templates and the tables listing previous speakers and session co-chairs will be made available to the 2018 Organizing Committee. 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.

Table 1. 2017 Abstract Categories with notes on revisions, additions and deletions.

01 Intracellular Dynamics: Cytoskeleton, Organelles & Trafficking	Renamed from "Cell Biology" to make distinct from other sessions; added "Organelles"
02 Cell Biology & Signal Transduction	
03 Cell Division and Growth Control	Added "cell cycle" topic from previous "Cell cycle and Cell Death" session
04 Cell Death and Immunity	Merged topics from two sessions with fewer abstracts: "Cell cycle and Cell Death" and "Immunity and Pathogenesis"
05 Physiology, Metabolism and Aging	Renamed "Organismal Growth" to "Metabolism" to reflect new trends and make distinct from 03 Cell Growth Control
06 Gametogenesis	Removed "Organogenesis" from this to separate session
07 Stem Cells	
08 Neural Development and Physiology	Added in "Physiology" taken from previous "Neurophysiology and Behavior"
09 Neural Circuits and Behavior	Replaced "Neurophysiology" with "Neural Circuits" to reflect current circuits trend and links to behavior
10 Models of Human Disease: Neurodegeneration and Neurological Disorders	Due to large number of abstracts, split Models of Human Disease into two sessions
11 Models of Human Disease: Developmental and Physiological Disorders	Due to large number of abstracts, split Models of Human Disease into two sessions
12 Evolution and Population Genetics	Replaced "Quantitative" with "Population"
13 Evolution and Development, other species	Expanded Evolution for new session to accommodate growing number of abstracts
14 Patterning, Morphogenesis and Organogenesis	Merged "Pattern Formation" that had fewer abstracts with "Organogenesis" and added "Morphogenesis"
15 Regulation of Gene Expression	
16 Chromatin and Epigenetics	
17 RNA Biology	Debated merging with other categories due to low number of abstracts; no consensus, so kept for abstract submission
18 Techniques and Technology	Changed "Resources" to "Technology", and made a stand-alone session with invited and selected speakers
19 Educational Initiatives	No talks given outside of workshops

Table 2A. 2017 Abstracts Submitted and Allocated Platform Talks
Notes on **primary choice** abstracts submitted, talks requested, allocated and selected.

Platform Session	Abstracts (1° choice only)	Platform talk req	Poster only	% Talks requested	Talks allocated	Talks allocated % of abstracts in category	Talks allocated % of talks req in category
01 Intracellular Dynamics: Cytoskeleton, Organelles & Trafficking	39	27	12	69.2%	8	20.5%	29.6%
02 Cell Biology & Signal Transduction	46	29	17	63.0%	14	17.4%	27.6%
03 Cell Division and Growth Control	32	23	9	71.9%	8	25.0%	34.8%
04 Cell Death and Immunity	31	14	17	45.2%	7	25.8%	57.1%
05 Physiology, Metabolism and Aging	60	30	30	50.0%	14	13.3%	26.7%
06 Gametogenesis	33	11	22	33.3%	7	24.2%	72.7%
07 Stem Cells	34	21	13	61.8%	8	23.5%	38.1%
08 Neural Development and Physiology	28	13	15	46.4%	8	28.6%	61.5%
09 Neural Circuits and Behavior	41	22	19	53.7%	8	19.5%	36.4%
10 Models of Human Disease: Neurodegeneration and Neurological Disorders	49	22	27	44.9%	8	16.3%	36.4%
11 Models of Human Disease: Developmental and Physiological Disorders	30	14	16	46.7%	8	26.7%	57.1%
12 Evolution and Population Genetics	60	35	25	58.3%	14	13.3%	22.9%
13 Evolution and Development, other species	19	11	8	57.9%	4	42.1%	72.7%
14 Patterning, Morphogenesis and Organogenesis	63	42	21	66.7%	14	12.7%	19.0%
15 Regulation of Gene Expression	65	37	28	56.9%	14	12.3%	21.6%
16 Chomatin and Epigenetics	48	25	23	52.1%	8	16.7%	32.0%
17 RNA Biology	14	9	5	64.3%	4	57.1%	88.9%
18 Techniques and Technology	19	7	12	36.8%	9 (2)*	10.5%	28.6%
19 Educational Initiatives	5	0	5	0.0%	0	NA	NA
TOTAL	716	392	324	54.7%	156	21.8%	39.8%

* 2 selected from abstracts, 7 invited

Table 2B. 2017 Abstracts Submitted and Allocated Platform Talks
Notes on total of **primary & secondary choice** abstracts submitted per session and talks requested, allocated and selected.

Platform Session	Abstracts (1° and 2° choices)	Platform talk req	Poster only	% Talks requested	Talks allocated	Talks allocated % of abstracts in category	Talks allocated % of talks req in category
01 Intracellular Dynamics: Cytoskeleton, Organelles & Trafficking	67	45	22	67.2%	8	11.9%	17.8%
02 Cell Biology & Signal Transduction	129	79	50	61.2%	14	10.9%	17.7%
03 Cell Division and Growth Control	72	41	31	56.9%	8	11.1%	19.5%
04 Cell Death and Immunity	46	22	24	47.8%	7	15.2%	31.8%
05 Physiology, Metabolism and Aging	120	60	60	50.0%	14	11.7%	23.3%
06 Gametogenesis	62	28	34	45.2%	7	11.3%	25.0%
07 Stem Cells	48	30	18	62.5%	8	16.7%	26.7%
08 Neural Development and Physiology	69	38	31	55.1%	8	11.6%	21.1%
09 Neural Circuits and Behavior	65	31	34	47.7%	8	12.3%	25.8%
10 Models of Human Disease: Neurodegeneration and Neurological Disorders	57	25	32	43.9%	8	14.0%	32.0%
11 Models of Human Disease: Developmental and Physiological	78	39	39	50.0%	8	10.3%	20.5%

Disorders							
12 Evolution and Population Genetics	91	52	39	57.1%	14	15.4%	26.9%
13 Evolution and Development, other species	41	23	18	56.1%	4	9.8%	17.4%
14 Patterning, Morphogenesis and Organogenesis	117	77	40	65.8%	14	12.0%	18.2%
15 Regulation of Gene Expression	175	95	80	54.3%	14	8.0%	14.7%
16 Chomatin and Epigenetics	97	55	42	56.7%	8	8.2%	14.5%
17 RNA Biology	36	23	13	63.9%	4	11.1%	17.4%
18 Techniques and Technology	52	21	31	40.4%	9 (2)*	3.8%	9.5%
19 Educational Initiatives	5	0	5	0.0%	0	NA	NA
TOTAL	1427	784	643	54.9%	156	10.9%	19.9%

* 9 talks total. 2 were selected from abstracts; 7 were invited.

Table 3. 2017 Drosophila Meeting Platform Sessions & Co-Chairs

Platform Session	Co-chairs	
Stem Cells	Gary Hime	Univ. of Melbourne, Australia
	Tina Mukarjee	Institute for Stem Cell Biology, Bengaluru, India
Neural Circuits & Behavior	Nilay Yapici	Cornell University, Ithaca, NY
	Gwyneth Card	HHMI Janelia Research Campus, Ashburn, VA
Models of Human Disease: Developmental & Physiological Disorders	Dirk Bohmann	University of Rochester, NY
	Rene Galindo	University of Texas Southwestern Medical Center, Dallas
Physiology, Metabolism and Aging (I & II)	Daniel Promislow	Univ. of Rochester, NY
	Benoit Biteau	Univ. of Washington, Seattle
Regulation of Gene Expression (I & II)	Bob Johnston	John's Hopkins Univ., Baltimore, MD
	Jack Bateman	Bowdoin Univ., Brunswick, ME
Cell Biology and Signal Transduction (I & II)	Jeff Axelrod	Stanford Univ., CA
	Mihaela (Ela) Serpe	NIH/NICHD, Bethesda, MD
Evolution of Development (talks 1-4) RNA Biology (talks 5-8)	Artyom Kopp	UC Davis, California
	Urs Schmidt-Ott	Univ. of Chicago, IL
	Nick Sokol	Indiana University, Bloomington
Intracellular Dynamics: Cytoskeleton, Organelles, and Trafficking	Julie Brill	The Hospital for Sick Children, Toronto, Canada
	Yohanns Bellaiche	Institut Curie, Paris France
Neural Development and Physiology	Pelin Volkan	Duke Univ., Durham, NC
	Makoto Sato	Kanazawa Univ. Japan
Evolution and Populations Genetics (I & II)	Kristi Montooth	Univ. of Nebraska, Lincoln
	Noah Whiteman	UC Berkeley, CA
Patterning, Morphogenesis and Organogenesis (I & II)	Jessica Treisman	NYU, Skirball Inst., New York
	Leslie Pick	Univ. of Maryland, College Park
Gametogenesis	Cordula Schulz	University of Georgia, Athens
	Alana O'Reilly	Fox Chase Cancer Center, Philadelphia, PA
Cell Death and Immunity	Kim McCall	Boston Univ., MA
	Henri Jasper	Buck Institute for Research on Aging, Novato, CA
Chromatin and Epigenetics	Melissa Harrison	Univ of Wisconsin, Madison
	Mia Levine	Univ. of Pennsylvania, Philadelphia
Cell Division and Growth Control	Don Fox	Duke Univ. Medical Center, Durham, NC
	Sharon Gorski	Simon Fraser Univ. & BC Cancer Agency, Vancouver, Canada
Models of Human Disease: Neurodegen. and Neurological Disorders	Serge Birman	ESPCI, Paris, France
	Doris Kretzschmar	Oregon Health & Science Univ., Portland, OR
Techniques and Technology	Hugo Bellen	Baylor College of Medicine, Houston, TX
	Julie Simpson	University of California, Santa Barbara

Table 4. 2017 Platform Session Postdoctoral Trainee Co-chairs

Platform Session	Co-chairs	
Stem Cells	Nicole Siddall	Univ. of Melbourne, Australia
Neural Circuits & Behavior	Ryan Williamson	HHMI Janelia Research Campus, Ashburn, VA
Models of Human Disease: Developmental & Physiological Disorders	Drew Stenesen	University of Texas Southwestern Medical Center, Dallas
Physiology, Metabolism and Aging (I & II)	Rebecca Kreipke	Univ. of Washington, Seattle
Regulation of Gene Expression (I & II)	Caity Anderson	John's Hopkins Univ., Baltimore, MD
	Kayla Viets	John's Hopkins Univ., Baltimore, MD
Cell Biology and Signal Transduction (I & II)	Qi Wang	NIH/NICHD, Bethesda, MD
Evolution of Development (talks 1-4)	Emily Delaney	UC Davis, California
RNA Biology (talks 5-8)	Arthur Luhur	Indiana University, Bloomington
Intracellular Dynamics: Cytoskeleton, Organelles, and Trafficking	Jean-Francois Groulx	UC San Diego, California
Neural Development and Physiology	Tetsuo Yasugi	Kanazawa Univ. Japan
Evolution and Populations Genetics (I & II)	Andy Gloss	UC Berkeley, CA
Patterning, Morphogenesis and Organogenesis (I & II)	Anja Katzemich	McGill, Montreal, Canada
Gametogenesis	Rafael Demarco	UCLA, California
Cell Death and Immunity	Imillce Rodriguez-Fernandez	Buck Institute for Research on Aging, Novato, CA
Chromatin and Epigenetics	Danielle Hamm	Univ of Wisconsin, Madison
Cell Division and Growth Control	Jessica Sawyer	Duke Univ. Medical Center, Durham, NC
Models of Human Disease: Neurodegen. and Neurological Disorders	Sabi Abdul-Raouf Issa	ESPCI, Paris, France
Techniques and Technology	Oguz Kanca	Baylor College of Medicine, Houston, TX

ACTION ITEM:
➢ Board should discuss whether the Fly Meeting Organizing Committee should have a mandate regarding nationality representation of invited speakers and session co-chairs.
➢ Mechanism for identifying new PIs for future New PI Forums.

3. Treasurer's Report: Micelle Arbeitman

Changes for 2016 can be summarized as follows:

- The 2016 Reserve balance is down $11,000 from 2015 because of $6,000 transferred to the Finnerty Award account and $5,000 used for TAGC travel awards for the Orlando meeting. Otherwise, there were no changes from 2015 because the Genetics Society took on all expenses/revenues associated with TAGC meeting.

- The Sandler balance is $68,384 and had a gain of $5716 and expense of $709.

- The Finnerty balance is $15,071 (up $886 - contributions plus $6000 transfer from Reserve) and (down $4394 - travel awards to students).

Table 1: Summary of expenses (see excel spreadsheet)

B. MEETING ATTENDANCE

Pre-registration 2017 (San Diego, CA):	1,121	$252,803
Estimated **Total registration 2017:**	**1,185**	**$270,000**
Pre-registration 2015 (Chicago, IL):	1,496	$313,373
Total registration 2015:	**1,569****	**$344,451**
Pre-registration 2014 (San Diego, CA):	1,335	$274,642
Total registration 2014:	**1,431**	307,377

Pre-registration 2013 (Washington, DC):		1,403	$268,795
Total registration 2013:		**1,555**	**$319,904**
Pre-registration 2012 (Chicago):		1,367	$234,928
Total registration 2012:		**1,537**	**$293,130**
Pre-registration 2011 (San Diego, CA):		1,328	$243,004
Total registration 2011:		**1,541**	**$307,237**
Pre-registration 2010 (Washington, DC):		1,529	$261,246
Total registration 2010:		**1,668**	**$306,393**
Pre-registration 2009 (Chicago):		1,383	$256,800
Total registration 2009:		**1,506**	**$294,266**
Pre-registration 2008 (San Diego) :		1,343	$214,856
Total registration 2008:		**1,447**	**$281,093**
Pre-registration 2007 (Philadelphia):		1,345	$234,000
Total registration 2007:		**1,507**	**$288,067**

C. ACCOUNT BALANCES
C.1. Drosophila Main Fund
Table 2: Summary of income and attendance since 1993

Meeting Year	Location	Net Income	Fund Balance*	# Meeting Attendees
1993	San Diego	$17,105	$ 25,146	1,165
1994	Chicago	2,800	27,946	1,222
1995	Atlanta	8,417	36,363	1,103
1996	San Diego	15,035	51,398	1,423
1997	Chicago	31,663	83,061	1,382
1998	Wash DC	21,522	104,583	1,378
1999	Seattle	(6,053)	98,530	1,366
2000	Pittsburgh	(56,060)	42,470	1,183
2001	Wash DC	71,656	114,126	1,627
2002	San Diego	60,661	174,787	1,552
2003	Chicago	(22,993)	151,794	1,603
2004	Wash DC	23,026	174,820	1,617
2005	San Diego	89,943	264,763	1,515
2006	Houston	6,196	270,959	1,402
2007	Philadelphia	16,663	287,622	1,507
2008	San Diego	(5,410)	282,212	1,447
2009	Chicago	(47,935)	234,277	1.506
2010	Washington, DC	27,082	261,359	1,668
2011	San Diego	64,471	325,830	1,541
2012	Chicago	(81,484)	244,346- 26,000 was transferred out 20,000 to Sandler and 6,000 to Vicky Finnerty)	1,537
2013	Washington DC	$2,921	$247,267	1,555
2014	San Diego	$6,982	$254,249	1,431
2015	Chicago	(21,457)	$232,793	1,569**
2016	Orlando	(11,000)	$221,793- $6K to Finnerty plus $5K in add'l Travel Awards for	

			TAGC	

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

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

Year	Investment Gain/transfers	Travel expenses	Supplies/ Mailing expenses	Net Income	**Balance**
1993				1417	25,964
1994				(451)	25,513
1995				1,595	27,108
1996				1,142	28,250
1997				1,119	29,369
1998				1,385	30,754
1999				877	31,631
2000				257	31,888
2001				(234)	31,654
2002				(846)	30,808
2003				(2,431)	28,377
2004				432	28,809
2005	1076	1,208	37	(169)	28,640
2006	1963	469	15	1,479	30,119
2007	2187	501	15	1,671	31,790
2008	-859	441	20	(1,320)	30,470
2009	1198	768		430	30,900
2010	947	1,482		(555)	30,345
2011	555	420		135	30,480
2012*	23,821	826		22,995	53,475
2013	6,847	1,171		5,676	59,151
2014	4,865	580		4,285	63,436
2015	369	428		(59)	63,377
2016	5,716	709		5,007	68,384

*Includes $20,000 transfer from meeting fund

C. 3. Vicky Finnerty Memorial Fund
Table 4: Summary of Finnerty Fund

Year	Contributions	Received from Dros	Awards	Net Income	**Balance**
2011	3,726			-	3,726
2012	4,102	6,000	3,726	6,376	10,102
2013	3,000	6,000	10,102	(1,102)	9,000
2014	960	6,000	6,000	960	9,960
2015	1,324	6,000	4,705	2,619	12,579
2016	886	6,000	4,394	2,492	15,071

58th ANNUAL DROSOPHILA RESEARCH CONFERENCE
As you can see from the information in the treasurer's report, I am anticipating a loss of approximately $33,000. Almost all of this amount is attributed to lower than expected registration income. However, exhibit and sponsorship revenue continues to make small increases each year. The reserves are still strong and can handle the loss but we will need to continue to increase registration costs to keep up with rising costs.

Registration:
The total registration number for 2017 as of March 5 is 1,160. This number is down approximately 25% which we anticipated it might be with the current funding situation and what we are seeing with other communities. In addition, San Diego usually has slightly lower attendance. The travel ban did not appear to make much of a difference as we did not have anyone who cancelled as a result of the ban. We don't, however, know if people that are not attending are doing so due to the travel ban. GSA currently does not collect information on country of origin for its members or conference attendees.

Hotel Rates and Pick-up:
While attendance is down, we should not be financially impacted by lower than normal room pickup in the form of attrition fees. When we re-signed with the Town & Country for 2020 we requested an additional buffer for 2017 moving our attrition fee trigger from 15% to 25% (industry standard is 15% or less. While this will not likely be something we can repeat, it certainly helped us this year. We had about 30 people go around the block (although we will get credit for them) and others are staying elsewhere or are local. It may be time to consider providing an incentive to encourage people to stay at the conference hotel.

Our pickup is important not only because cost-saving concessions are tied to it but there is the possibility that we would have to pay an attrition fee if we dip below 85% of our contracted block. Normally we are at 95% or more of our contracted block so it is rarely an issue. However, this is something that all groups continue to have challenges with, especially with the constantly changing pricing available on the Internet, Airbnb and hotel scalpers. While we are protected to some degree by adding a contractual clause that requires the hotel to do an audit against our registration list to look for those who did book in the conference block (resulting in 100+ room nights this year), we have no control over those that decide to stay elsewhere. Many groups have begun to charge a higher amount to those who do not stay at the contracted hotel.

FUTURE CONFERENCES
After the enthusiastic intellectual success of TAGC, the GSA Board has decided to hold the next meeting in 2020. The plans are just developing but I know GSA is hopeful you will once again join this meeting. You can see below the overwhelmingly positive stats for the meeting and with some adjustments in some of the logistical issues, it should be even better in 2020. If you do decide to join TAGC in 2020, we will attempt to move the already contracted for 2020 meeting in San Diego to 2021. Regardless of the outcome, Dros will not be responsible for any fees that may be associated with a date shift IF you do decide to be part of TAGC in 2020. As of now, the dates and rates have been confirmed through 2020 for Dros as follows:

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

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

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

2021-Open

Registrations - 2017

	Number
Faculty/Lab Tech Members	387
Faculty/Lab Tech NonMembers	64
Postdoc Members	175
Postdoc Nonmembers	41
Grad Student Members	260
Grad Student Nonmembers	59
Undergrad Members	111
Undergrad Nonmembers	26
Complimentary	37*
Early/Regular	**1,160**

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

Registrants by Country

United States	952	Israel	4
Canada	28	Chile	3
Germany	23	Denmark	3
UK	21	Singapore	3
Japan	15	Czech Republic	2
South Korea	15	Hong Kong	2
China	12	Portugal	2
France	10	Argentina	1
India	10	Colombia	1
Taiwan	10	Netherlands	1
Switzerland	8	Norway	1
Brazil	6	Russian Federation	1
Australia	5	Spain	1
Austria	5		
Italy	5	Total number of countries: 30 for 1160
Mexico	5	registrants
Sweden	5		

TAGC Highlights

75% of Dros attendees said TAGC met or exceeded their expectations
83% of Dros attendees were overall satisfied with the meeting. For only early career scientist that number goes up to 90%
90% of Dros attendees wanted TAGC to be held again in the future

55% of Dros attendees would like to see it organized by theme v 45% of Dros attendees would like to see it offered again in its current format.
76% of Dros attendees felt it was very or somewhat important to maintain some form of the regular meeting within the TAGC format.

