Minutes From 2023 Drosophila Board Meeting at Annual Drosophila Conference, March 1, 2023 at the Grand Sheraton Hotel in Chicago, Illinois.

1. Welcome and Introductions: The meeting was run by President Michelle Arbeitman and was in the hybrid format, with some participants joining the meeting remotely, via Zoom. All participants introduced themselves at the beginning of the meeting. The new and outgoing board members were welcomed and thanked for their service.

2. Approval of the minutes from 2022 meetings: The minutes from the previous North American Drosophila Board meeting was approved. These minutes and current officers of the Flyboard can be viewed at:
https://wiki.flybase.org/wiki/FlyBase:Fly_Board#The_Drosophila_Board_203-24

3. Brief Reports

a) Fly Board elections: Past-president Mariana Wolfner had a delayed flight and so was unable to attend the meeting. Michelle Arbeitman announced the results of the Fly Board Elections. The nominations committee included Alisa Armstrong*, Erica Bach, Lydia Grmai**, Ana-Maria Raicu**, Michael Welte, and Past-President Mariana Wolfner (*serving for a second year, **early career representatives). As in previous years, voting this year was between two candidates for each of the 8 positions up for election. The nominations committee outlined the methodology used to arrive at the final slate of candidates in their report. The results of the elections are as follows:
Vice President: *Sally Horne-Badovinac* (will serve as President in 2024)
Treasurer: *Jessica Treisman*
Northeast representative: *Barbara Mellone*
Mountain region representative: *Laurel Raftery*
Australia/Oceania representative: *Louise Cheng*
PUI representative: *Ruth Johnson*
Postdoc representative: *Shyama Nandakumar*
Trainee representative: *Shefali Shefali*
Although not present, Mariana pointed out that the elections garnered 300-400 votes for each position and were often closely contested races. People who were unsuccessful candidates this year could be renominated in future years. Other 'self-nominations' could be obtained from the community survey that was carried out earlier this year.

b) Treasurer: Jessica Treisman presented the Treasurer's report covering the activity and balance for the Drosophila Reserve Fund, Larry Sandler Fund and Victoria Finnerty Fund. As decided in previous years, ~5% of the reserve funds were used to fund travel awards and outreach awards to encourage trainee participation and DEI efforts in the Drosophila community. A committee constituted to best allocate these funds decided that outreach awards were more likely to be transformative than individual travel awards. Although only a few awardees were named, this was seen as a likely outcome of the awards being new and not being as well known. A suggestion was made that the successful awardees could be encouraged to write a blogpost to highlight their efforts that could be featured prominently on the GSA blog page and serve to draw more attention to these awards. Photos and field reports were also seen as a positive means to drive more traffic and attention to highlight opportunities that are not just limited to North America, as a few of the initial awards were made outside US and Canada (including Bosnia, Brazil, and Nigeria). The board thanked the committee who selected these awards (Jessica Treisman, Brian Lazzaro, Rachel Smith-Bolton, Blake Riggs, and Ana-Maria Raicu) for their hard work.

c) Sandler Award: Tim Mosca (chair) presented on the work of the Sandler Award Committee (Tim Mosca, Beverly Piggott, Filip Port, Sarah Signor, Deepika Vasudevan). They had 18 nominations, which were each ranked for Significance, Originality and Clarity of Abstract (the full process of selection is outlined in the Sandler committee report). The winner of the 2023 award is James O'Connor who also presented his thesis work at the 2023 meeting. One runner up (Xiaoran Guo) and three finalists (Lisa Baumgartner, Mireia Coll-Tané, and Zinan Wang) were also chosen to highlight their excellence. One strong recommendation made by the committee was *"to ensure Best Practices for DEI are engaged with this committee, more information should be solicited from candidates in the future regarding gender, ethnicity, protected group, or any other relevant information."* It was suggested that sometimes thesis advisors can be too busy or otherwise fail to nominate their students, and that any member of the thesis committee should be able to nominate for a Sandler award. In response, Tim Mosca replied that indeed, they do consider such nominations from other mentors (including postdoc mentors), not just the thesis advisor. Michelle Arbeitman suggested that pointing this out explicitly in the call for nominations and on the Wiki page would add more transparency to the awards and increase nominations (although this year the committee already read in excess of 1300 thesis pages).

d) Drosophila Image Award: Julie Brill (chair) presented a report on the Drosophila Image award on behalf of the committee (Julie Brill, Tina Tootle, Clemens Cabernard, Jose Pastor-Paréja, Amy Kiger, and Dan Bergstralh). 80 submissions were received for the award this year (51 images, 29 videos). The Image Prize winners were Bryce Bajar and Orkun Akin, and the video prize winners were Regan Moore, U. Serdar Tulu, and Dong Li. One issue that came up was that some submissions (3) were ineligible because the publication they were featured in was yet to be published in a journal, even though some were published as a preprint. This is important to ensure that images get submitted only once rather than in several years. Julie also pointed out that several submissions were incomplete as submitters did not follow the guidelines closely, despite previous years' applications being available on the website. They will incorporate a PowerPoint template in future years to make sure all the images are easily collected and to cut down on heterogeneity of information from different submitters. Suggestions were made to incorporate survey suggestions for future members of the Image award committee, and to invite this year's winner to be on the committee in future years (Julie mentioned she did do that this year). Michelle Arbeitman recommended putting these clear guidelines for the award on the Fly Board wiki page.