Main reasons people did not attend include:
- Prefer smaller meetings
- Cost to attend/availability of funding
- Scheduling conflict

Main complaints from meeting:
- Meals either not included, cost prohibitive or inability to leave the property for a quick bite
- Too many sessions/agenda too packed
- Not enough cross-over between communities
- Distance from posters/exhibits to other meeting space

Stats as compared to recent meetings:

	TAGC Overall	Dros Only @TAGC	Dros 2015 Chicago	Dros 2014 San Diego	Dros 2017 San Diego (est)
# of abstracts	2,182	706*	999	968	787
# of attendees	3,015	1066**	1,569	1,431	1200
Percentage Faculty/PI	43%	40%	37%	37%	40%
Percentage Postdoc	17%	17%	15%	19%	20%
Percentage grad	32%	34%	35%	35%	28%
Percentage undergrad	8%	9%	12%	9%	12%

*244 Additional through PEQG

5. GSA and the Drosophila Board: Lynn Cooley

The Genetics Society of America values the *Drosophila* community, and is grateful for the opportunity to serve fly researchers. The following topics will be useful prior to discussions that will be held at the FlyBoard meeting in San Diego.

TAGC 2016 and beyond

Suzy Brown, GSA Senior Meetings Director, has in her report described TAGC highlights, garnered from the overall evaluation of the meeting. To recap:

- Members of the fly community (including those registering primarily as population & quantitative traits) comprised 706/2182 meeting abstracts (32%) and 1066/3015 (35%) of attendees. Clearly, this is a significant portion of the overall TAGC meeting population.
- As followed the general trend for the meeting, Dros attendees included 40% faculty/PIs, 34% graduate students, 17% postdocs, and 9% undergraduates.
- 75% of Dros attendees said TAGC met or exceeded their expectations

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- 83% of Dros attendees were overall satisfied with the meeting. When considering early career scientists only, that percentage increases to 90.
- 90% of Dros attendees wanted TAGC to be held again in the future
- 55% of Dros attendees would like to see it organized by theme v. 45% of Dros attendees would like to see it offered again in its current format.
- 76% of Dros attendees felt it was very or somewhat important to maintain some form of the regular meeting within the TAGC format.
- The main reasons stated for those not attending TAGC:
    o prefer smaller meetings
    o cost to attend/funding availability
    o schedule conflict
- Primary complaints about TAGC:
    o meals either not included, cost-prohibitive meal plan, or difficulty in leaving the property for a quick meal
    o too many sessions/packed agenda
    o not enough cross-community sessions or opportunities to socialize/network
    o (long) distance from posters/exhibits to main meeting space

In general, the GSA Board and meetings staff feel that the primary stated complaints about TAGC can and will be addressed for the next TAGC meeting, *tentatively* planned for 2020.

Questions for discussion

That said, at the FlyBoard meeting (Dros, 2017) Suzy Brown will present these and other relevant statistics, and she and Lynn Cooley will discuss with FlyBoard members questions that include the following:

1. TAGC
    a. For the next TAGC, what kind of balance would the community want in terms of topic/theme- v. community-focused session? The former could include speakers and attendees across a wide range of model organisms, while the latter would be for Dros. scientists only.
    b. We've proposed holding TAGC every four years. That timeframe is still under discussion, but in general, what does the FlyBoard think?

2. The GSA Board would like to invite the FlyBoard President or past-President as a member of the GSA Board (ex-officio). We believe this would increase transparency in terms of the relationship between GSA and FlyBoard, allow GSA to better understand & respond to your community's concerns, allow for more frequent communications, and yield mutual opportunities as yet unknown.

3. The Gruber Foundation approached GSA with the idea of GSA hosting the Awards Ceremony and the Keynote for the Gruber Prize in Genetics http://gruber.yale.edu/genetics. This would be done at TAGC (every 4 years or so).
    a. The award ceremony for the Gruber Genetics prize has been done frequently at the ASHG meeting, but will not continue.
    b. Every 5 years, they present the award at the International Congress of Genetics (ICG), with 2018 being the next one.
    c. During non-TAGC or non-ICG years, the Gruber Foundation would like to present the Award & host a Keynote at a GSA-sponsored meeting (most likely Worm or Dros) or at another event.
    d. Ceremony is ~10 minutes /emphasis is on the lecture as value added to conference (~45-60 minutes).
    e. GSA would like to accept the Gruber Foundation's proposal, and is asking for

your feedback on whether the Dros community would be tentatively open to hosting the Awards Ceremony and Keynote at a Dros meeting (every ~3 years or so).

      f.   A list of Genetics Laureates is available here http://gruber.yale.edu/genetics-laureates. The awardee's research is typically notable and interesting enough that a keynote is applicable to a wide range of geneticists, regardless of whether the awardee's field of study necessarily dovetails with the model organism meeting (e.g. Dros or Worm).

4. Announcement: GSA is an official partner of the March for Science (MfS), *www.marchforscience.com,* which will be held April 22, 2017 in DC as well as at over 300 satellite cities. We'd like to encourage you, your families and friends to attend and get the word out about this important, awareness-raising event.

ACTION ITEMS:
➢ Future TAGC meetings - what kind of balance re. topic/theme- v. community-focused session
➢ FlyBoard member on the GSA Board
➢ Gruber Prize

6. Sandler Lectureship Committee: Bob Duronio

Committee members:
Bob Duronio, University of North Carolina at Chapel Hill (Chair)
Kim McCall, Boston University
Laura Johnston, Columbia University
Tin Tin Su, University of Colorado at Boulder

Chair 2018:
Kim McCall, Boston University

Total 2017 Nominees: 23
Total Male Nominees: 13   Total Male advisors: 17
Total Female Nominees: 10   Total Female advisors: 6

Winner:
Danny Miller (Ph.D. mentor: Scott Hawley). Dr. Miller obtained his Ph.D. in Physiology with Honors in 2016 from the University of Kansas Medical Center and the Stowers Institute for Medical Research. He currently is enrolled in the final MD portion of his MSTP program. Dr. Miller used whole genome sequencing to characterize recombination during meiosis. His comprehensive analysis, which required a sophisticated combination of computational and experimental protocols, provides one of the highest resolution data sets describing the distribution of crossovers and gene conversions in any animal genome. Dr. Miller demonstrated that, unlike recombination, gene conversion (which arises from the same type of double strand breaks that result in recombination) is not subject to either interference or the centromere effect, both of which suppress recombination. Furthermore, and of great value to the greater *Drosophila* community, Dr. Miller identified the inversion breakpoints, gene disruptions, and chromosome regions not effectively balanced on several balancer chromosomes. The bulk of Dr. Miller's thesis work describing these findings was published in three 2016 articles appearing in *Genetics*, *PNAS*, and *G3*. He also published a first authored G3 paper in 2012 that formed the foundation for the later studies. In addition, during graduate school Dr. Miller was a contributing author on six additional manuscripts (4 of which were from the Hawley lab).

Runners up:

1st Celine Santiago, University of Pennsylvania (Ph.D. mentor: Greg Bashaw)
2nd Mira Pronobis, University of North Carolina, Chapel Hill (Ph.D. mentor: Mark Peifer)

Notes on process:
Of the 23 nominees, the committee selected 5 finalists for which the whole PhD thesis was evaluated. One of these five was from Valentino Gantz, who was also nominated last year by his advisor, Ethan Bier. The chair unfortunately missed the stipulation that a student can only be nominated once, and when the committee recognized the chair's error during their deliberations, Dr. Bier was notified and Dr. Gantz's thesis was removed from consideration.

2017 Nominees:

Nominee	Gender	Thesis advisor	Gender
Ronald Alfa	M	Seung Kim	M
Giuseppe Bosso	M	Giovanni Cenci	M
Ben Jiwon Choi	M	Brian McCabe	M
Erik Clark	M	Michael Akam	M
William Constance	M	Darren Williams	M
Alyssa Coyne	F	Daniela Zarnescu	F
Shaun Davis	M	Herman Dierick	M
Kyle Eagen	M	Roger Kornberg	M
Ines Fragata	F	Margarida Matos	F
Valentino Gantz	M	Ethan Bier	M
Tom Hill	M	Andrea Betancourt	F
Shadi Jafari	F	Matthias Alenius	M
Chun Wai Kwan	M	Urs Schmidt-Orr	M
Sarah Levinson	F	Ross Cagan	M
Hongjie Li	M	Henri Jasper	M
Danny Miller	M	Scott Hawley	M
Mira Pronobis	F	Mark Peifer	M
Theresa Reimels	F	Cathie Pfleger	F
Leah Rosin	F	Barbara Melione	F
Celine Santiago	F	Greg Bashaw	M
Heather Turner	F	Michael Galko	M
Jen Urban	F	Erica Larschan	F
Yiliang Wei	M	David Arnosti	M

7. Victoria Finnerty Undergraduate Travel Award (Alexis Nagengast, Chair)

This year we received 13 applications for the Victoria Finnerty (VF) Undergraduate Travel Award and funded the top 7 for a total of $3844. We again awarded a maximum amount of $599 because recipients do not have to pay taxes on amounts less than $600. One reward of $250 was less but more than what was requested by the applicant.

We did not designate a recipient to receive the Larry Sandler Undergraduate Travel Award designation this year because of prior confusion around the method to recognize the recipient and a change in personnel at GSA. Beth Reudi, former Director of Education and Professional Development, was no longer at GSA when it was time to review the applications. Last year she had requested that the awardee receive an extra ribbon on her/his poster to mark the Sandler distinction so that this designation would not require a new award mechanism separate from the Victoria Finnerty Travel Award. I didn't know Beth was no longer at GSA until mid-October, two weeks after the deadline for applications. I worked with Mary Rose Stoltz at GSA and she was very helpful but not experienced with the application process. This did not seem like the year to try

something new. We did request that the criteria be changed next year to state that only one nominee from each lab be allowed.

The awardees are:
- James Cevallos (Poster #417C), UCLA, $250
- Jenna Harris (Poster #392B), Georgia State, $599
- Madison Hupp (Poster #567C), Kennesaw State, $599
- Matthew Riccetti (Poster #445A), University of Dayton, $599
- Ryan Salemme, (Poster #382A), John Carroll University, $599
- Liesl Strand (Poster #584B), University of Washington, $599
- Courtney Willet (Poster #571A), Kennesaw State, $599

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

This year's selection committee was Alexis Nagengast (chair and PUI Drosophila board representative), Sarah Certel, Justin DiAngelo, Jim Erickson and Matthew Wawersik. Amanda Norvell, incoming PUI rep, will be on the committee next year and take over as chair in 2018.

ACTION ITEM:
➤ New mechanisms for endowing more travel awards?

8. Image Award: David Bilder
This year's competition 63 total submissions, including 14 videos.

The winners this year were:
➤ **Helen Weavers**, for her video 'Systems Analysis of the Dynamic Inflammatory Response to Tissue Damage'.
➤ **Yali Zhang**, for his image of 'The basis of food texture sensation in Drosophila'.

The runner-ups were:
➤ **Yusuke Hara**, for his video 'Non-invasive Tension Estimation during the Early Stage of Dorsal Closure**'**
➤ **Tvisha Misra**, for her image illustrating that different cellular hypoxic states correlate with tracheal supply in the brain.

David Bilder will make the Award presentation at the meeting.

After 13 years, I am looking to step away from the Award and pass it on to another caretaker, after a transition to hand over the ropes. Before stepping away, I like the idea of creating a poster with some of the ~150 great images that we've collected, for people to hang in their labs/fly rooms. One option for distribution is to include a (foldable) poster with ADRC registration that attendees could pick up (saving postage fees); another is to mail it out as an incentive to labs when they sign up for the FlyLab mailing list at Bloomington. Suzy got some quotes for 19x27 100# coated posters for a little less or more than a dollar each depending on 1000 or 2000 posters. I'm wondering if the Board would like to consider either 1). Directly sponsoring this, 2). Adding a charge option (like T-shirts) for next year's meeting fee, or 3). Encouraging me to seek an outside sponsor (GSA? Microscope company?).

Another nice thing to do would be to create some screensavers that people could download from the site and put on their computers. These could be in themed collections (neuroscience, cell biology, etc.) selected from the archive. Should be straightforward --if a Board member is enthusiastic, we'd be happy to have some help with this.

ACTION ITEMS:
- ➢ Should FlyBoard sponsor Image Award Posters and/or screensavers?
- ➢ Add a charge option to ADRC registration?
- ➢ Seek outside sponsor?

9. 2018 & 2019 Fly Meetings Update (Tin Tin Su)

2018 organizers are Tin Tin Su, Giovanni Bosco, Pam Geyer, and Noah Whiteman.

The organizers plan to study the platform sessions and how well they work at the 2017 meeting, before deciding on what to keep. There is a number of changes to the program for 2017, along with several new additions such as new PI forum, PI Happy Hour, a stand alone technique session, and Science Slam. They will also take a close look at these to see how well they work and decide after whether they are appropriate to keep for 2018.

We are currently considering a list of speaker suggestions. Our plan is to get the sessions and invited speakers sorted out within two weeks after the 2017 meeting.

10. Drosophila Board Election Report (Ken Irvine)

The Elections Committee consisted of Ken Irvine (Chair), Ela Serpe, Helen McNeill, Mark Peifer and Justin Kumar. Mark and Justin served last year and will rotate off next year, Ela and Helen were new recruits to the committee. Next year's chair will be David BIlder. Ken will remind him to organize the committee and to select two new members to serve 2-year terms.

The Chair solicited nominations from outgoing regional representatives and from the elections committee, and compiled a list of all nominees. Each member of the Election Committee then ranked the nominations for each open position. The rank orders from all committee members were used to assemble a final ordered list. The Chair contacted the top-ranked nominees to ask them to stand for election. A number of candidates declined, but as we had a long list of qualified candidates we were able to come up with two excellent candidates for each position. With the help of Jim Thurmond and Thom Kaufman, a ballot including two candidates for each position, along with short biographies and links to their lab websites, was disseminated to the fly community by email on Nov 14, 2016, with a deadline for voting of Dec. 2nd, 2016. A reminder email was sent on November 28th.

Election emails and candidate statements are appended to the end of the Agenda.

The winners of the election were:
Bruce Edgar, President (2018)
Michelle Arbeitman, Treasurer (through 2020)
Celeste Berg, Mountain representative (through 2020)
Kim McCall, New England representative (through 2020)
Amanda Norvell, Primarily Undergraduate Institutions representative (through 2020)

Coral Warr, Australia representative (through 2020)

The turnout for this election was good, with a total of 652 votes cast, compared to a historical average of around 500 votes. The ballot included a statement that "*Only scientists who use Drosophila as a research organism are eligible to vote.*" Unlike last year, there was no indication that any voting outside of the fly community occurred.

We had also intended to select a trainee representative for the board. Our intended procedure was to have interested individuals self-nominate, and the elections committee would then choose the best candidate. However, there were no nominations. The appeal for nominations was included in the elections email, with the following text:

"**New This Year: Trainee Representative***. We are adding a trainee representative to the Fly Board. The trainee representative should be a PhD student or Post-doc, and will be expected to serve a 2-year term. Interested candidates should self-nominate by sending to Ken Irvine (mailto:irvine@waksman.rutgers.edu) 1) a current CV, 2) an ~1-2 page statement describing your qualifications and interest in serving on the fly board, and 3) a letter of recommendation from your current mentor, which must include a statement confirming financial support for your attendance at Fly meetings while serving on the board. The trainee representative will be selected by the elections committee from amongst nominations received by Dec 1*st* 2016.*"

Some possible explanations for the lack of nominations:
1) Lack of advertising for the new position.
2) Not enough time for people to give adequate consideration to joining the board.
3) Lack of financial support for trainee representatives.
4) A two year commitment may be difficult for trainees.

ACTION ITEMS:
➢ The position could be advertised at the Fly meeting to people more time to consider whether they want to be a candidate for this position.
➢ Is a two-year term appropriate?
➢ Does the board want to provide any support for the trainee representative (eg, waive meeting registration fees)?

11. Janelia Drosophila Ecosystem Meeting: David Bilder

At the 'Drosophila Research Ecosystem' meeting last year in Janelia, a number of initiatives were proposed to improve the community.   Some of these have been completed (Kudos to Ken!), while others (including those in my bailiwick) are moving slowly ahead. Updates on major items are below.

-**White Paper revision** (Ken Irvine): completed, posted at Flybase.
-**Fly Board charter revisions** (Ken Irvine): completed, now updated at Flybase.
-**ADRC Innovation ideas** (Howard Lipshitz): completed. Some of the ideas have been adopted by this year's organizers. Others are listed in the 2016 Board Meeting Notes.

-**Communications and Advocacy** (Andrea Page-McCaw, Andreas Prokop, Michelle Arbeitman, Sarah Certel, Alexis Nagengast, Gio Bosco): covered separately
-**Validated commercial antibody list**: Bing Zhang, Thom Kaufman: covered separately

-**Meeting Report** (David Bilder): My approach was to write –instead of a standard narrative meeting report—a piece that also gave an overview of the current status of the Fly Research Ecosystem, which would also allow for pro-fly advocacy and provide a citable document for some of the strengths of the community and its resources. Ken and I have a decent draft, entitled 'Taking Stock of the Drosophila Research Ecosystem' that we plan to submit soon, perhaps to Genetics.

-**Fly worker contact list for communication** (David Bilder): I'd like to formally propose to the Board that an opt-in registration of Fly groups at stock centers, starting with Bloomington, be initiated. While not a perfect system, discussion at Janelia and last year's Board meeting indicated that this would be more useful, comprehensive, and sustainable than other options.
Kathy and Kevin have worked out some of the following details:
-all new accounts will be asked to 'opt-in' to receive emails from FlyBoard (as well as a separate option for emails from Bloomington)
-existing users will be prompted by separate SurveyMonkey email
-the request will link to a (Flybase-hosted?) web page that explains the importance of the contact list and an example of the small number of yearly emails that can be expected (1 x: Fly News, Sandler and Image Award announcement, ADRC announcement, critical advocacy issues that might arise?)
-further encouragement will be given at the President's address at the ADRC
-list maintenance will be coupled to culling of inactive accounts after ~4 years
-a separate list for non- Bloomington account holders will be offered by email registration and by 'Register as a Flyperson'. Maintenance on this list is an open question.
-when the Bloomington accounts are up and running, notes can be compared with VDRC and Kyoto (which may have different privacy policies) to see how many others would be captured if the process is extended to these stock centers.

-**Standardized reagent table for fly publications**, to promote reproducibility and ease the burden on FlyBase curators/annotators (Norbert Perrimon): Norbert and Flybase are working with Cell Press and Genetics on this to establish a paradigm to bring to other journals. Cell has folded some suggestions from Norbert into the 'STAR Methods'. With Genetics, Lynn Crosby of Flybase has designed a more rigorous Author Reagent Table template. There are issues that still need to be worked out (e.g. use of identifiers) and of course promotion and acceptance amongst both authors and journals. Work is ongoing.

-**Encouragement of donations of useful stocks to public stock centers**, to ease the open sharing and convenient access of reagents (Kevin Cook, Nick Brown): Bloomington is interested in taking useful stocks, including those frequently requested from individual labs, as well as characterized strong/null alleles in genes not currently represented in Bloomington. This should be publicized along with other ways to help the community –in the President's address, in FlyNews, and in the article that Ken and I are writing. Incidentally, the following represents our current status about alleles (thanks to Nick and Gillian) –note the relatively low coverage of nulls: Mutant alleles have been generated for 56% of genes, including 77% of the genes orthologous to human genes. About 2/3 of the genes with mutant alleles have only transposon insertion alleles, which may not be functionally null, whereas 21% have more standard mutant alleles, with 8% confirmed null alleles (for those with human orthologs, these numbers are 32% and 11%). For the genes with null alleles, about half have a null allele available at stock centers

New energy as well as new initiatives are welcome from Board representatives and the community at large.

12. Alliance of Genome Resources meeting report (David Bilder)

This meeting will work through plans for the integrated MOD databases, and will take place on March 6th. Norbert, Thom, Brian, Hugo and I will update the Board on the outcomes.

13. Primarily Undergraduate Institutions: Alexis Nagengast

The undergraduate plenary session and mixer in the past has been organized by Beth Reudi, former GSA Director of Education and Professional Development. However, she is no longer at GSA and there is no undergraduate plenary session or mixer this year. As was tried last summer at The Allied Genetics Conference, the traditional Drosophila Research and Pedagogy at Primarily Undergraduate Institutions Workshop has been split into two different workshops. The pedagogy workshop (Integrating Research and Teaching) focuses on undergraduate education at all types of institutions and not just PUIs. The undergraduate research workshop (Spotlight on Undergraduate Research) will include five talks from undergraduate students.

Activities at this year's meeting are:
  • Integrating Research and Teaching at PUIs at 7:45 pm on Thursday.
  • Spotlight on Undergraduate Research at 1:45 pm on Friday.

Amanda Norvell from The College of New Jersey will be the new PUI representative. She will join the Victoria Finnerty Undergraduate Travel Award Committee this year and become chair in 2018.

14. Advocacy & Communications (Andreas Prokop, Stephanie Mohr)

Background: At the Janelia Drosophila Resources workshop in February 2016, two groups were established, one to work on Community Outreach (led by Andreas Prokop, Stephanie Mohr and Scott Hawley) and one to work on Advocacy (led by Gio Bosco and Andrea Page-McCaw). Since the efforts of these committees were similar it was decided to merge to committees into one group. David Bilder asked Andreas Prokop to be the 2017 committee chair.

1. FlyBase icons
Andreas Prokop and Stephanie Mohr worked with Susan Russo Gelbart at FlyBase to develop a proposal for modifying the left-hand icons on the FlyBase home page. The goal was to highlight resources for outreach and community. As part of this effort, we have drafted a community website (see **Appendix 3**) that would serve as a new, easily updatable place for fly community news, events, and online resources for various audiences.

Here is a low-resolution image of a mock-up of the proposed new icon layout as it would appear on FlyBase home (left); a higher-res look at the proposed new icons section (right).

2. Mission, challenges and ideas for solutions.

A) Mission for the science communication committee

It is the overarching aim of the science communication committee to promote active communication with a wide range of relevant audiences as well as within the community of fly researchers - with a view to strengthening the standing of *Drosophila* in society and research. The concrete goals are:

1. To raise general awareness and recognition (among the wider public, clinicians, decision makers and politicians) of the importance of *Drosophila melanogaster* as a pillar in the process of scientific discovery, and its immediate relevance for our understanding of many diseases and the advance in biomedical sciences, evolutionary biology, bioinformatics and other related areas.

2. To animate more non-fly researchers to use *Drosophila* or engage in collaborations with *Drosophila* laboratories.

3. To raise the standards of knowledge about *Drosophila* as a model among those who already use or plan to use *Drosophila* for their research.

4. To improve the means and culture of horizontal communication and exchange within the community of fly researchers, with a view to fostering efficient exchange of research tools and strategies and also building para-scientific networks of science communication.

B) Defining the challenges

B1. The challenges we face today with respect to teaching and research:

Twenty years ago, the standing of invertebrate model organisms, such as *Drosophila*, was still unrivalled, and the fly community had a strong presence in decision making bodies. *Drosophila* was accepted as a uniquely powerful and irreplaceable boundary object linking genetics to

biology (Keller, 1996), and it was frequent practice to learn about fly genetics in schools. This view has changed:

– Today also vertebrates have become boundary objects (fish, frog, mouse), and especially CRISPR is seen as the magic bullet in many systems able to replace invertebrate model organisms. At first sight, it seems logic to put more weight on those organisms which are closer to humans.

– In times of political drive towards "translational research", we are faced with widespread misconceptions about the importance of fundamental biology, and fly research (even into disease) is naturally restricted to fundamental biology. It is not apparent to many contemporary scientists, clinicians and decision/policy makers that fly research can be a very powerful contributor to the translational pipeline (arguably to a far greater degree than mouse ever can).

– Due to technology development, classical genetics is being overshadowed by modern "omics" approaches; it has lost its original appeal in schools and at universities (Redfield, 2012). Therefore, the majority of students has never been and will never be in contact with flies. This has major impact on the general standing of flies in research.

Our task is therefore to communicate the advantages of flies, including speed, efficiency, cost-effectiveness, the enormous power of combinatorial genetics, and the ways in which flies fuel the translational pipeline. We need to innovate the use of flies as a teaching tool in schools and at universities. For example, in universities applied fly genetics provides efficient, active learning means to convey fundamentals of classical genetics (Fostier et al., 2015), and *Drosophila* can be used as a teaching tool in schools to convey many curriculum-relevant topics involving memorable classroom experiments that reflect relevant contemporary research (poppi62.wordpress.com/2015/08/28/school-flies).

B2. The challenges to our communication:

Since the 30s, the *Drosophila* community shared information through the *Drosophila Information Service* (Kelty, 2012). Importantly, DIS was sent out to a member of the community only if he/she actively "*contributed a stock-list of mutant fruit flies available in their labs (and thereby was willing to share these mutants by mail or in person)*" (Kelty, 2012). This active contribution is an important concept that likely was one of the pathways to success of DIS and further helped to shape a strong fly community. DIS lay at the roots of the Red Book (interim versions have appeared in volumes 62, 64, 65 and 68) (Lindsley and Zimm, 1992) and also "*FlyBase grew directly out of the DIS – numbers 73 and 74 (1994) are printed versions of the contents of the database*" (Kelty, 2012).

FlyBase quickly became the new central point of call for our community, and especially during the early years, we all registered at FlyBase so that we could be found and find others. This was a mild version of "signing up" to the community, perhaps enough to give us a certain feeling of corporate identity and certainly providing a fairly reliable overview of who was a member of the community. Furthermore, due to lack of other information sources, we may have looked more closely at additional information (beyond genes and genetic tools) provided in the side bar of the FlyBase front page, and FlyBase may therefore have worked, at least to a degree, as a conveyor of "para-genetic" information relevant to our community, thus fulfilling an important second role that DIS used to play.

Nowadays, due to efficient search engines, registration at FlyBase has become obsolete. This means we have no reliable mailing lists anymore and can only guestimate how many drosophilists there are worldwide. As a further complication, social media and search engines make us feel well informed - not realising that we are often not informed at all about important

matters because we were not alarmed to look for them. In consequence, community information in the FlyBase side bar is far less likely to be read, and there is little hope that newsletters would be opened by many - adding to the problem of not having reliable mailing lists anyway. To give a few examples, I still meet many that have never heard of the Genetics Training package we published in 2013 (Roote and Prokop, 2013), and Lisa Meadows at VDRC reports that they have to use their own compiled customer lists to inform about important innovations but have no means of reaching the wider community. Any new resource will depend on word-of-mouth.

FlyBase is the obvious starting point if we are to improve the situation. If I recall correctly, FlyBase counts 300K visitors and 1.5 mio page views per month. This is a unique opportunity and, in my view, we could make efficient use of it. Thus, the FlyBase front page is currently not well designed to support community information exchange, nor does it give good visibility to existing community resources, which tend to be woven into gene queries but hard to recognise as independent entities. The Fly Wiki (http://flybase.org/wiki/FlyBase:External_Resources) is trying to address this issue by providing resource lists and links. However, many of us seem not to know about it, and the relation between FlyBase and those community resources might not be sufficiently obvious. There is a need for greater transparency.

In the latter context, it also needs to be highlighted that not all our community resources are of scientific nature, but they may address issues of science communication, education or training. Great examples are Ashburner's laboratory handbook (Ashburner et al., 2005), fly pushing (Greenspan, 2004), the green bible (Campos-Ortega and Hartenstein, 1997), the blue bible (Bate and Martínez-Arias, 1993), FlyMove (Weigmann et al., 2003), interactive fly (Brody, 1999), the atlas of fly morphology (Chyb and Gompel, 2013), the genetics training package (Roote and Prokop, 2013), lords of the fly (Kohler, 1994), the unsung hero book (Brookes, 2001/2002) or the making of a fly (Lawrence, 1992). These are only the tip of the iceberg and YouTube, journals and blogs are full of great resources that get unfortunately lost in the noise of the web. In consequence, we spread our message thin and tend to re-invent the wheel (because there is little awareness of existing resources) without reaching greater impact. For example, did Fly book have the impact that was hoped for?

We need a one-stop shop that bundles all this information, categorises it in a transparent way and makes it accessible for wider use. Importantly, such a one-stop shop needs an "official status" so that it is taken serious and finds wider acceptance. For example, the Manchester Fly Facility has taken first steps in this direction by providing a comprehensive list of science communication, training, history and education resources (http://www.flyfacility.ls.manchester.ac.uk/forthepublic), but it lacks the required authority to be accepted as a true community resource.

Apart from failing to inform our community, not promoting community resources has an important further negative knock-on effect: user statistics stay relatively modest, providing little incentive/justification to maintain the effort - a risk that many community resources may face. For example, fly Move and the Manchester Fly Facility initiatives are the most consequent initiatives that I am aware of, but both suffer the same problem: lack of interest within the community. I recently talked to Christian Klaembt about it, and they stopped Fly Move primarily because of lack of interest, once the money ran out. To illustrate the situation further: after giving a much applauded talk about science communication to a packed lecture theatre at the EDRC two years ago, there was no increase in visitor numbers on our web sites, not even on the same day. Our two resource websites have in the range of 22K (droso4schools) and 40K views (Manchester Fly Facility) over several years (about 10K p.a.), and that is simply not enough to justify time invested in front of local line managements. Merely by channeling more visitors towards community resource sites, we would not only raise awareness of their existence but also provide an incentive for those who maintain those resources - and the willingness of members of our

community to develop and share general resources has always been one of our key strengths. I believe that improved visibility (hence recognition) will inspire and animate members of our community to provide and improve our resource and strategy pool.

In conclusion, the key goal of *Drosophila* science communication and advocacy is NOT primarily the development of new communication resources, and there are plenty in existence already. The key goal MUST be to develop strategies for making resources transparent and capitalise on them efficiently. For this we need to:

1. improve the means and culture of communication and information exchange within our community.

2. bundle all our resources on a well-accepted platform to make them transparent and stimulate their use.

This will have positive impact on research, outreach, training, education and advocacy.

C) Defining terms relevant to the science communication committee

There is confusion about the various terms describing the communication of science; they include: public outreach, public engagement, science communication, advocacy, widening participation, knowledge exchange, as well as dissemination and marketing. Many of these terms seem to have their specific connotations but are nevertheless often used interchangeably (Illingworth et al., 2015). Furthermore, they show strong overlap with other areas of activity, which include training and education; education/training and science communication can often be viewed as two sides of the same coin.

It is essential that we are clear about our objectives and respective target audiences. For this, I propose to take a pragmatic approach by introducing a clear nomenclature for areas of activities relevant to the fly community, and to define them in a way that provides a sensible classification as basis for future action and strategy development. As the overarching term, I suggest to use the term science communication. This can be broken down into:

1. Public engagement: communicating with non-scientists as well as scientists from unrelated fields

2. Advocacy (separated out from 1): communicating with politicians and decision makers

3. School education (separated out from 1): introducing *Drosophila* in schools - as a teaching tool or to inspire/enthuse pupils about science; collaborations with teachers; continued professional training for teachers

4. Training: raising knowledge standards of university students, postgraduate students and postdocs about the uses of *Drosophila*, with a view to inspiring students to use *Drosophila* for their research and also building a pool of well-informed ambassadors

5. Marketing: raising awareness about resources and strategies within our community, as well as with specific target audiences (e.g. make school resources known to teachers)

6. Horizontal communication: fostering and improving the means and culture of sharing information within our community

D) Concrete suggestions:

D1. Committee structure

I propose to form one committee, which oversees the 6 tasks listed above. I propose to publish names of those on the committee within the Fly Board section of FlyBase, thus enhancing external recognition of their voluntary efforts and providing authority that can help to perform the task (e.g. convince conference organisers to have a slot for science communication).

D2. FlyBase front page

Stephanie Mohr has made a series of very helpful suggestions to improve the current front page of FlyBase (see appendix). However, these do not yet represent the required step change in our approach. I strongly propose a more drastic approach (see appendix) designed to address a whole range of issues:

- It would de-clutter the front page and take out redundancy

- It would have a stimulating effect; for example, when the design was shown to the communication committee last year, there was an immediate firework of ideas - and this is the spirit that we need in our community.

- It would make FlyBase user-friendly on hand-held devices

- It would reach 300K viewers each month, and raise chances that they look not only at (1) FlyBase but also into the equally weighted tiles regarding (2) Horizontal communication, (3) Public engagement, Advocacy, School education and Training, and (4) Research resources. Through clearer emphasis on the different areas relevant for our community we would provide new opportunities to re-ignite Horizontal communication, improve transparency and accessibility of resources, and clearly improve the marketing aspect.

Changing the front page of FlyBase is a rather political issue, but it should be seriously discussed by the committee because it is, in my view, the most powerful of all options. Please, consider that these changes would leave the core function of FlyBase untouched and it would not enhance the work load of the FlyBase team because the additional three areas would be overseen by people outside FlyBase (I am happy to take over the third tile). At the moment we would need a declaration of will as an incentive to apply for money to pay web designers - certainly not astronomic amounts!

D3. Areas of activity

For most areas of activity mentioned in C, resources and strategies have already been developed (see examples below). The key challenge is to promote resource dissemination and marketing, so that members of our community can make use of them during their science communication work, and get hopefully inspired to improve them or develop and share new resources. Merely by enhancing the use of what we have already, we will achieve significant impact!

a. Public engagement

Existing outreach and communication resources are listed on the Manchester Fly Facility web site (http://www.flyfacility.ls.manchester.ac.uk/forthepublic). As discussed elsewhere, science communication is likely to be most efficient if organised as an objective-driven long-term initiative (Prokop and Illingworth, 2016). Currently the best example of such an initiative is the Manchester Fly Facility which has established a sound basis of resources, ideas and strategies which the fly community can capitalise on: a web page explaining fly research (https://droso4schools.wordpress.com/why-fly), a web page comparing fly and human organs (https://droso4schools.wordpress.com/organs), educational films (now beginning to be translated into other languages;

https://www.youtube.com/channel/UCRUW0eMYSbFsdGtBpNVmPjg/videos), articles explaining strategies and resources (Patel and Prokop, 2015; Patel and Prokop, 2017), and a newly published repository with resources for science fairs and school visits (Prokop and Patel, 2016). This effort can only survive if it is picked up by the fly community and developed into a culture where many of us share in a little, to jointly make a huge difference. For this, we need a common sci comm platform.

b. School education

Existing school resources are listed on the Manchester Fly Facility web site (http://www.flyfacility.ls.manchester.ac.uk/forthepublic/outreachresources). The visionary flag ship initiative was Fly Move (flymove.uni-muenster.de), but its development has seized about a decade ago. Currently, the Manchester Fly Facility is likely the most active initiative, as summarised on a recent blog post (https://poppi62.wordpress.com/2015/08/28/school-flies). Here mentioned are the objective-driven long-term "droso4schools" initiative which is accompanied by teacher resources (Prokop and Patel, 2015), a website (https://droso4schools.wordpress.com), as well as articles in school and scientific journals (Harbottle et al., 2016; Patel et al., 2017). These resources are being used in several countries already (one lesson was recently translated into Spanish), but their wider use and development through *Drosophila* researchers worldwide will be the only way to get more teachers on board. These would become highly effective multiplicators of our key messages, thus gaining significant momentum and implanting an understanding of fly research in society.

c. Training

Complementary to Fly Pushing (Greenspan, 2004), the Manchester Fly Facility has developed fly training resources that use applied genetics to teach fundamentals of classical genetics (Fostier et al., 2015; Prokop, 2013a; Prokop, 2013b; Roote and Prokop, 2013) (Genes to Genomes blog: http://genestogenomes.org/guest-post-maintaining-a-strong-drosophila-community-starting-with-students). If drosophilists worldwide would join in using existing or newly developed resources on university courses, this would be an enormously efficient promotion of *Drosophila* in research.

d. Marketing

A number of strategies can be tried:

- The sheer presence with greater visibility on the FlyBase front page (section D2) would be a major step forward to get resources, strategies and info out into our community.

- We should take a systematic approach at having slots for science communication on each and every fly conference worldwide. I personally have presented about science communication on a couple of international conferences (Prokop, 2015; Prokop, 2016), or organisers agreed to show our slides (https://ndownloader.figshare.com/files/6021738).

- We should target all relevant societies to help us in our advocacy campaign. I am already working with the British Society of Developmental Biology, as well as The Node, on an advocacy campaign about Developmental Biology (thenode.biologists.com/advocacy/outreach), and fly will be closely woven into that. But there are many other societies, such as SDB, GSA, GfE, British Genetics Soc, ASCB etc with which we should establish collaborations to promote our case. It needs to be made clear that our initiative can be used as a model initiative for other scientific fields or model organism communities.

- We should try to involve GSA or CoB in sponsoring an advocacy competition in which we give prizes for the best online advocacy resources, be it websites or short videos, or an

elevator pitch competition. This might be a way to get especially young people involved. Once having thought about the matter in depth, this is likely to keep many of them going.

e. Horizontal communication

Here, the FlyBase front page seems the most promising way forward by equipping one tile with a modern blog-like functionality with short scrollable headlines that can be clicked for further info. Key is the equal weight of this tile aside the other three tiles, hence its improved prominence (see appendix).

f. Advocacy

This is the area I know least about.

Appendix 2. References to Advocacy & Communication Report
Appendix 3. Advocacy and Communications FlyBase cover mock-up
Appendix 4. Advocacy and Communications FlyBase cover (2016)

ACTION ITEMS:
➢ Form Advocacy and education committee; add member names on FlyBoard Wiki page.
➢ FlyBase website cover page alterations?
➢ Funding mechanism for Community Advocacy Webpage

15. Cryopreservation Workshop (Toshiyuki Takano-Shimizu)

The NIH – sponsored workshop was held Workshop held on Wednesday, July 13, 2016 Orlando World Center Marriott, Orlando, FL

Cryopreservation potentially protects valuable stocks from mutations, reduces storage space, decreases maintenance costs, and prevents stock loss or contamination. There are a few of successful reports for cryopreservation of Drosophila embryos. However, a reliable and cost-effective method has not yet been established in Drosophila mainly because the developmental window for successful cryopreservation of embryos is very short and the timing of the window varies among strains.

In this situation, the workshop sponsored by the Office of Research Infrastructure Programs in the Division of Program Coordination, Planning and Strategic Initiatives and the National Institute of Neurological Diseases and Stroke was held to evaluate the potential and practicality of developing efficient preservation methods of Drosophila stocks. The speakers presented new approaches for cold storage and diapause as well as potential cryopreservation targets, sperm, embryos, and larvae. Other speakers provided practical strategies to extend life span and therefore to reduce maintenance labor and cost, based on micro-environmental treatments including fluctuating thermal regime and diet choice, which could be more useful for individual labs. We also heard about robotic and instrument development for optimizing preservation protocols and dehydration.

In summary, the participants agree the necessity of developing easy-to-use and efficient preservation methods and further research not only for long-term cryopreservation methods but also for medium-term storage methods that extend life-span.

Appendix 5: Final Report of the NIH Workshop: Cryopreservation of Drosophila Strains

16. Commercial Antibody Verification (Bing Zhang, Thom Kaufman)

Background: At the request of David Bilder and Ken Irvine, Bing Zhang and Thom Kaufman were tasked to collect information about commercial antibodies. Such a site is being set up on Flybase, and the following letter was written to the community. The letter contains a Google Sheet weblink, with the idea that each lab can enter information about commercial antibodies in use in their lab. This information will then be posted on FlyBase for general use.

Dear Fly Colleagues,

Increasingly more of us face a difficult bottleneck in our research: the lack of antibodies for most fly antigens. Currently, there are three sources of antibodies: 1) home-made ones, 2) mAb from the U of Iowa Hybridoma Bank, and 3) commercial Abs. The home-made Abs are often limited in supplies whereas most commercial Abs are not made against fly antigens.

Out of desperation many labs have purchased commercial Abs (including those from the Hybridoma Bank) and tested their cross reaction with fly antigens. It is not uncommon for many labs to independently test expensive commercial Abs that may have failed in other labs. On some occasions this approach has been successful. However, this information is often buried in the Method section or not well described in publications. It is not collected in one place that is easily accessible to fly scientists.

The Fly Board has initiated a '**Commercial Antibody Verification'** community drive to fulfill this Ab gap. We cordially invite you to help gather the information of commercial Abs that you have used (successfully or not) in your research. Once completed this information will be shared with the entire fly community via a searchable database. We believe this database will be complementary to the existing antibody database on FlyBase (http://flybase.org/wiki/FlyBase:Antibodies) and extremely valuable to all fly researchers. Please click on the **Google Sheet Link** below and enter the Ab information. Feel free to share this information with fly labs which may not be on the current emailing list.

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

It will take some considerable effort from each lab to do this but the payback is sizable for you and the fly community. Thank you for your assistance!

Sincerely Yours,

Bing Zhang and Thom Kaufman

16. FlyBase: Norbert Perrimon

For the past twenty-four years, FlyBase has provided a centralized resource for Drosophila genetic and genomic data to enable researchers to further their research. FlyBase has three main goals. 1. To continue curation of literature and reagents relevant to Drosophila research, so that researchers can continue to rely on FlyBase to find the latest innovations in the field. We 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. 3. To facilitate more integrative analyses and approaches, FlyBase continues to expand its utility as a platform for integrating and displaying large-scale studies, transcriptomics and proteomics data sets. In addition, FlyBase improves access and display of tools available within the community, and incorporate the most useful data sets and tools for visualizing complex data sets to enable more researchers to take a more global approach to their genetic research.

The past year has been quite busy at FlyBase. In this report to the Fly Board, we have included a section describing the main accomplishments (see section I. FlyBase U41 grant 2016 Accomplishments, on page 2). Importantly, we recently submitted the Flybase competing renewal and have included the Specific Aims of the proposal to help the Fly Board evaluate our long term plans (see section II. FlyBase U41 grant renewal Specific Aims on page 18).

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

We thank the community for continued support.
Norbert Perrimon (on behalf of FlyBase)

I. FlyBase U41 grant 2016 Accomplishments
1. FlyBase Data Capture Specific Aims

1.a. Through a combination of manual curation, direct user submissions and automated text mining, FlyBase will triage and curate the primary genetic/genomic research literature on D. melanogaster and allied species.

Some summary statistics on the growth of bibliographic and genetic/phenotypic data in FlyBase are presented in Table 1. Increases each year are quite similar and reflect the constant and considerable activity of the Drosophila community as well as the ability of FlyBase to keep up with the data flow.

TABLE 1: CURRENT FLYBASE STATISTICS COMPARED W/ PREVIOUS TIMEPOINTS (ALL DATA FROM FLYBASE WEB SITE RELEASE NOTES)				
Category	May 9th, 2014	Sept. 3, 2015	Nov. 20, 2015	Oct. 18, 2016
General Counts	FB2014_03	FB2015_04	FB2015_05	FB2016_05
Number of References in FlyBase	208,148	212,340	212,991	216,377
----- Research papers	91,496	94,736	95,195	97,811
----- Pers. Communications	5,719	6,057	6,109	6,264
Number of Fly Strains	124,904	140,101	141,104	141,106
D. melanogaster Genetic Stats	FB2014_03	FB2015_04	FB2015_05	FB2016_05

Number of Gene records	31,713	32,085	32,078	31,998
----- Genes w/ Gene Models	17,294	17,717	17,716	17,747
----- Genes w/o Gene models	14,419	14,368	14,362	14,251
Number of Alleles	166,864	176,557	176,891	180,306
----- Alleles of Genes w/ Models	148,440	158,510	158,860	162,474
----- Alleles of Genes w/o Models	18,424	18,047	18,031	17,832
Number of Chromosomal Aberrations	20,207	20,276	20,286	20,677
----- Total Deficiencies	8,610	8,703	8,712	8,768
----- Deficiencies w/ Mapped Endpoints	2,154	2,341	2,341	2,405
Number of TE Insertions	149,600	168,193	168,395	171,612
----- TEs Localized on Genome Seq.	65,455	68,130	68,188	69,403

Publications: More than 3,500 potentially relevant publications were identified in PubMed via automated scripts; ~3,000 (83%) were verified by eye and their citations added to FlyBase. ~56,000 Digital Object Identifiers (DOIs) and ~24,400 PubMed Central IDs (PMCIDs) for all publications in the bibliography have been added to FlyBase. DOIs can be used to provide hyperlinks to journal webpages, while PMCIDs provide a direct hyperlink to free full text content at PubMed Central; both ID sets are available for querying and download. Existing scripts for searching PubMed were overhauled, resulting in increased efficiency and automation. PubMed abstract text, PMCIDs, and links to 'related publications' (e.g., commentaries on specific research papers) are now captured, and a system to identify and update missing PMCIDs (that are not always available at the time of the bibliography update) has been established.

Paper Triaging: Authors continue to respond well to our automated email system ('EmailAuthor'), triaging and associating key genes to 55% of all newly published papers via the online 'Fast-Track Your Paper' (FTYP) tool. Triage flags for 'models of human disease' and 'gene group data' were added during this period. The Support Vector Machine (SVM) system (developed by WormBase) that is used to automatically identify papers containing certain data types now also flags papers containing models of human disease. Papers not submitted by authors to our FTYP tool (1291) were first-pass skim/triage curated. This involves curating genes mentioned as experimental subjects in the papers in order to create gene-to-publication links in FlyBase and adding data-type-specific triage flags to prioritize papers for further curation. We will retrain the SVM for the 'new allele' and 'new transgene' data types to try to improve their accuracy. We have investigated and tested several approaches/tools (including NCBI PubTator) for automated gene identification, with the aim of pre-seeding FTYP forms and automating gene-to-reference associations when author submissions are not forthcoming. Our test of PubTator revealed that it will be very useful and is being incorporated into our triage pipeline. We will design 'data templates' for authors to complete upon submission/acceptance of their papers. These will list the specific fly stocks and other reagents used in the paper, thereby increasing the speed of curation and facilitating experiment reproducibility.

Gene Expression: 92 papers were curated for wild type expression patterns. Curation is concentrated on genes that have little or no curated expression pattern data in FlyBase, and on expression pattern data at post-embryonic stages. 77 papers have been curated for neural expression as part of our collaboration with the Virtual Fly Brain project. The Virtual Fly Brain curator will clear the current backlog and keep up with new publications.

Physical Interactions: 3340 physical interactions were curated from 328 papers. Since the incorporation of the DPiM protein interaction dataset, >95% of the papers curated represent "low-throughput" studies in which interactions are supported by multiple lines of evidence. We have also curated 7 large-scale interaction datasets. The current set of interaction comprises ~16K distinct pairwise gene-gene interactions involving ~4K genes from ~1.2K papers and ~20K experiments. We have developed effective SVM triaging that recognizes papers containing physical interaction data, complementing the curator/author flagging system. We have worked with an external collaborator, EsyN (www.esyn.org), to create tailored physical interaction graphs in our gene and interaction reports. We have also trained and continue to oversee physical interaction curation by a curator at University of New Mexico. The UNM curator will help curate physical interactions from 400 papers to keep pace with new published physical interactions and reduce the 2014-2015 backlog. We will provide FlyBase interaction data as a bulk download file in standard psi-mitab format. We will improve the clarity of reports for RNA-protein interactions, distinguish "high-throughput" and "low-throughput" interactions in reports and bulk files, integrate gene group data, especially regarding protein complexes, with physical interaction data to provide context to the pairwise interactions and import interactions from other databases (with provenance clearly marked). The current corpus comprises 24,413 interactions representing 18,155 distinct pairwise gene-gene interactions involving 4,595 genes, curated from 1,987 publications. 48% of these interactions are curated from "low-throughput" studies.

Sequence Features: 1,189 features were curated from 408 references. Genome feature curation (mapping of features that can be localized on the genome, including mutations, rescue fragments, transgenic construct insertions and aberration breakpoints) was brought up to date mid-2015. Current identification of important papers is based on flags generated by user (FTYP) and curator triaging. We will continue curation of new papers flagged for "genome feature" and evaluate 756 papers that have the "new allele" flag as potential sources of genome features to curate. Initial estimates are that 85% of these papers contain curatable data.
GSA article mark-up: 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, has continued uninterrupted. 106 articles were QC checked by a FlyBase curator in the current time period.

Genetic/phenotypic curation: 789 papers, representing 29% of all newly published papers, have been fully curated for genetic/phenotypic data in the current period. (Note: This number is less than our target of ~1,000 owing to staff turnover.) Our goal is to keep up with the number of new curatable papers published, expected to be ~1,000 papers/year based on current triage and publication levels.

Non-transposable element-based insertions: Previously, 'insertion records' were only created for transposable element-based insertions. They are now also created for DNA inserted into the genome by techniques such as homologous recombination and CRISPR, allowing links to be made between the insertions and relevant allele and stock reports on the website. An associated data retrofit has also been performed.

1.b. From direct submissions, from high-throughput data generation groups and from the capture of information in appropriate supplementary tables of primary research papers, FlyBase will incorporate large-scale genetic and genomic data and metadata, with a particular emphasis on data that map to the genome, describe reagents such as stocks and clones, or inform the phenotypes/functional roles associated with the ~15,000 genes encoded by the D. melanogaster genome.

Supplemental data: Since April 2015, standard genetic/phenotypic literature curation has included all relevant material from the supplementary data as well as that in the main body of a paper. We have also stopped creating separate reference reports for supplements - all material is now curated under a single reference. We will merge the legacy reference reports for supplemental data with the associated report for the main paper.

Bulk datasets: FlyBase has incorporated select high-throughput datasets (and associated metadata) deemed to be of high value to the community. To date, this has largely consisted of RNA-Seq and transcription factor binding studies from the modENCODE project, although some array-based and RNA-Seq expression studies from other groups have also been incorporated. This endeavor extends to the curation of large-scale reagent collections, such as RNAi or GAL4 driver sets, as most of the processes and tools for data collection, integration and reporting are the same.

In the past year, five large-scale dataset/collections have been incorporated.
- Transcription start site data from Thomas Gingeras' lab (RAMPAGE, 36 developmental stages), displayed in GBrowse as RNA-Seq profiles along with peak calls.
- Transcription start site data from MachiBase (oligo-capping, 6 stages and 1 cell line), displayed in GBrowse as RNA-Seq profiles.
- Transcription factor and histone modification data from Eileen Furlong's lab, displayed in GBrowse as discrete peak calls (binding regions): 28 ChIP-chip tracks for 13 mesodermal transcription factors at various points of embryogenesis, and 7 ChIP-Seq tracks for histone modifications and RNA Pol II in purified mesodermal cells.
- Realigned small RNA-Seq data from Eric Lai's lab, consolidated from 277 RNA-Seq samples into 44 distinct conditions: 26 cell lines, 13 developmental stages and 5 tissues. Data are displayed as RNA-Seq coverage tracks in GBrowse. These data have also permitted the Lai lab to calculate miRNA expression levels across these 44 conditions - these data have been incorporated and we are currently working on gene expression displays for the miRNA gene reports.
- Over 49,000 P{acman} BAC clones from the CHORI-321 and CHORI-322 libraries have been added to FlyBase, displayed as GBrowse tracks and listed in the "Reagents" section of relevant gene reports.

The majority of our effort has been to overhaul how we curate and display the dataset/collection metadata, motivated by the goal of creating a comprehensive and well-indexed catalog of datasets/collections that will make it easier for users to find datasets/collections of interest. Key improvements include 1) making formal relationships of datasets to genes, reagents, etc., 2) implementing an assay CV to permit searching/browsing of datasets by technique and 3) distinguishing projects, biosamples, assays and results derived from the analysis of an assay(s) as distinct types of entities to improve report organization and allow for the curation of complex relationships between datasets. This overhaul is at an advanced stage, with curator tools and quality control systems in place, a retrofit of pre-existing metadata to the new standards is complete, and dataset report designs are finalized. We will work with developers to implement the dataset reports in the next few months. Completion of the dataset metadata overhaul is the first priority, which will allow two other ambitious projects to move ahead. First, we will work to incorporate some or all of the data and metadata for thousands of D. melanogaster RNA-Seq datasets that are being realigned and analyzed by the NCBI and Brian Oliver's group. This will include the standardization of related anatomy, stage, cell line and strain metadata.
Second, we will work on a pipeline to automatically pull dataset metadata from various data repositories to build a comprehensive and integrated catalog of Drosophila datasets (in addition to

the RNA-Seq datasets); we will then work to index these using our various FlyBase CVs and features (genes, cell lines, strains, etc.).

Review curation: 550 reviews (published between 2015-2016) were curated, resulting in ~6,000 new gene-to-reference associations.

modENCODE data: As reported last year modENCODE RNA-Seq datasets (the developmental, tissue, cell line and treatments profiles, comprising 110 samples), realigned to the new *D. melanogaster* Release 6 reference genome assembly, were incorporated. These data are visible in GBrowse, and used to calculate RPKM expression values reported on gene reports and forming the basis of the FlyBase RNA-Seq search tools. These tools allow the user to interrogate the expression data for Expression Profile, Expression Similarity or by Levels by Exon or Genomic Region. We are currently collaborating with Eric Lai to obtain the modENCODE expression profiles of the miRNA genes.

Improved annotation of transgenic construct alleles: We will enhance our current curation strategy so that users can more easily see and find particular types of reagents. For example, we are currently investigating better ways to capture information on 'tags' (*e.g.,* GFP or nuclear localization signals), and we are considering adding new controlled vocabulary terms to describe the functional state of coding regions (*e.g.,* 'dominant negative', 'constitutively active', 'wild type - endogenous promoter').

1.c. By manual review of available evidence, FlyBase will continue to maintain a comprehensive, high quality gene model annotation set of the RNAs and proteins encoded by the D. melanogaster genome.

Gene Model Annotation: The results and analyses of our comprehensive gene model reannotation effort were published in two papers in 2015. Matthews *et al*. 2015 includes extensive comparisons between a recent annotation set (R6.03) and the last annotation set generated prior to incorporation of HTD (R5.24), describes difficult or subjective annotation calls, and discusses future challenges. Crosby *et al*. 2015 describes the many exceptional and non-canonical (but biologically real) gene model annotations, and how FlyBase has flagged such cases. Subsequent to these publications the gene annotation effort resulted in the review of 195 genes and 33 new annotations were created, 24 of which are new lncRNAs. In the current report period 39 new gene models (primarily new miRNA genes and small conserved ORFs within 5' UTRs) were created. The latter are primarily small ORFs based on assessment of predictions in Mackowiak *et al. 2015* and new miRNAS from miRBase Release 21. From the data presented in **Table 2** one can see that the *D. melanogaster* genome has become stable in terms of gene model annotation. We will continue to annotate new genes or exons based on RNA-Seq analyses from the NCBI and Brian Oliver's group. We do not anticipate many large-scale changes in gene models or the number of genes. However, there are likely to be refinements of exon/intron structure and changes in the sizes of 5' and 3' UTRs. Additionally, we will see the prediction and annotation of many additional anti sense RNAs. We will fold into the assessment above: new TSS flags (primarily RAMPAGE and modENCODE CAGE data); provide sequence feature curation of piRNAs and siRNAs and annotate regions from which these small RNA species are derived as well as keep current with models flagged based on new data in the literature.

Table 2 provides documentation on the gene model annotation changes seen in 2014, 2015 and 2016. It is apparent that change has dampened and that the genome at least with respect to its eukaryotic compartment has become more stable. There are fewer new genes and many fewer splits and merges.

Dmel Release	GENE MODEL CHANGES FROM PREVIOUS RELEASE					
	NEW	RESTORED	DELETED	MERGED	SPLIT	COMPLEX
Calendar Year 2014 (for comparison with reporting year, below)						
Rel_5.55	120	0	3	8->3	0	0
Rel_5.56	528	3	1	12->6	0	0
Rel_5.57	0	0	0	0	0	0
Rel_6.01	0	0	31	2->1	0	0
Rel_6.02	344	3	16	48->15	0	0
Rel_6.03	123	3	0	4->2	0	0
TOTALS	**1,115**	**9**	**51**	**74->27**	**0**	**0**
Calendar Year 2015						
Rel_6.04	24	0	1	0	0	0
Rel_6.05	9	0	0	0	0	0
Rel_6.06	0	0	0	2->1	2->4	0
Rel_6.07	0	0	0	0	0	0
Rel_ 6.08	0	0	0	2->1	0	0
TOTALS	**33**	**0**	**1**	**4->2**	**2->4**	**0**
Calendar Year 2016						
Rel_6.09	0	0	1	0	0	0
Rel_6.10	18	0	2	6->3	0	0
Rel_6.11	0	0	0	0	0	0
Rel_6.12	0	0	0	0	0	0
Rel_6.13	0	0	0	0	0	0
TOTALS	**18**	**0**	**3**	**6->3**	**0**	**0**

TABLE 2: MAJOR CHANGES TO D. MELANOGASTER GENE MODELS BY CATEGORY (ALL DATA FROM FLYBASE WEB SITE RELEASE NOTES)

Table 3 presents statistics on numbers and lengths of various gene products or their parts (exons, introns). Increase in numbers largely reflects the identification of new gene products or transcript isoforms. Increase in mean lengths reflects identification of new isoforms and additions of 5' or 3' UTRs to known products. Again the rate of change in the last year (Rel_6.08 => 6.13) in the number of metrics of gene size and number is indicative of the relative maturity of the *D. melanogaster* annotated genome.

TABLE 3: CURRENT FLYBASE GENE MODEL ANNOTATION STATISTICS ON SEQUENCED BDGP STRAIN (iso-1) COMPARED W/ PREVIOUS TIMEPOINTS (ALL DATA FROM FLYBASE WEB SITE RELEASE NOTES)

Category	06Nov2012	04Nov2013	12Nov2014	20Nov2015	18Oct2016
***D. melanogaster* Annotation Statistics**	**Rel_5.48**	**Rel_5.54**	**Rel_6.03**	**Rel_6.08**	**Rel_6.13**
# of Protein-Coding Genes	13,945	13,942	13,918	13,919	13,929
----- Mean Length Genes (bp)	6,638	6,635	6,911	6,935	6,962
Protein-Coding Transcripts	27,781	29,375	30,385	30,447	30,482
----- Mean Length mRNA (bases)	2,828	2,867	2,879	2,880	2,881
# of Exons	74,918	76,477	77,654	77,688	77,689
----- Mean Exon Size (bases)	522	531	539	539	539
# of Introns	57,296	58,263	58,518	58,538	58,534
----- Mean Intron Length (bp)	1,620	1,641	1,695	1,700	1,704
rRNA Genes	160	161	147	147	147
tRNA Genes	314	314	314	313	313
snRNA Genes	31	31	31	31	31

snoRNA Genes	288	288	288	288	288
miRNA Genes	239	238	238	304	256
Long non-coding RNA Genes	710	1,483	2,446	2,469	2,468
Long non-coding RNA Transcripts	896	1,757	2,871	2,909	2,908
Pseudogenes	189	197	301	310	314
Natural TE Insertions (BDGP Strain)	5,604	5,604	5,578	5,578	5578

1.d. For other Drosophila species, FlyBase will work with genome assembly and annotation groups to facilitate data submission to GenBank and develop a priority list, in concert with the Drosophila genome evolution community, for selectively incorporating other species genome data in FlyBase.

At the time of the last renewal the gene models for the sequenced genomes of the 11 non-melanogaster species analyzed as part of the NHGRI-funded "12 *Drosophila* Genomes Project" dated back to 2006, were principally *'ab initio'* predictions and were quite stale. For comparative analyses and to better inform features on the *D. melanogaster* genome, we felt it would be valuable to improve these annotations. FlyBase and NCBI collaborated to upgrade these annotations, taking advantage of current *D. melanogaster* annotations and the availability of species-specific RNA-Seq data for the other species to improve the predictions of the NCBI GNOMON annotation pipeline. In addition, for one of the species, *Drosophila simulans*, which was known to have severe assembly quality issues, a new assembly was contributed to GenBank by Hu *et al.* 2013. In FlyBase public releases FB2015_01 and FB2015_02, the upgraded *D. simulans* assembly replaced the previous one, and new annotation sets were provided for *D. simulans*, *D. yakuba*, *D. erecta*, *D. ananassae*, *D. pseudoobscura*, D. *willistoni*, *D. virilis* and *mojavensis*. The other three species were not upgraded because of either low quality assemblies (*D. sechellia* and *D. persimilis*) or absence of RNA-Seq data (*D. grimshawi*). Better assemblies and RNA-Seq data are now available for *D. grimshawi* we are collaborating with NCBI to run the GNOMON pipeline and make the improved annotation sets publicly available. We are also in the process of obtaining the RNA-Seq data used for the improved annotations and these will be presented in our GBrowse 'TopoView' tracks for these species. It should be noted that extensive development was required to create a robust pipeline for validation and incorporation of GNOMON annotations.

1.e. Through user submissions via wikis as well as FlyBase manual curation, FlyBase will incorporate data that will permit integrative views of the information in individual gene reports, such as pathway summaries and diagrams, macromolecular complexes and gene family descriptions.

Gene group curation: We have continued to build the Gene Groups resource, in which related sets of *D. melanogaster* genes (gene families, macromolecular complexes and functionally related gene products) are compiled based on published literature, and used to produce report pages listing member genes alongside useful download/analysis options and external links. Improvements to the accuracy and consistency of GO annotations and gene nomenclature occur in tandem with this effort. This year, we have added 255 groups, including the OXPHOS system, heat shock proteins, spliceosomal complexes, ion channels, tRNAs and translation factors. There are now 555 gene groups in total, comprising 3,519 unique genes (= 20% of genes located to the sequenced genome). We continue to work with the HUGO Gene Nomenclature Committee (HGNC) to enable reciprocal links between our pages and their 'Gene Family' pages.
Gene Snapshots These are new, short summaries shown at the top of each *D. melanogaster* gene report page that are designed to provide a quick overview of the function of a gene's products. We contacted authors predicted by an automated algorithm to be experts on a given gene and asked them to provide a couple of sentences/bullet points on the function and main biological roles of the gene product, preferably using terms suitable for a general, non-Drosophilist audience.

FlyBase curators then revised these responses to produce the final summaries. So far, we have contacted 1,371 authors for information on a total of 3,858 genes, and have received contributions from 708 authors (51.6% response rate) on 1,796 genes. We will continue to contact authors until we have received summaries for 90% of the most extensively studied genes. We will provide summaries for genes with relatively minimal available data by automated methods.

Human disease model curation: This is part of regular genetic literature curation and first appeared in the FB2014_02 release. In 2014-15, a Human Disease Model Report was developed, with the goal of providing a less specialized entry point into FlyBase for users specifically interested in models of human disease. This report includes tabulated data and links from other relevant FlyBase reports, a description of orthology relationships, links to outside sources, a free-text overview, and references, including reviews. The initial set of disease model reports included extensive summation of the work done in flies for each specific disease model. This effort was the most labor-intensive aspect of the disease model curation. In 2016, we shifted to more rapid curation of new disease models, omitting the summation of experimental results. We describe these as "framework" reports. We have expanded our disease model curation guidelines to accommodate "postulated" disease models, *i.e.*, new disease-gene associations. These include several recent studies in which initial associations based on GWAS in humans are supported by phenotypic assessments of orthologous genes in flies.

In the FB2014_06 release, there were 2,778 disease annotations from 566 references, involving 1,753 alleles from 824 genes. Models of 146 different human diseases had been annotated (approximately two-thirds of which are of neurological diseases). In 2015 1,027 Disease Ontology (DO) annotations been added to 207 references, representing 89 different human diseases. SVM text mining was used to identify all relevant papers published since 2010 containing disease model information. In the current reporting period 356 human disease reports were created (framework reports, parent reports and stub reports) and 1057 associations were made to papers reporting Human disease related data (including new papers curated to existing disease model records).

A list of genes that have Disease Ontology terms associated as part of allele curation is maintained and is used to identify new human disease models that require curation. Currently, there are ~180 genes from this list that are not represented by a human disease model report. Many of these do not correspond to existing diseases associated with an orthologous human gene, and thus may represent postulated disease models. A goal for the coming year is to eliminate this backlog and maintain curation of newly described disease models. Disease model data curation and presentation is still evolving, both at FlyBase and within the AGR. Based on the evolution of the AGR effort goals and approaches may change significantly.

A manuscript describing these reports and the more formalized Disease-Ontology-based gene/allele curation was published in the 'Spotlight on *Drosophila* issue of Disease Models and Mechanisms (Millburn *et al.* 2016).

Pathways We will start developing pathway pages based on the model used for the Gene Groups project. These pages will eventually house pathway displays derived from LEGO models.
1.g. FlyBase will contribute to broad biological ontology efforts and connect FlyBase genetic/molecular objects to the appropriate ontological terms.

Gene Ontology (GO) annotation: The total number of Gene Ontology (GO) annotations held is now 308,676. A majority of protein-coding genes and all named and sequence-localized genes now have at least one GO annotation. Recent work has focused on improving the quality and consistency of annotations by revising terms for related sets of genes as part of the gene group approach (described below); >6,500 annotations have been made as a direct result. In addition, we

have reviewed and added GO terms to all previously unannotated genes that have a human ortholog with an OMIM entry. We will continue to review this current disease model annotation approach as part of our active involvement in the relevant working group of the AGR.

There has been a net increase of 251 terms in the last year, most of these related to neuroanatomy as part of our collaborative work with Virtual Fly Brain. The number of referenced publications has also increased (from 816 to 856), as has the percentage of terms with definitions (from 86% to 91%). In parallel, the structure of the ontology has been significantly improved. These enhancements are the result of a combination of approaches, including a systematic review of undefined terms by organ system (ongoing, with the last system currently being reviewed) and the removal of erroneous or deprecated terms (ongoing). Any changes to terms have been accompanied by any necessary retrofits to existing annotations.

Additionally, 220 terms were added to describe datasets, which will be used to improve the curation of large-scale datasets. We will review the current set of phenotypic class terms in order to decide if the current scope is adequate. We will generate an ontology for grouping functional tags in order to allow improved categorization of transgenic alleles.

A collaboration of web developers and GO curators has resulted in a new summarized view of the data in the GO, phenotype and anatomy sections of report pages, using the ontology structure to group related annotations. A first step was to generate slim versions of the ontologies. These were used to label ribbon displays of ontology-based GO annotations similar to what is done at MGI. These will be made public in early 2017 with the release of FlyBase 2.0.   The anatomy and phenotypic class ontologies will be developed similarly.

We will continue to use the 'gene group' curation model for focused GO annotation over the coming year - we aim to review in excess of 1,000 genes in this manner. Specifically, we shall target non-coding RNAs (ncRNAs) for GO curation in the coming year - there are currently 3,436 ncRNA genes in FlyBase, 2,782 (81%) without any GO annotation. We will start by reviewing the "housekeeping" classes of ncRNAs (e.g., rRNA, snoRNA), before moving on to regulatory ncRNAs. We will also implement the Protein2GO annotation tool within the coming year, and continue preparations for adopting the Noctua tool (for LEGO annotations).

2. FlyBase Data Integration Specific Aims

2.a. On a weekly cycle, FlyBase will run QA/QC and data integrity checks on all captured data and incorporate the data passing these checks into the central Chado_Production database.

The FlyBase central database group has continued to process curation and annotation data produced by FlyBase curators into the central Chado database on a weekly basis. As part of this process, extensive weekly validation checks were carried out and problematic records were returned to curators for resolution. Less frequent updates to ontologies were similarly validated and incorporated. As new data became available from bulk data providers (*e.g.,* GDP, DGRC, BDSC, REDfly, miR-Base, TRIP), these data updates were validated and loaded into the central FlyBase Chado database, as were updates of NCBI-provided alignment evidence for *D. melanogaster* and eight other species (*D. ananassae*, *D. erecta*, *D. pseudoobscura*, *D. simulans, D. yakuba, D. mojavensis*, *D. virilis* and *D. willistoni*).

2.b. On a bi-monthly cycle, FlyBase will freeze the final Chado_Production instance and produce a Chado_Reporting instance for a new public data release.

On the planned schedule, the 5 Chado_Reporting instances were produced and delivered to the FlyBase group responsible for production of the new FlyBase web site releases.

3. FlyBase Data Access/Dissemination Specific Aims

3.a. On a bi-monthly cycle, FlyBase will convert the Chado Reporting instance into a new public release of the FlyBase web site, including all information and tools necessary for robust searching and browsing of the entire corpus of FlyBase.

Public Releases of FlyBase: 5 release cycles were produced on schedule. **Table 4** lists the dates and some of the major new or improved features of the public releases in 2016.

TABLE 4: 2015 & 2016 FLYBASE RELEASES			
Release Date	*Release ID*	*Dmel annotation version*	*Notable Events*
October 2016	FB2016_05	Dmel Release 6.13	JBrowse beta; Gene Groups update; New antibody linkouts
July 2016	FB2016_04	Dmel Release 6.12	Gene Snapshots; *R. norvegicus*, 3 new algorithms added to Orthologs DIOPT search; Gene Groups update
May 2016	FB2016_03	Dmel Release 6.11	New protein domains GBrowse track; Transcription start site data; Small RNA-Seq data; DIS entries updated; Chromosome maps; ID Converter upgrade mitochondrial genome assembly; Automatically Generated Summary updated.
March 2016	FB2016_02	Dmel Release 6.10	New orthology data and query tool; miRNA annotation set update; Systematic nomenclature for *D. melanogaster* tRNA genes; P{acman} clones now in GBrowse gene reports.
January 2016	FB2016_01	Dmel Release 6.09	External Resources pages; New video tutorials; P{acman} clones; Histone modification and TFBS data for embryonic mesoderm: GBrowse tracks; Community pages tool.

FlyBase 2.0: We continue development work toward FlyBase 2.0, a completely new version of our web site. Core code libraries were completed and the development of a few existing web applications was started. Applications worked on include Simple Search, Report pages, HitLists, Fast-Track Your Paper, and BLAST. The new web site will be implemented in early 2017.

GBrowse2: Migration to GBrowse 2 was fully completed with the retirement of GBrowse 1.x from the current FlyBase website. The TopoView glyph was updated to include user configurable options such as a scaling algorithm, titled vs. vertical display, and the ability to select sub tracks. We are integrating GBrowse 2 into our new FlyBase 2.0 version of the web site.

JBrowse: JBrowse has been adopted by the AGR initiative as the common genome browser used by all the participating MODs. We have incorporated more than 50% of the tracks in GBrowse into this tool. Several of our tracks are custom configured (notably TopoView) and will require special coding to allow their display in JBrowse. We also use exported image views from GBrowse to populate several of our report pages. Those images allow interactive links to be inserted so the

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user can migrate among different reports. JBreowse does not support this capability. Thus until JBrowse developers provide it we will need to maintain both browser tools.

FlyBase in the Amazon Cloud: We have migrated our frontend distribution and backend data servers (DNS, JIRA, load balancers, and backend servers) into the Amazon Cloud. This move should reduce our costs for server hardware and allow us to increase or decrease our server capacity deployment as needed to adequately serve the user community. We have also partnered with the Open Science Data Cloud (OSDC) initiative to host FlyBase data on their cloud service.

Network Resources and Reagents pages: We have created new Network Resources and Reagents pages. These are derived from our current listing of community resource links and are intended to provide easy access to popular resources, pulling together groups of topic-specific information and links (including reagent links, network resource links, useful publications, techniques, *etc.*) into a better organized presentation and increased visibility. Popular resources were assembled for CRISPR, RNAi, Stock Centers, and Antibodies. Access to this information can be made from the FlyBase home page. The data and links are being provided in a wiki environment. This path was taken to allow easy editing of links and resources by all members of the FlyBase staff. Experience has taught us that some of these resources can be volatile and incorporation into the main database inefficient.

Other improvements: A new search interface and report sections for human disease Information and gene groups were added to the home page. We have added access to DIOPT functionality to allow wider access to information on orthology relationships with special emphasis on linkage to the other MODs and human genes. This effort will aid in the development of AGR searching and integration.

3.b. On the same bi-monthly cycle, FlyBase will produce bulk files for download of key structured datasets from the FlyBase ftp site as well as the Open Access Cloud.

During 2015, the FTP site and compute intensive release pipeline tasks were moved to Amazon Web Services (AWS). Moving to AWS reduces the amount of time required for system administration and simplifies service upgrades as our hardware demands (cpu, disk space, memory) increase. We will continue this migration of FlyBase data and tools to the cloud.

3.c. FlyBase will maintain a robust set of links to other appropriate on-line data resources.

Network Resources: As noted above we have completely overhauled the Network Resources Page and created a new instance in a wiki format. This should allow easy editing by curators and developers and facilitate maintenance of lists of network resources that tend to be more volatile than other data types. Also as noted above we have moved access to these resources to the home page and reorganizing the types into coherent sets that will bring together all resources that are relevant to specific technologies *e.g.,* CRISPR, RNA-Seq, RNAi *etc.*

3.d. FlyBase will periodically update gene model annotation sets at GenBank and provide RefSeq annotation sets for D. melanogaster and other Drosophilidae.

During 2016, FlyBase prepared and submitted 10 genome annotation updates to GenBank and RefSeq. These included *D. melanogaster* (genome annotation R6.07 and mitochondrion iso1) and the eight non-melanogaster genomes managed by FlyBase for which FlyBase implemented entirely new annotation sets, produced by the NCBI Gnomon pipeline: *D. simulans* (R2.01), *D.*

pseudoobscura (R3.03), *D. ananassae* (R1.04), *D. yakuba* (R1.04), *D. erecta* (R.1.04), *D. willistoni* (R1.04), *D. mojavensis* (R1.04), and *D. virilis* (R1.02).

4. FlyBase Development Pipeline Specific Aims

4.a. *From our own observations as well as input from the SAB and the broader community, FlyBase will periodically make assessments of new data types to incorporate into the production FlyBase pipeline.*

As noted above, we have brought in new data types related to *Drosophila* models of human disease, gene groups and *Drosophila* strains.

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

Proforma Validation Software (Peeves): Work has continued on our Proforma Validation Scripts (Peeves), which perform QA/QC checks on curation records prior to loading to identify any errors/omissions, thereby streamlining the weekly loading process. Specifically: (i) checking has been implemented for several existing proformae (physical interaction, sequence feature, database, and cell line) that previously lacked Peeves checks; (ii) checking has been added for a new 'species' proforma, which is used to enter basic taxonomic data on species that are new to FlyBase (needed, for example, when a fluorescent protein from a novel species is used in a transgenic construct); (iii) checking of the dataset proforma fields has been updated to reflect the new specification for this data type.

Triaging/SVM scripts: We have written wrapper scripts to automatically perform the individual steps in the SVM triaging process. A script has also been written to compute the precision and recall for the SVM text-mining results, making it easier for us to monitor the accuracy for each data type flag.

Ontology Infrastructure: The ontology server that runs Jenkins, a continuous integration server that performs several checks to the ontology after every change, was replaced. In addition, the ontology repositories were moved from SourceForge to GitHub, another web-based repository hosting service, following concerns about the longevity of SourceForge.

Other Curation Software: Other software improvements needed for efficient curation have been carried out in response to curator requests.

4.c. *FlyBase will continue to work with text mining groups to implement automated procedures for data capture wherever possible.*

Support Vector Machines: As noted above (section 1.a.), we continue to work with WormBase and Textpresso to improve SVM for automatic triaging of the literature.

5. FlyBase Community Interaction and Outreach Specific Aims

5.a. *FlyBase will continue to work with the Drosophila research community to identify new opportunities for direct user data submissions.*

Fast-Track Your Paper (FTYP): Extensive work on a new version of the FTYP tool was completed in 2015. The new version of FTYP is more readily extensible and provides the project with more

opportunities for direct user submissions. Additionally, the new tool provides the user the ability to upload large groups of genes reported in publications. This is especially relevant to highthroughput papers reporting on genome wide studies of gene expression. We will continue to add new author tags to indicate novel data types e.g., we added a tag for Human disease. Additionally, in order to make markup easier for both the author and the curators we will begin using the NCBI PubTator tool, which accurately finds 87% of gene mentions in PubMed abstracts. These computationally recovered gene paper associations can be used to populate the FTYP tool and allow these associations for papers that are not Fast Tracked by the authors.

EmailAuthor: As part of the FTYP effort we will to rewrite the EmailAuthor software so that it is easier both to maintain and to add new features.
5.b. FlyBase will provide training in the best use of the FlyBase web interface through workshops at annual Drosophila conferences, at other appropriate research conferences and through workshops at large centers for Drosophila research.

Community Advisory Group: We have continued to send regular surveys to the FlyBase Community Advisory Group (FCAG), which now comprises >550 members representing *Drosophila* labs from 41 countries. We have carried out four surveys in the current period on topics ranging from a general survey on the future direction of fly research, to more targeted surveys on the layout of web pages and the annotation of transgenic constructs. The average response rate is 52%. Changes made as a direct result of FCAG responses include finalizing the content/format of the new Gene Group reports and improving the GBrowse track layout. We will continue to send out regular surveys to increase community input into upcoming changes and new features.

Conference attendance: During 2016, staff from all three sites (Harvard, Cambridge and Indiana) manned a help desk in the FlyBase demonstration room and gave scheduled presentations at The Allied Genetics Conference (TAGC) and the European *Drosophila* Research Conference.   TAGC meeting was a meeting of several model organisms whereby staff had an opportunity to interact with members of other MODs. We shared a booth with WormBase and SGD. Additionally, a comprehensive review describing the data content, organization and available tools in FlyBase was published (Marygold *et al*. 2016).
5.c. FlyBase will also provide training through development of tutorials and other on-line documentation.

Documentation: In conjunction with the Web Development Committee, we have significantly improved the FlyBase help documentation. All help pages have now been migrated from static, developer-managed pages to wiki pages that can be edited by all project members. Having the help documents in this format will make them easier to maintain and update, thus reducing the time and effort needed to keep them current. Many help pages were reviewed and updated, e.g. the Report Help pages, and new pages created where necessary. Based on user feedback, we started to make short video tutorials to help users get the most of FlyBase tools and features. Ten videos have been made todate, most of them recently, with >2,000 combined views, and can be found on the 'FlyBase TV' YouTube channel (https://www.youtube.com/channel/UCG-KSNq46vkezAwbrVQojYA).

Social Media: We Promote FlyBase using social media, particularly Twitter. FlyBase Tweets were used to draw attention to new or little known features, *e.g.,* Network Resources page tweets resulted in the addition of over 20 new network resources to the page based on user response.
5.d. FlyBase will maintain its project-wide help desk to provide support to users with data/web interface questions or suggestions.

The FlyBase model for help desk is that it is a distributed responsibility of all project members. All members receive all help emails, and the email is answered by one or more project members as they see fit. Sometime, help emails trigger extensive group discussions and lead to changes in the web site or in FlyBase policies. To ensure that all help mails are answered, one project member is responsible for tracking help mails for a month and then turns that responsibility over to another project member. This continues to be an effective way to answer user inquiries and to ensure project-wide understanding of user issues.

6. FlyBase Web Site Usage Statistics

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 per month during the most recent period was 1.1 million, with a high of 1.3 million and a low of 933k. The periodic dips all correlate with expected holiday patterns.
FlyBase sessions (visits) for the period of Dec-Oct from 2014-2016. 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 per month during the most recent period was 148k, with a high of 168k and a low of 127k.

FlyBase users for the period of Dec-Oct from 2014-2016. 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 devices and/or browsers. The average number of users during this period was 49k/month, with a high of 55k and a low of 41k.

"Data Class Usage", shows the top pageviews per month for FlyBase data class reports. The usage pattern is unchanged from our last report in 2012 with Genes, Stocks, References and Insertions topping the list.

Pageviews by FlyBase Data Class

- Genes
- Stocks
- References
- Insertions
- Alleles
- Constructs
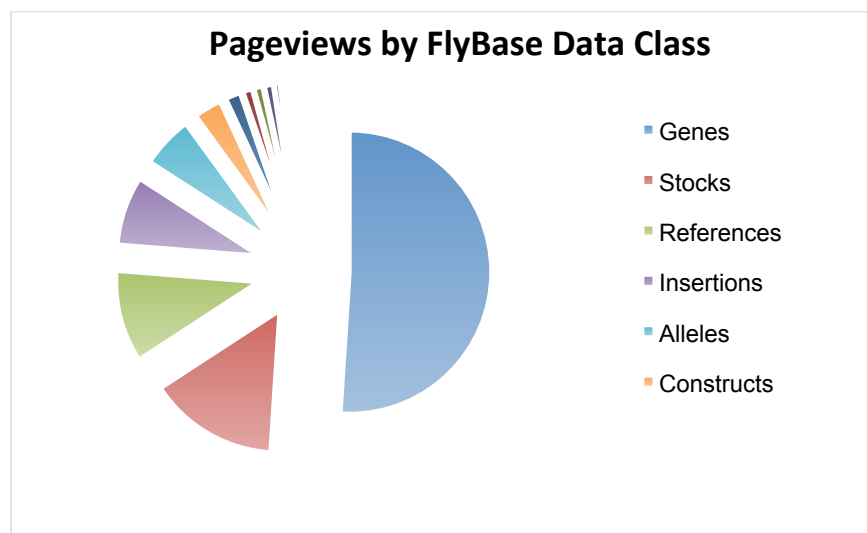
"FlyBase Tool Usage", shows that our top 5 tools are Simple Search, BLAST, GBrowse, Jump to Gene, and Vocabulary reports. This is unchanged over previous reports as well.

FlyBase Tool Usage

Legend:
- Simple Search
- BLAST
- GBrowse
- Jump2Gene
- Vocabulary Report
- Data Type Tab
- Batch Download
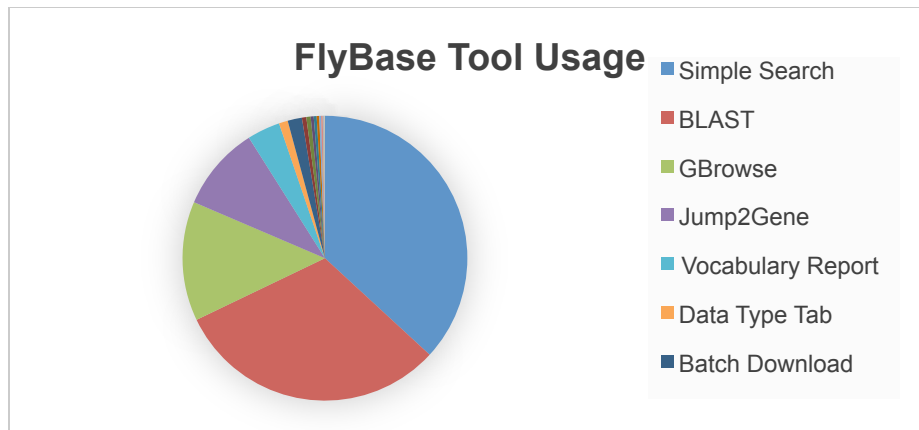
FlyBase-authored publications 2015/2016

Marygold SJ, Antonazzo G, Attrill H, Costa M, Crosby MA, dos Santos G, Goodman JL, Gramates LS, Matthews BB, Rey AJ, Thurmond J; FlyBase Consortium. (2016) **Exploring FlyBase Data Using QuickSearch.** Current Protocols in Bioinformatics. In Process at NIHMS

Marygold SJ, Attrill H, Lasko P. **The translation factors of Drosophila melanogaster**. Fly. 2016 August 5;:1-10. PubMed PMID: 27494710.

Marygold SJ, Crosby MA, Goodman JL; FlyBase Consortium (2016). **Using FlyBase, a Database of *Drosophila* Genes & Genomes.** In *Drosophila*: Methods and Protocols, Second edition, vol. 1478 (C. Dahmann, ed.) p. 372. Springer, New York.

Kahsai L, Millburn GH, Cook KR. (2016) **Phenotypes Associated with Second Chromosome P Element Insertions in *Drosophila melanogaster*.** G3 (Bethesda) 6(8):2665-2670. PubMed PMID: 27317776; PubMed Central PMCID: PMC4978919.

Millburn GH, Crosby MA, Gramates LS, Tweedie S. **FlyBase portals to human disease research using Drosophila models. Disease models & mechanisms**. 2016 March;9(3):245-52. PubMed PMID: 26935103; PubMed Central PMCID: PMC4826978

Attrill H, Falls K, Goodman JL, Antonazzo G, Millburn GH, Rey A, Marygold SJ; FlyBase Consortium (2016). **FlyBase: Establishing a Gene Group resource for *Drosophila melanogaster*.** Nucleic Acids Res. 44(D1):D786-D792.

Lu J, Marygold SJ, Gharib WH, Suter B. (2015) **The Aminoacyl-tRNA Synthetases of *Drosophila melanogaster*.** Fly 9(2):53-61. PubMed PMID: 26761199; PubMed Central PMCID: PMC4826098.

Gramates SL, Marygold SJ, dos Santos G, Urbano JM, Antonazzo G, Matthews BB, Rey AJ, Tabone CJ, Crosby MA, Emmert DB, Falls K, Goodman JL, Hu Y, Ponting L, Schroeder AJ, Strelets VB, Thurmond J, Zhou P, **FlyBase Consortium. FlyBase at 25: Looking to the future.** Nucleic Acids Research. 2016 October 30. PMC Journal - In process

II. FlyBase U41 grant renewal Specific Aims (submitted February 2017)

Aim 1. FlyBase community interaction and outreach. FlyBase will continue to meet user community needs. We will: **a.** Enable accelerated incorporation of published data by identifying new opportunities for direct user data submissions and improving existing tools; **b.** Maintain project-wide help desk *via* email; **c.** Provide in-person training through presentations and demonstrations at Drosophila and other conferences; **d.** Provide on-line training through

maintenance and development of documentation and video tutorials; **e.** Publicize updates and new features through various media, including an email-based Newsletter, our Twitter feed and peer-reviewed publications; **f.** Enhance community-driven webpages and portals; **g.** Solicit and respond to feedback from research community *via* the FlyBase Community Advisory Group; **h.** Collaborate with Model Organism Database and biocuration communities to find common solutions to shared goals.

Aim 2. FlyBase literature and large-scale data curation. To efficiently and effectively capture the most relevant published data, we will: **a.** Identify and incorporate all publications describing Drosophila research into FlyBase on a weekly basis; **b**. Hone first-pass curation pipelines by improving text-mining-based triaging methods and incorporating automated gene-to-reference associations; **c**. Use the triaging output to focus expert manual curation on key genetic, phenotypic, genomic, expression and physical interaction data**; d.** Curate new data types, in particular more in depth phenotypes at the molecular and cellular level, pathways, antibodies, GAL4 line expression, and phenotypes/interactions involving small molecules/chemicals; **e.** Adopt Gene Ontology Consortium tools to streamline functional annotations using the Gene Ontology, adding a new focus on non-coding RNAs; **f.** Work with researchers to incorporate large-scale datasets and associated metadata; **g.** Coordinate with external groups to improve access to images of expression patterns, especially neural expression; **h**. Develop and improve ontologies and quality control scripts required for curation. To improve access to curated data, we will: **a**. Provide graphical summaries of GO, phenotypic and expression data**; b.** Organize functionally related genes into Gene Group and Pathway reports**; c.** Provide short gene summaries solicited from experts; **d.** Improve categorization of transgenic alleles so that particular classes of reagents may be more easily identified and grouped.

Aim 3. FlyBase and human genetics. To make FlyBase a database more useful to human genetics, translational research, and personalized medicine, we will: **a.** Enhance ontology-based curation of experimental models of human disease using common annotation criteria (in coordination with the AGR); **b.** Expand and make more efficient creation of disease-centric integrated reports; **c.** Improve accessibility to experimental and orthology-based data through an integrated search interface; **d.** Improve representation of human genes and transgenes in FlyBase; **e.** Expand the Gene2Function (G2F) portal, including access to human disease-related data; **f.** Refine and expand curation of molecular and cellular data relevant to human disease models; **g.** Obtain feedback from our Human Disease Advisory Committee and other colleagues with expertise in translational research.

Aim 4. FlyBase and population genetics. Sequence data for >1,000 genomes of *D. melanogaster* isofemales, found from adults in different geographical locations, are available, however the data are not integrated in a single access portal to enable easy comparison with the D. melanogaster reference genome and annotations. We will incorporate these natural variation data into FlyBase into graphics to indicate nucleotide positions where sequence variations exist, frequency of these variants in the studied populations, and whether or not alternative alleles to the *D. melanogaster* reference allele sequence, have fixed in any given lineage. Users will be able to easily expand their scope of investigation to consider whether mutant alleles occur as standing variation alleles in natural populations.

Aim 5. FlyBase web and tool development. To make the FlyBase web site current with technology, we will: **a.** Build modern front-end applications, expose data *via* improved public API, perform and maintain testing to improve stability; **b.** Adopt JBrowse as an additional format for genome browsing; **c.** Use cloud services to reduce costs; **d.** Develop new search and display tools

and pages to accommodate new data types; **e.** Streamline release and archival process; **f.** Expand and maintain documentation tools; **g.** Maintain stock center data.

Aim 6. FlyBase data integration and broader community development pipeline. To ensure consistent quality, we will: **a.** Run QA/QC on all captured data and incorporate into the central production database, weekly, freeze the production instance and produce an instance for a public data release, bi-monthly; **b.** Periodically assess new data types to incorporate into production, based on observations and input from the SAB and broader community; **c.** Develop necessary curation and QA/QC methods, database modules, web site features and bulk reports to accommodate new data types; **d.** Provide data access and dissemination by: producing bulk files of key structured datasets to correlate with bi-monthly releases; maintaining robust links to on-line data resources; working directly with NCBI to periodically update gene model annotation and provide RefSeq annotation sets for *D. melanogaster* and other Drosophilidae.

18. Bloomington Stock Center (Kathy Matthews, Kevin Cook, Annette Parks, Sam Zheng, Cale Whitworth, Thom Kaufman)

Stock Holdings as of 3/3/2017

- 59,663 stocks with 62,843 unique genetic components
- 11,814 annotated *D. melanogaster* genes are associated with alleles or constructs in the collection
- 3,314 registered user groups, 2,033 of which ordered stocks in 2016
- 6,889 registered users, 2,948 of whom ordered stocks under their own name in 2016

2016 Use Statistics

- 217,072 samples shipped in 13,521 shipments
- 3.6 orders per stock on average, range 0–134; 67% of stocks ordered at least once, 20% ordered 6 or more times, 5 stocks ordered >100 times, the most popular stock was *MTD-GAL4* (#31777), which expresses GAL4 uniformly in the germarium and throughout oogenesis.

Growth

2,625 stocks were accessioned in 2016:

- 809 Transgenic RNAi Project stocks
- 423 UAS-human-cDNA insertions from Douglas Armstrong, Travis Johnson & Coral Warr
- 325 *P{IT.GAL4}* enhancer trap insertions from the InSITE Project
- 141 GFP-tagged transcription factors from the modERN Project
- 127 GFP-tagged proteins from RMCE of *Mi{MIC}* insertions from the GDP
- 89 GAL4 swap-ins into *Mi{MIC}* insertions from Hugo Bellen & colleagues
- 78 LexA enhancer trap insertions from Lutz Kockel
- 23 HACKed QF driver insertions from Chris Potter
- 18 HACK donor stocks from Chris Potter
- 14 Modified histone cluster transgenes from Hillary Graves
- 13 Voltage indicator transgenes from Tom Clandinin, Mike Nitabach & Vincent Pieribone
- 8 Isogenic stocks with sequenced Wolbachia strains from Luis Teixiera
- 570 stocks from other donors

Staff now consists of 48 stockkeepers (22 full-time equivalents) and 9 managers/scientists.

Grant Funding We are in year 3 of a 5 year grant from NIH, $440,923 direct costs. Increased income from user fees is paying for growth of the collection.

New Stocks We expect to add ~5,150 new stocks in 2017:

- o 2,250 Transgenic RNAi Project stocks
- o 1,000 Mi{MIC} and CRIMIC insertions from the Gene Disruption Project
- o 700 InSITE Project stocks
- o 700 UAS-human-cDNA stocks from Hugo Bellen, Sue Celniker & colleagues
- o 500 stocks in all categories from the community at large

Pruning We plan to discard ~1,700 stocks including ~300 assorted low-use stocks and ~1,400 redundant transposon insertion stocks in April 2017.

Scientific Advisory Board

- o Hugo Bellen, Baylor College of Medicine (chair)
- o Nancy Bonini, University of Pennsylvania
- o Lynn Cooley, Yale University
- o Susan Parkhurst, Fred Hutchinson Cancer Research Center
- o Norbert Perrimon, Harvard Medical School
- o Benjamin White, NIH, National Institute of Mental Health

19. VDRC stock center (Lisa Meadows)

The VDRC (**www.vdrc.at)** is a **non-profit** research infrastructure. Its mandate is to maintain and distribute transgenic RNAi lines and other resources to Drosophila researchers, both locally and worldwide, and to further develop and expand VDRC resources according to the emerging new technologies and community needs.
Core funding from the Austrian Federal Ministry for Science and Research and the City of Vienna currently covers ~30% of total running costs. The remaining 70% of the costs must be recovered from user fees, which have not been increased since June 2014. Current funding will continue until June 2020.

Key changes during 2016
1. Major website redesign
2. ~400 shRNA lines added
3. Some KK control lines added
4. Further lines added to "Other Resources", thereby increasing diversity – including deficiencies, markers, tagged transgenes, miRNA sensors, piRNA and piRinternalA biogenesis reporters, CRISPR/Cas9 lines.

Usage Statistics 2016
- Registered users worldwide: **2,565**
- Stocks delivered externally in 2016: **49,104** in **1,650** separate orders
- Total stocks delivered to Drosophila community since 2007: >**1,200,000**.

Resources as of Mar 2017
Total stocks currently available to the community: **36,587**
- 26,585 RNAi lines (16,763 in GD, 9,822 in KK and 373 in the shRNA collection).
- 18 toolkit stocks used for the construction of the RNAi collections.

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

- 8,457 enhancer-GAL4 lines (VTs, Vienna Tiles). Expression patterns annotated in adult brain and embryo. Searchable databases available.
- 880 Tagged FlyFos TransgeneOme (fTRG) lines.
- A small, but growing number of plasmids and stocks made available to the community from Private Stock Collections.
- 13,848 DNA constructs used for the generation of the GD collection.

Services
VDRC is open to donations of highly used stocks for integration into its community stock center collection, complementary to other stock centers.
In addition, we offer a Private Stock Keeping Service to maintain and distribute personal fly stock/plasmid collections on a cost recovery basis and also offer a fly food service.
See VDRC policy for stock keeping services.

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

20. Kyoto Stock Center, Japan: Toshiyuki Takano-Shimizu

21. Species Stock Center, UC Berkeley: Patrick O'Grady

22. Drosophila Gene Disruption Project Current Report, May 2016-April 2017 (Bellen, Perrimon, Spradling Laboratories)

Funding support for the GDP (NIGMS R01 GM06785) has entered year 15 (Bellen et al., 2011; Spradling et al., 2011). We continue to utilize the MiMIC collection as the foundation for our current project. We have tagged about 500 genes with GFP and these are now available from the BDSC (Nagarkar-Jaiswal et al., 2015). The GFP tagged genes allow numerous manipulations (Neumuller et al., 2013; Nagarkar-Jaiswal et al., 2015). Two teams have developed a very useful and efficient strategy to insert an artificial exon that encodes the T2A GAL4 in MiMICs inserted in coding introns (Diao et al, 2015; Gnerer et al., 2015). This typically creates a null allele and leads to the production of a GAL4 in the endogenous spatial and temporal expression pattern of the gene of interest, permitting numerous elegant manipulations. We have currently adopted this strategy and tagged 600 MiMICS and have started depositing them in BDSC. The goal is to create about 1500 different genes tagged with GFP or/and T2AGAL4. This project will be finalized this year.

Another aim is to expand the GDP collection by inserting a small MiMIC-like swappable insertion cassette into 2,500 genes that currently have no MiMIC insertion using CRISPR (a.k.a. CRIMiC). We had technical issues with construction of the vectors and efficiency of obtaining CRIMiC insertions that have slowed our progress. However, we have now solved these issues and have an 70% success rate in producing the CRIMIC constructs (done in Norbert Perrimon's lab) and a 65% success rate upon injection and integration. We have prioritized 2,500 target genes based on the fact that they have human homologues. So far we have obtained insertions in about 400 genes not previously tagged by MiMICs using this technology. These cassettes contain T2AGAL4 but can be converted to SA-GFP-SD (an artificial exon) to tag the gene of interest (Venken et al., 2011). We have prepared several hundered more constructs and are ramping up our injection team inject team to attain our goals as this project is very labor intensive. Indeed, we need to inject 600-700 embryos for each construct (versus 50 for UAS-human cDNA constructs, see below).

Finally, we are creating new tools that will be discussed in the method section at the this meeting: the include FLIP-FLOP and double header (Nagarkar-Jaiswall et al., 2017).

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

We obtained support from ORIP (NIH resources) to create a UAS-human cDNA library (ORIP, R24) and are in the first year of support for this project (2016-2021). Much of our understanding of the genetic basis of development and the physiological processes

in human is derived from studies in model organisms. Studies in flies have provided critical insights into the *in vivo* molecular function of conserved genes, and allow one to test the potential pathogenicity of variants that are associated with human diseases. Such experiments are timely, due to the recent advent of whole-exome sequencing (WES) and whole-genome sequencing (WGS) as clinical diagnostic tools, thereby increasing the need for functional gene studies in model organisms.

Conceptually, it is possible to systematically mutate fly genes and replace them with the human homologs to assess if they function similarly in the fly. We use the T2A-GAL4 system based on MiMICS to create mutations and then drive the UAS-cDNA-HA constructs to assess rescue (Bellen and Yamamoto, 2015). Our success rate of rescue of fly mutations with human cDNA's is 50 - 70% (our sample is too small to be more precise). The limiting step is the lack of a human cDNA library capable of expression in Drosophila*.* Such a library will greatly facilitate the development of studies of human genes in Drosophila. It will allow the research community to investigate human gene function in flies, and to study homology and orthology between human and Drosophila genomes. In addition, because these cDNA clones can be easily modified to incorporate variants, this library will facilitate the use of Drosophila studies in clinical genomics interpretation, especially for variants of unknown significance (Yoon et al., 2017; Chao et al., 2017).

There are currently ~10,000 human genes that are annotated to be conserved in Drosophila*.* We are using Gateway compatible human cDNA clones developed by Dr. Marc Vidal (Harvard) from the Mammalian Gene Collection library (MGC) as well as private cDNA libraries collected by Ken Scott (at BCM) and Coral Warr (Monash, Australia). The clones are sequence-validated full-length cDNA clones and 8,000 of the conserved genes are represented in these collections of clones. We estimate that ~7,000 will be useful at this stage (the ones that are larger than 5kB are underrepresented). We are subcloning these cDNAs into the pUASTg-HA.attB vector for site-specific integration. The library will be available for either direct injection into flies or mutagenesis in order to generate variant forms for DGRC. About 600 UAS-cDNA clones have been generated so far and we are ramping up the production.

We will insert 1,500 pUASTg-HA-human cDNA constructs into a defined Drosophila locus by ϕC31 integrase mediated transgenesis. We will select genes for transgenesis based on the following criteria: genes known to cause genetic diseases, genes that can be manipulated with available MiMIC insertions and genes that are prioritized by the users, Drosophila and human biologists. This will allow to directly test functional replacement of genes for which there is an ongoing need to determine gene and variant function. We have injected 450 constructs so far with 100% efficiency. We anticipate to finish the production of these 1500 strains and about 400 VUS in the next two to three years. If support and time permits we will create more stocks. The stocks are being deposited in the BDSC.

References related to GDP, MiMIC, and human cDNA libraries

Bellen HJ, Levis RW, He Y, Carlson JW, Evans-Holm M, Bae E, Kim J, Metaxakis A, Savakis C, Schulze KL, Hoskins RA, Spradling AC (2011) The Drosophila Gene Disruption Project: progress using transposons with distinctive site-specificities. *Genetics* 188:731-43.

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

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

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

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

Venken KJT, Schulze KL, Haelterman NA, Pan H, He Y, Evans-Holm M, Carlson JW, Levis RW, Spradling AC, Hoskins RA, Bellen HJ (2011) MiMIC: a highly versatile transposon insertion resource for engineering *Drosophila melanogaster* genes. *Nature Methods* 8:737-743.

23. Harvard Drosophila RNAi Screening Center (Stephanie Mohr)

I. About the DRSC
Funding. The *Drosophila* RNAi Screening Center (DRSC) is funded by NIH NIGMS R01 GM067761 (N. Perrimon, PI, S. Mohr, Co-PI). The current funding extends through Nov. 2019.

Mission. The DRSC supports functional genomics projects in *Drosophila* cultured and primary cells by the community either on-site at our screening center or off-site at another location. Over the years, the type and number of functional genomics screens, analyses, and other projects supported by the DRSC has grown. We now offer RNAi, miRNA, ORF, and CRISPR-related services, and have a growing suite of bioinformatics software tools freely available online. Last year we re-did our website, now at http://fgr.hms.harvard.edu/

Usage. We continue to see a trend towards focused library screens and custom projects, but some genome-wide screens are still done and proposed.
In the past year, we
- Hosted on-site or provided reagents for projects by researchers based in nine US states (CT, MA, MI, NC, NY, OH, PA, TX, WA) and four non-US countries

- Provided data analysis or data access support for six projects (CA, IL, MA, PA, WI)
- Wrote six letters of support for new projects (MA, MO, NH, UT, WA)

II. Libraries and services
We continue to offer the following libraries and services in addition to the new libraries and services listed in *Section III*.

Libraries for cell-based, arrayed-format screens (for on-site or off-site use)
- Genome-wide RNAi
- Focused RNAi libraries
  - Autophagy-related
  - FDA (see below)
  - Kinases & phosphatases
  - Membrane-bound organelle-related
  - RNA binding
  - Transcription factors & DNA binding
  - Transmembrane domain-containing
  - Ubiquitin-related
- miRNA over-expression
- miRNA "sponges"
- UAS-ORFs

Services
- Access to reagents for assay development, low-throughput, or follow-up studies
- Assay development and optimization support (consultation, equipment access)
- Bioinformatics support for screen data analysis, visualization, and integration (no fees)
- Cell culture, automated cell dispensing (training, equipment)
- Collaborations on production of custom CRISPR engineered cell lines
- High-throughput screening (training, equipment)
  - Molecular Devices SpectraMax Paradigm "plate reader" (luminescence, fluorescence, spectrophotometry)
  - GE IN Cell automated high-content imaging (see below)
- Smaller high-content imaging projects or others using our assay readout instruments
  - PCR templates for making dsRNA in your lab ("cherry-picks")
  - 96-well custom dsRNA synthesis ("custom IVT")

III. New libraries, equipment, and approaches
New Library: RNAi reagent library targeting fly orthologs of known targets of FDA drugs. We generated a library of dsRNAs based on our genome-wide collections that targets high-confidence fly orthologs of high-confidence targets of FDA-approved drugs (excluding GPCRs). The rationale is to quickly identify targets for which it will be possible to use drugs, rather than RNAi reagents, in mammalian follow-up studies. The library has already been screened and is openly available to the community (standard cost-recovery fees apply).

New Equipment: State-of-the-art high-throughput imaging at the DRSC. In 2016, we applied for funding from the HMS Tools and Technology program, and together with matching funds from Howard Hughes Medical Institute, were able to purchase a GE IN Cell 6000 automated confocal, epifluorescence, and bright field imaging system and supporting plate-handling robotics. The instrument offers a number of significant advantages over our previous system, including more flexibility in imaging and sample formats (slides, plates), bright field imaging with DIC and phase options, non-proprietary TIFF format image files, and LED-based illumination. We are very excited to continue to offer 60x confocal screen imaging, now with the added benefit of bright field and flexibility of support for imaging of larvae, tissues, and other types of samples.

We are grateful to NIH NIGMS, Harvard Medical School's Tools and Technology program, and Howard Hughes Medical Institute, whose support made this possible.

New Approach: CRISPR pooled screens. Ram Viswanatha, a postdoc in the Perrimon lab, has led development of genome-wide CRISPR pooled screens and has promising results identifying both drop-out and selection 'hits' with this technology. We have begun two pilot collaborations with other laboratories and welcome others.

IV. New bioinformatics resources
Major update to the DIOPT ortholog prediction tool. Dr. Claire Yanhui Hu and team recently updated the DRSC Integrative Ortholog Prediction Tool. Altogether, we
- updated the underlying data for all species and all algorithms
- added an estimate of confidence in a given ortholog prediction (high, moderate, low)
- added an indication of whether or not a given ortholog prediction would also be the best match if the reverse query was done
- added the ability to search a gene vs. all species
- added the ability to search for paralogs within a species.

For an "all" search, you can click to view a summary table, giving a quick sense of in what model species the gene has been conserved. The table has links to sequence alignments of all relevant orthologous across the nine organisms so users can evaluate the conservation of specific domains and amino acids. The table also links to gene reports with summary information about gene function such as publications, gene ontology terms, and molecular interactions. These updates to DIOPT are part of our overall effort to create new functionality and user interfaces for various user groups that facilitate mining of model organism data for functional annotation and other applications.

http://www.flyrnai.org/diopt

Summary Table of the Best Predicted Ortholog

Cell Content: Gene symbol(s) of best predicted ortholog (DIOPT Score of Max Score)

Species Gene ID	Gene ID	Search Term	Fission yeast	Budding yeast	Worm	Fly	Zebrafish	Frog	Rat	Mouse	Human	MultiSequence Alignment	Gene Report
FBgn0004009	34009	wg	----	----	cwn-1 (3 of 11)	NA	wnt1 (11 of 12)	wnt1 (9 of 9)	Wnt1 (7 of 10)	Wnt1 (11 of 12)	WNT1 (11 of 12)	generate alignment	generate report
FBgn0004644	42737	hh	----	----	qua-1 (4 of 11)	NA	shha,shhb (10 of 12)	dhh (6 of 9)	Shh (10 of 10)	Dhh,Shh (10 of 12)	SHH (11 of 12)	generate alignment	generate report
FBgn0000382	45278	csw	pyp1 (1 of 8)	PTP2,PTP3,PTP1 (1 of 11)	ptp-2 (6 of 11)	NA	ptpn11a (8 of 12)	ptpn6 (4 of 9)	Ptpn11 (8 of 10)	Ptpn11 (10 of 12)	PTPN11 (10 of 12)	generate alignment	generate report

Drosophila Gene Expression Tool (DGET). We recently published our new tool for mining modENCODE and other RNAseq datasets (Hu et al. 2017). The tool complements similar mining tools at FlyBase by providing a quick and easy way to search using a list of genes. Here is an example of a search of only the RNAseq data from the Spradling lab focusing on sub-regions of the gut. This was also our first experience using the BioRXIV preprint server.

http://www.flyrnai.org/tools/dget/web/
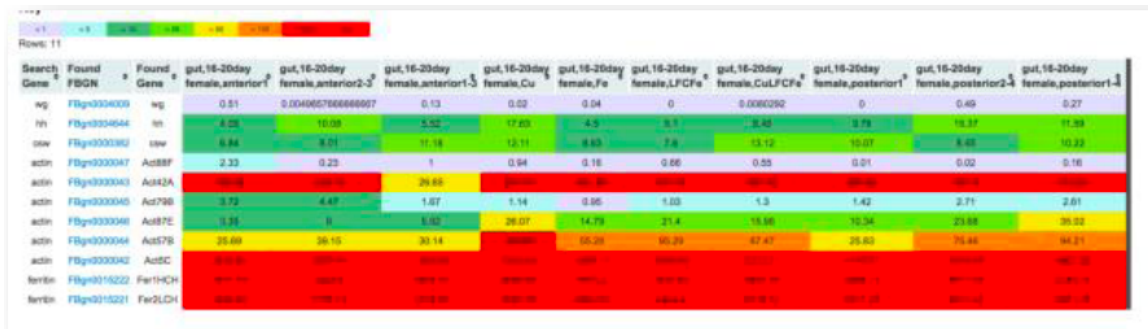
Drosophila Protocols Portal. We continue beta-testing of a site that brings together publications, YouTube videos, lab web pages, etc. with protocols, providing a centralized search of these distributed resources. Our overall plan is that the resource proves useful to the community, it will be migrated to and maintained by FlyBase.
Thus far, we have not received feedback—***if you like it and use it, please let us know!***
http://www.flyrnai.org/tools/protocols/web/

Here is a screenshot of a search with the term "Media" – as you can see, several types of resources are retrieved.
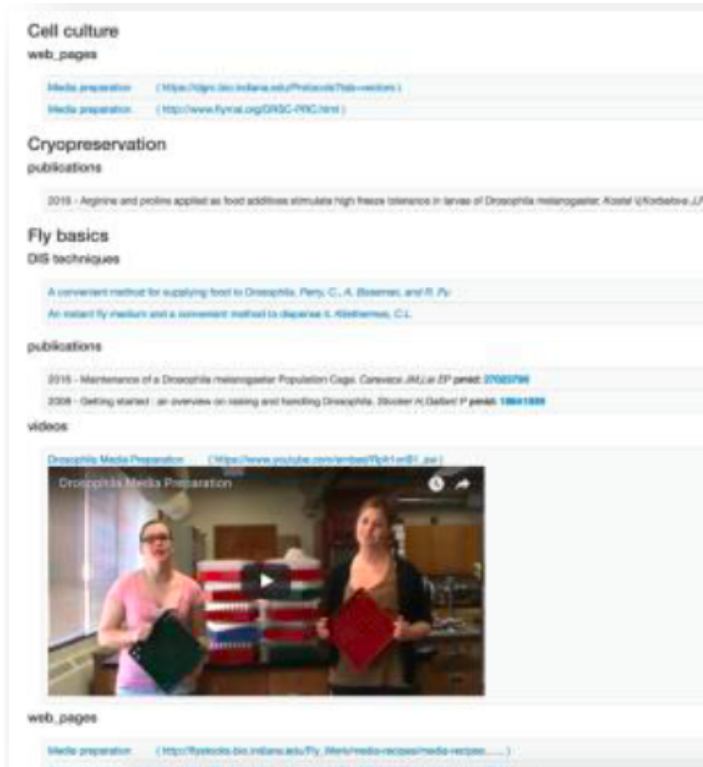
VI. Spreading word of DRSC/TRiP offerings

- Hosted a workshop on Functional Genomics at TAGC 2016
- Presented at the Boston Area Drosophila Meeting (Sept. 2016)
- Presented at the International Congress of Entomology (Sept. 2016)
- Have posters at ADRC 2017

VII. Summary of next directions for the DRSC

In the near future we plan to:
- Continue support of on-site and off-site *Drosophila* cell RNAi screens
- Facilitate CRISPR pooled screens with collaborators
- Launch new online tools for mining of model organism data

VII. "FlyBi" large-scale binary interactions project

We are collaborating with the CCSB/Vidal lab and BDGP/Celniker lab on a large-scale binary interaction project funded by NHGRI. As mentioned previously, we transferred ~10,000 ORFs from BDGP into Gateway entry vectors; this collection is available at the DGRC and other plasmid repositories. We are now doing the large-scale yeast two-hybrid screens. Initial quality analysis experiments done following the first of several iterations of the large-scale screen suggests a rate of binary interaction detection that is similar to the rate of detection of known binary interactions in the literature. More information at http://flybi.hms.harvard.edu.

IX. Recent publications co-authored by DRSC staff

Wangler MF, Hu Y, Shulman JM. Drosophila and genome-wide association studies: a review and resource for the functional dissection of human complex traits. *Dis Model Mech*. 2017 Feb 1;10(2):77-88. PMID: 28151408.

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Housden BE, Muhar M, Gemberling M, Gersbach CA, Stainier DY, Seydoux G, Mohr SE, Zuber J, Perrimon N. Loss-of-function genetic tools for animal models: cross-species and cross-platform differences. *Nat Rev Genet*. 2017 Jan;18(1):24-40. PMID: 27795562; PMCID: PMC5206767.

Vinayagam A, Kulkarni MM, Sopko R, Sun X, Hu Y, Nand A, Villalta C, Moghimi A, Yang X, Mohr SE, Hong P, Asara JM, Perrimon N. An Integrative Analysis of the InR/PI3K/Akt Network Identifies the Dynamic Response to Insulin Signaling. *Cell Rep*. 2016 Sep 13;16(11):3062-74. PMID: 27626673; PMCID: PMC5033061.

Mohr SE, Hu Y, Ewen-Campen B, Housden BE, Viswanatha R, Perrimon N. CRISPR guide RNA design for research applications. *FEBS J.* 2016 Sep;283(17):3232-8. PMID: 27276584; PMCID: PMC5014588.

X. Recent publications of studies done using DRSC resources

Helenius IT, Haake RJ, Kwon YJ, Hu JA, Krupinski T, Casalino-Matsuda SM, Sporn PH, Sznajder JI, Beitel GJ. Identification of Drosophila Zfh2 as a Mediator of Hypercapnic Immune Regulation by a Genome-Wide RNA Interference Screen. *J Immunol*. 2016 Jan 15;196(2):655-67. PMID: 26643480; PMCID: PMC4707113.

Wang H, Becuwe M, Housden BE, Chitraju C, Porras AJ, Graham MM, Liu XN, Thiam AR, Savage DB, Agarwal AK, Garg A, Olarte MJ, Lin Q, Fröhlich F, Hannibal-Bach HK, Upadhyayula S, Perrimon N, Kirchhausen T, Ejsing CS, Walther TC, Farese RV. Seipin is required for converting nascent to mature lipid droplets. *Elife*. 2016 Aug 26;5. PMID: 27564575; PMCID: PMC5035145.

Vinayagam A, Kulkarni MM, Sopko R, Sun X, Hu Y, Nand A, Villalta C, Moghimi A, Yang X, Mohr SE, Hong P, Asara JM, Perrimon N. An Integrative Analysis of the InR/PI3K/Akt Network Identifies the Dynamic Response to Insulin Signaling. *Cell Rep*. 2016 Sep 13;16(11):3062-74. PMID: 27626673; PMCID: PMC5033061.

Swenson JM, Colmenares SU, Strom AR, Costes SV, Karpen GH. The composition and organization of Drosophila heterochromatin are heterogeneous and dynamic. *Elife*. 2016 Aug 11;5. pii: e16096. PMID: 27514026; PMCID: PMC4981497.

Zanotto-Filho A, Dashnamoorthy R, Loranc E, de Souza LH, Moreira JC, Suresh U, Chen Y, Bishop AJ. Combined Gene Expression and RNAi Screening to Identify Alkylation Damage Survival Pathways from Fly to Human. *PLoS One*. 2016 Apr 21;11(4):e0153970. PMID: 27100653; PMCID: PMC4839732.

Chen X, Xu L. Genome-Wide RNAi Screening to Dissect the TGF-β Signal Transduction Pathway. *Methods Mol Biol*. 2016;1344:365-77. doi: 10.1007/978-1-4939-2966-5_24. PMID: 26520138.

24. Harvard Transgenic RNAi Project (Jonathan Zirin)

The Transgenic RNAi Project (the TRiP) has entered its first year of its third round of funding (NIGMS R01-GM08494; N. Perrimon, PI; ends June 2020). We thank the board for their steadfast support in securing the grant. With this new funding, the TRiP is transitioning 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 **~13,604** Fly stocks, with **~1,050** in production and **~85** nominated. These completed stocks, in production and nominated represent **~10,230** unique FBgns which we calculate covers **74%** of the genes in the fly genome (**84%** of highly conserved genes).

TRiP RNAi Stocks at BDSC					
Generation	**Vector**	**Hairpin**	**# Stocks**	**Use in**	**Ref**
1st Generation	VALIUM1	dsRNA	678	soma	19
	VALIUM10	dsRNA	1808	soma	18
2nd Generation	VALIUM20	shRNA	8639	soma, germline	17
	VALIUM21	shRNA	97	soma, germline	17
	VALIUM22	shRNA	1616	soma, germline	17

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

In addition to the TRiP RNAi stocks (see Table), the TRiP, via the BDSC, also provides the community with the **"TRiP Toolbox"**, which includes injection stocks for labs wishing to generate their own RNAi lines and commonly used GAL4 lines with UAS-Dcr2 (only for long dsRNAs not shRNAs) to enhance message knockdown. In addition, all of the TRiP vectors, including vermillion and white versions of vectors for over-expression, are available to the community through the plasmid repository of the DF/HCC DNA Resource Core at HMS. In 2012 the TRiP, in collaboration with Eric Lai (Sloan-Kettering Institute) and David Van Vactor (HMS), provided the BDSC with 102 microRNA

transgenes (the UAS-LUC-mir collection) for conditional expression of fly micro RNAs (Bejarano et al., 2012). In addition, we advised the VDRC with the design of their new UAS-RNAi lines using short hairpin microRNA (shRNA) (http://stockcenter.vdrc.at/control/about_shrna).

In 2016 the BDSC sent **75,364** subcultures of TRiP stocks (**798** of these were Toolbox and **708** were UAS-LUC-mir stocks) to **1,375** different user groups in **43** countries (A. Parks, personal communication). As of Feb 23, 2017 there were **12,837** TRiP stocks in distribution at the BDSC and the TRiP expects to send **800-1000** new RNAi stocks to Bloomington in 2017.

Number of TRiP Stocks Shipped by BDSC Yearly (data from A. Parks)

Year	
2016	~75000
2015	~79000
2014	~68000
2013	~67000
2012	~60000
2011	~48000
2010	~29000
2009	~13000
2008	
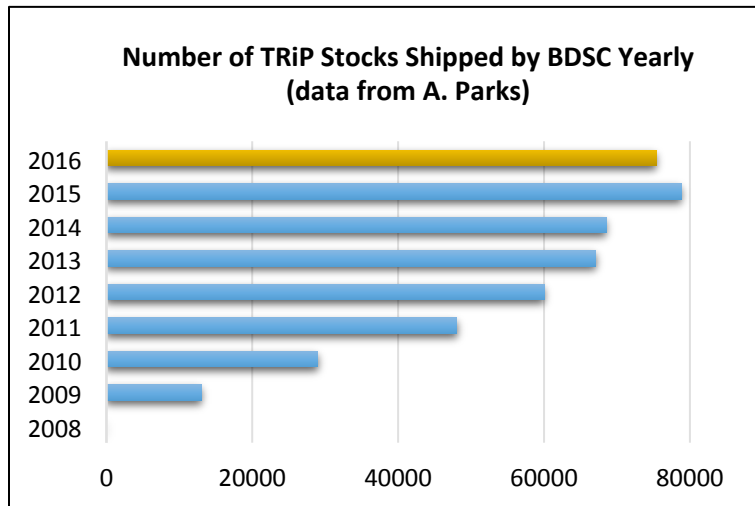
Validation of the TRiP lines
The TRiP continues its curation of reagents via the **RNAi Stock Validation and Phenotypes Project (RSVP)** (http://fgr.hms.harvard.edu/rsvp) at HMS, a web resource that allows users to search and view information about knockdown efficiency (qPCR data) and phenotypes (text and when available, images) for specific RNAi fly stock/Gal4 driver combinations (supported by the TRiP's NIH grant as well as a grant from the NCRR/ORIP). The production pipeline for RSVP qPCR validation and phenotyping was pioneered by Richelle Sopko, a Perrimon Lab Postdoc, who found that on average, 60-80% of TRiP stocks display knock down efficiencies of >50% (Sopko et al. 2014). Curation of the lines for RSVP allows us to decide which of lines are suboptimal and need to be discarded and/or remade. RSVP includes results curated by FlyBase for other major stock collections, such as phenotypes associated with VDRC fly stocks, and we hope in the future to also include CRISPR stock validation. Currently on RSVP there are **>8,400** data entries for **>5,200** TRiP lines representing **>3,750** fly genes. In addition, the RSVP contains **23,451** data entries extracted from FlyBase for **17,782** RNAi lines representing **11,346** genes.

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

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

The TRiP-OE collection is based on work from Perrimon lab postdoc, Ben Ewen-Campen and Shualing Lin of Tsinghua University, which demonstrated that CRISPR/Cas9-based transcriptional activation is effective in vivo in Drosophila (Lin et al., 2015). TRiP-OE sgRNA stocks are crossed to a stock in which Gal4 directs expression of a catalytically inactive dead Cas9 (dCas9) fused to a highly active chimeric activator called VPR (composed of the VP64, p65, and Rta domains) (Chavez et al., 2015). In the resulting progeny (Gal4>dCas9-VPR; sgRNA-gene), the gene of interest is overexpressed in the Gal4 domain. To date the TRiP has produced **208** TRiP-OE stocks with an additional **541** constructs injected and **330** constructs cloned. We expect to produce **>1500** TRiP-OE stocks in the remainder of 2017.
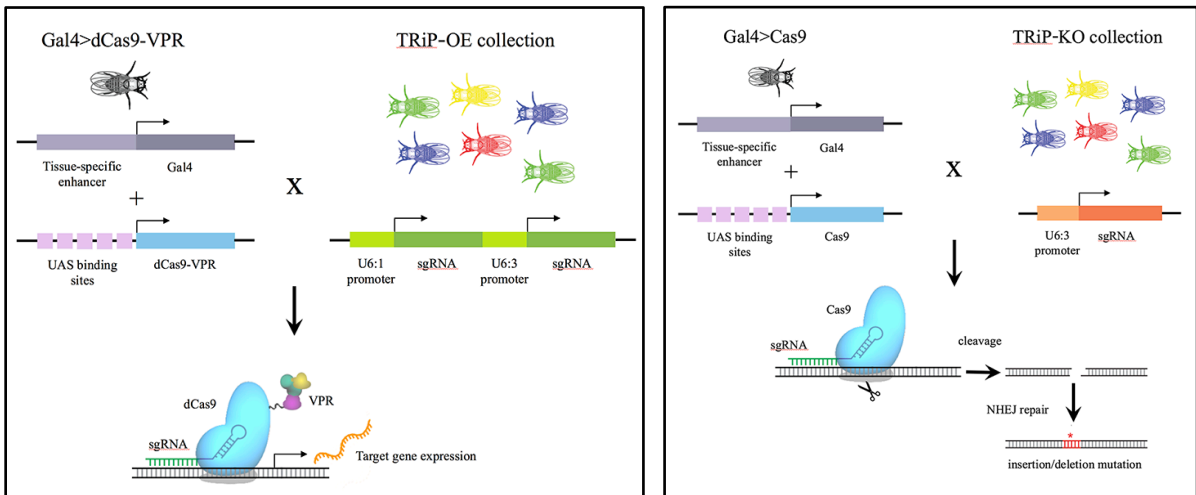
2. TRiP-CRISPR Knockout (TRiP-KO)

We, and others, have found that the CRISPR/Cas9 system efficiently generates double strand breaks (DSBs) in Drosophila, which can be used effectively to generate mutations or for genome engineering approaches (Ren et al., 2013). TRiP-KO flies ubiquitously express sgRNAs targeting gene coding sequence. Mutant animals or tissue-specific mosaics can be produced by simply crossing TRiP-KO flies to germline-specific-Cas9 or somatic tissue-specific-Gal4>Cas9 flies, respectively. To maximize coverage of the genome for the benefit of the research community, production of TRiP-KO stocks is coordinated with similar efforts headed by Drs. Fillip Port and Michael Boutros at the German Cancer Research Center (http://www.crisprflydesign.org/) and Drs. Shu Kondo and Ryu Ueda at The NIG, Japan (https://shigen.nig.ac.jp/fly/nigfly/cas9/). To date the TRiP has produced **594** TRiP-KO stocks with an additional **896** constructs injected and **286** constructs cloned. We expect to produce **>1700** TRiP-KO stocks in the remainder of 2017.

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 TRiP-OE stocks. Additional wild type Cas9 toolbox stocks are also available for generating mutant mosaics in the soma, or generating small deletions and modifications in the germline. **55**

TRiP CRISPR/CAS9 Toolbox lines are complete and have been shipped to BDSC for distribution.

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.

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

A. Introduction
This is our 25th year anniversary! 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.

Since the sequencing and finishing of the euchromatic portion of the genome, we have continued to improve and extend the assembly and quality of the heterochromatic portion. We have also moved into functional genomics. Release 6 was made public last year (GenBank and FlyBase) and we hope to integrate PacBio sequencing to produce the next version of the genome sequence. We continue to characterize the transcriptome using next generation RNA sequencing and to validate gene and transcript models by analysis of full-length cDNAs. We mapped the modENCODE transcriptome data to Release 6. We continue to use the cDNAs to generate resources for proteomics studies and as templates for probes to determine spatiotemporal gene expression patterns in the embryo.

B. Reference Genome sequence

After completion of the Release 6 genome sequence, our efforts to improve the genome are centered around incorporating the PacBio long-read whole genome shotgun assembly (MHAP) into Release 6 with the goal of producing an integrated consensus assembly that will become Release 7. There is currently no budget for these studies.

C. cDNA Clone Resources

The Gateway expression-ready clone collection to be used to generate a Y2H map (Mohr, Perrrimon, Vidal, Celniker) has been sequenced using a pooling and random shotgun strategy using one lane of the Illumina HiSeq. We submitted the sequence to GenBank as full-length cDNA clones when they are finished and as ESTs when they are incomplete. The accession numbers for the 890 clones submitted full-insert sequenced to GenBank are KX531261-KX532150. The rest of the submission to the SRA is under SRA accession is SRP091922

The following are our summary statistics of clones submitted to GenBank - DNA sequence for 258,891 cDNA clones, of which 22,184 were fully sequenced and 18,946 fully support a FlyBase Release 6.13 protein model. The Gold Collection of cDNAs whose amino acid translation matches a FlyBase model with 100% identity, now contains 13,180 clones. From the Gold Collection, we have produced 10,389 expression-ready donor clones lacking the native stop codon (for making C-terminal fusion constructs) and 10,470 expression-ready donor clones containing the native stop codon (for making N-terminal fusion constructs). Using the donor clones, we have generated sets of expression clones in different vectors with a variety of tags (Table 1).

Table 1. Summary of Expression Clones.

Collection	Vector	Promoter	N-term Tag	C-term Tag	ORF Stop Codon?	System	Past year (2/2016-3/2017)	Total
XO	pDNR-Dual	T7	--	6xHN	No	*E. coli*	0	10,389

XS	pDNR-Dual	T7	--	--	Yes	*E. coli*	0	10,470
MXO	pMK33-CTAP-BD	Metallothionein	--	TAP	No	Cell culture	0	1960
FMO	pMK33-CFH-BD	Metallothionein	--	Flag-HA	No	Cell culture	95	10,146
UFO	pUAST-CFLAGHA-BD-PHI	UAS	--	Flag-HA	No	Gal4-UAS	0	7,110
URO	pUAST-C-mCherry-BDatt	UAS	--	mCherry	No	Gal4-UAS	0	245
UGO	pUAST-C-eGFP-BDatt	UAS	--	eGFP	No	Gal4-UAS	0	230
URS	pUAST-N-mCherry-BDatt	UAS	mCherry	--	Yes	Gal4-UAS	0	247
UGS	pUAST-N-eGFP-BDatt	UAS	eGFP	--	Yes	Gal4-UAS	0	237
MSN	pMK33-BD	Metallothionein	--	-	Yes	Cell culture	0	71
GEO	Gateway Entry	-	--	-	No	Y2H*	778	10,664
MSNP	pMK33-N-NoTag-BD-Puro	Metallothionein	--	-	Yes	Cell culture	0	83
MNEP	pMK33-N-EGFP-Puro-BD	Metallothionein	eGFP	-	Yes	Cell culture	0	94
RMO	pMK33-C-mCHERRY-BD	Metallothionein	--	mCherry	No	Cell culture	0	12
GMO	pMK33-C-EGFP-BD	Metallothionein	--	eGFP	No	Cell culture	0	10
CCO	pCopia-C-Clover-BD	Copia	--	Clover	No	Cell culture	346	346
CRO	pCopia-C-Clover-BD	Copia	--	mRuby2	No	Cell culture	345	345
GCO	pCopia-C-EGFP-BD	Copia	--	eGFP	No	Cell culture	23	23
ECD	pECIA2	Metallothionein	--	Fc; V5; 6xHN	No	Cell culture	0	207
ECD	pECIA14	Metallothionein	--	Alkaline Phosphatase; Flag; 6xHN	No	Cell culture	0	207
hGUHO	pUASg-HA.attB	UAS	--	3xHA	No	Gal4-UAS	160	160

hGUHO	pGW-HA.attB	UAS	--	3xHA	No	Gal4-UAS	238	238

*Not colony purified

Table 2. Summary of clones available at the DGRC:

Collection	Past year (Feb 2016 – March 2017)	Cumulative
AU (Gold)	96	11,975
XO	0	9,685
XS	0	9,600
MXO	0	1961
FMO	0	10,051
UFO	0	7,110
ECD	0	414

D. Embryonic Gene Expression

We continue to collect embryonic spatiotemporal gene expression data from high throughput *in situ* hybridizations using the Gold Collection clones as templates for RNA probes. Annotations assigned by stage to each gene are now included in the FlyBase gene reports. In addition to the wild type gene patterns, we are collecting expression patterns for CRM-driven reporter constructs from the Rubin/Janelia collection and have started to incorporate these experiments into the public database (http://insitu.fruitfly.org) with links to the FlyBase sequence feature reports for these constructs. Our homepage includes a separate browse tab for the CRM experiments to improve accessibility. This year we released a new version of the gene report pages. The improved gene reports will include graphical summaries of the stage specific organ system annotations and a graphical representation of the associated modENCODE RNA-seq data. The updated version also allows searches by all known gene name synonyms and human ortholog names. We continue to add new search and discovery tools based on computational image and annotation analysis. We have recently published an advanced method for modeling spatially local gene interactions and networks with our dataset. An interactive viewer based on the annotated patterns of 708 site-specific transcription factor genes, using self-organizing maps to show relationships among transcription factor expression patterns in the context of organ system development, can be accessed at http://insitu.fruitfly.org/som. We are active participants in the development of image analysis within the open source image analysis platform FIJI (fiji.sc). We are starting to use our recently finished open source microscope automation software for automated slide loading and imaging with commodity hardware. To date annotated experiments for 8066 genes, documented with over 125,000 images, have been deposited into the public database.

E. ENCODE model organism Project - modERN (Bob Waterston, Susan Celniker, Kevin White, Valerie Reinke and Mark Gerstein)

The ENCODE model organism project is an independent R01 submitted to complete the study of fly and worm transcription factors (those defined as having a currently recognized DNA-binding domain) determining their genomic DNA binding sites in animals using the ChiP-Seq assay as was perfected in ENCODE. The application was funded and started in August 2014. To date the Celniker lab has produced 328 transgenic GFP tagged-TF fly lines and deposited 270 at the Bloomington Stock Center. Two lines are in the process of being balanced and the remainder are being verified before sending to the BSC. The White Lab has performed ChiP-Seq for 269 lines, 14 from ModENCODE, 255 from modERN. The data is being processed through the ENCODE pipeline and is being distributed through the ENCODE DCC. In addition we produced TF knock-down RNAi followed by RNA-seq experiments for a number of TFs (~26 sequenced – 23 more in process). Once validated the RNA-seq files will be submitted to the SRA

A grant to generate the remaining GFP tagged-TF fly lines and additional RNAi TF experiments was submitted to NHGRI January 2017 with Bob Waterston as PI.

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

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

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

H. Funding
The BDGP is funded almost exclusively by NIH grants (NIGMS). An R01 (SEC) funds the spatiotemporal gene expression studies and was renewed last year 2015. Image analysis research for the spatiotemporal expression studies is funded through an NIH BISTI grant to Erwin Frise. The competitive renewal was resubmitted February, 2016 but was unsuccessful. We are also funded under subcontracts from Harvard University (Perrimon, PI, Celniker, co-PI) to participate in the analysis of the Y2H data, the University of Washington (R. Waterston, PI, Celniker and White, co-PIs) to participate in a consortium performing ChIP-seq analysis of transcription factors in embryonic

development and just recently from Baylor College of Medicine (Bellen, PI, Celniker, co-PI) to construct human ORF clones for expression in flies.

27. DGRC: Andrew Zelhof

Key Changes to Report: None

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

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

Peter Cherbas, Associate Scientist
Lucy Cherbas, Associate Scientist

Use Statistics:
The DGRC serves ~3266 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 2016, demand for our "products" (cDNA clones, vectors, and cell lines) remains substantial; we shipped 3586 individual items at a value of $189,773 in 2016.

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

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

Newsletter:
We have initiated a "quarterly" newsletter. The newsletter will announce any changes or additions to the DGRC collection. Upon receiving please distribute among your lab.

New and Future Collections:
1. Resurrected cell line ML-DmBG2 and it is now available to the community.
2. Trojan Exon Vectors from Dr. Benjamin White

3. ~650 tagged transcription factors in BACs for phiC31 integration from Dr. Kevin White – available after the fly meetings.

Coming soon: A UAS-human ORF clone collection (several hundred) from Dr. Travis Johnson.

Website Improvement:
1. Integration of cell line usage in publications with Flybase: We have expanded the literature references for each cell line. In collaboration with FlyBase we now include all papers that make use of cell lines available from the DGRC. References can be viewed by clicking on the "References" tab; they are associated with searchable keywords.
2. Integration of DGRC cDNA collections (eg. GOLD, Tagged-ORFs) with Flybase: At the request of the DGRC, FlyBase is extending its import and presentation of cDNA collections. FlyBase will be adding a new section within the 'Stocks and Reagents portion' of each FlyBase gene report, which will include a direct link to the relevant DGRC gene-specific reagent listing.
3. Integration of common vector, GOLD clone and Tagged-ORF clone usage in publications: Citations that specifically reference any of the above, as found in our Google Scholar search, will be added to the relevant vector or clone page.

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

Grant Renewal: We will be submitting the renewal proposal for the deadline of May 25th, 2017.
1. We would like to say thank you for all of the labs that responded to our call for citations (Jan 2013-Feb 2017).
   - For example, we have confirmed and curated 700+ citations through labs and Google Scholar.
2. We also hope for the same response when we ask the research community to supply letters of support for the renewal application.

Resource Development: We have recently initiated a survey of transformation efficiency and CRISPR/Cas9 efficiency of gene tagging across modENCODE cell lines. The DGRC maintains over 100 stable cell lines and these cell lines have become an integral part of the toolkit for research. In particular, there are 25 Drosophila melanogaster cell lines (modENCODE cell lines) that have been characterized by whole-genome tiling microarray analysis of total RNA, permitting researchers to choose the most appropriate cell line for investigations into gene function and cellular biology. Furthermore, with the advent of CRISPR/Cas9 the ability to manipulate the genome of these cells has decreased the reliance on transient transfections and increased the utility of stable cell lines. Nonetheless, CRISPR/Cas9 manipulations have been limited to only a couple of cell types and thus there is a need to provide a systematic survey of the ability to manipulate as many different lines as possible. Our goal is to establish a baseline/minimum set of conditions applicable to as many modENCODE cell lines for transfections and CRISPR/Cas9 manipulations and reveal and note potential differences between cell lines to consider in planning experiments.

Poster 704B and Booth: Please contact us for any guidance and collaborations.

Scientific Advisory Board: No changes

27. DIS: Jim Thompson

Volume 99 (2016) of Drosophila Information Service was published on our web site (www.ou.edu/journals/dis) in early January. It continues to attract a broad range of research reports, technique articles, teaching activities, and general notices. We now distribute printed copies through www.lulu.com, a company that prints on demand at a lower cost than we had been able to offer earlier. Other advantages are rapid delivery and having no unused copies to store. Volume 97 (2014) and 98 (2015) are now available. Volume 99 (2016) has been temporarily delayed because one or more of the articles had some embedded commands that blocked correct conversion into the required printer format. As soon as those commands have been located and eliminated, volume 99 will be available on that site.

First published in 1934, DIS remains an active source for research, teaching, and technique articles relevant to our field. We continue to respond to other requests for assistance in locating information for researchers and graduate students. Most submissions occur in response to our traditional "Call for Papers", in which we are assisted by the excellent help of Josh Goodman, FlyBase, University of Indiana. But we already have several recent submissions for volume 100, to be published soon after the end of December 2017. Free access to each new issue is provided on our web site soon after the issue is completed at the end of December. But submissions are accepted at any time. Manuscripts can be sent to James N. Thompson, jr., Department of Biology, University of Oklahoma, Norman, OK 73019; jthompson@ou.edu.

APPENDICES.

Appendix 1.   PI Early Career Forum Schedule.

Guy Tanentzapf, chair
Welcome & Introductions
8:50-9:00 am

SCIENCE TALKS

Bergstralh, Daniel T.	9:00-9:15
LaRocque, Jeannine R.	9:15-9:30
Chiolo, Irene	9:30-9:45
Chambers, Moria C.	9:45-10:00
Loza-Coll, Mariano A.	10:00-10:15
Rideout, Elizabeth J.	10:15-10:30

Coffee break
10:30-11:00

Velazquez	
Ulloa, Norma	11:00-11:15
Jepson, James E.	11:15-11:30
Pearce, Margaret	11:30-11:45
Villa-Cuesta, Eugenia	11:45-12:00
Siekhaus, Daria E.	12:00-12:15
Miura, Pedro	12:15-12:30

LUNCH
12:30-14:00 with
FlyBoard members

Shahrestani, Parvin	14:00-14:15
Lott, Susan E.	14:15-14:30
Amodeo, Amanda A.	14:30-14:45
McKay, Daniel J.	14:45-15:00

PANEL DISCUSSION
15:00-16:30
featuring Melissa Harrison, Judith Leatherman, Blake Riggs and Tina Tootle

PI SOCIAL
16:30-18:00

Appendix 2. References to Advocacy & Communications.

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Appendix 3. Advocacy and Communications FlyBase Cover (2016).

Appendix 4. Advocacy and Communications FlyBase cover mock-up.

Appendix 5. Report of the NIH Cryopreservation Workshop.

These appendices can be accessed via the following Dropbox link:

https://www.dropbox.com/sh/jtatl0ys1s7gzne/AAB2269i8qJ-AFqtU3a2okMna?dl=0