e) Drosophila Community Service Award: Michelle Arbeitman presented the selections for the inaugural Community service awards on behalf of the committee (Michelle Arbeitman, Kevin Cook, Amy Kiger, Nadia Singh, and Nasser Rusan) that were instituted by the flyboard last year. Three awardees were chosen this year for gathering and organizing information that drives Drosophila research: Dr. James Thompson (Drosophila Information Services), Dr. Thomas Brody (Interactive Fly), and the Flybase Curatorial Team (FlyBase). Nominations submitted will be automatically considered for future year awards. Michelle would also like to prominently feature the call for nominations on the Drosophila meeting web site in future years (on par with the Sandler and the Image awards) to encourage and solicit a deeper pool of nominations. In response to a question, Michelle clarified that this award is for people who do or have done work for the fly community, rather than an award for fly people to do service work in their communities.

f) GSA Conferences: Suzy Brown reported to Flyboard on behalf of GSA. Many details of the relationship and agreement between GSA and Fly Board are in the filed report. Suzy reported that organizers of #DROS23 have done a great job with nearly 1600 participants (90% of whom have chosen to attend in person) from 25 countries. Less than 3% of talks will be given online.

However, in keeping with GSA commitment to hybrid meetings, all talks will be streamed and recorded for later viewing for a few weeks. This year's meeting has a 'Pay It Forward' theme and a 'Come Fly with me' mentoring session for various career prospects for trainees. There was also a description of the neighborhood program, initiated by Alana O'Reilly, using "neighborhoods" led by early career scientists to improve the understanding of science in the public, specifically within systemically minoritized populations. In discussing future Drosophila conferences, Suzy mentioned that next year's meeting will be part of #TAGC24 in Washington, D.C. with the meeting returning to San Diego in 2025 and possibly back to Chicago in 2026. GSA is making a strong emphasis on childcare awards for future meetings. Michelle suggested that some trainee award money could be used to support childcare costs at #TAGC24, although this decision would have to be made much earlier than in previous years if that were to happen. A board member pointed out that the definition of care could be expanded to also include those caring for elderly parents. Finally, Tim Mosca pointed out that other communities including the C. elegans community is also instituting its own equivalent of the Larry Sandler Award. Everyone thanked Suzy and GSA for their hard work throughout the year but especially leading up to the fly meeting.

g) #Dros23: Savraj Grewal reported to Fly Board on behalf of the #Dros23 committee (Savraj Grewal, Angela DePace, Mia Levine, Jennifer Jemc Mierisch, and Lucy O'Brien). Savraj thanked Suzy and GSA for their help with organizing the conferences and helping fulfil the vision of the committee. Savraj talked about the 'Pay it forward' theme of the meeting: to " recognize all we have received from mentors, peers, trainees, and colleagues and accept responsibility for repaying their gifts of attention, insight, and opportunity to others. We also acknowledge the barriers many face in joining and participating in our community. We accept responsibility for doing our part to make the fly field a welcoming, creative, and caring community for everyone." He described the process by which Keynote speakers and plenary and session speakers were selected, including committing 4 slots of early-stage PIs to showcase their science. The keynote speaker for the meeting is Yukiko Yamashita and the ten plenary speakers are: Amanda Amodeo, Allison Bardin, Edan Foley, Sally Horne-Badovinac, Karla Kaun, Erin Kelleher, Mustafa Mir, Caroline Palavicino-Maggio, Kausik Si, and Lesley Weaver. New to the meeting are (1) a commitment to new PIs, (2) a community building session, and (3) a community vision board. In response to a question, Savraj clarified that in some cases, the main organizers removed some selected speakers to prioritize talks given by early-stage investigators or trainees instead of established PIs. Michelle suggested that trainees could be encouraged to self-nominate for session chair slots for future fly meetings including at #TAGC24. Savraj pointed out that even though the main organizers represent diverse aspects of fly biology, they are only still considering a smaller subset of possible Drosophila researchers for plenary talks. A system in which people can nominate others or themselves for plenary talks (like through a community survey) would be good to remove bias. Savraj also mentioned in his report that reimbursing some of the registration or travel costs might encourage more trainee co-chair self-nominations. Michelle asked what frequency of such self-nominations would be useful. In response to a suggestion, Michelle clarified that the community survey is something distinct from the fly meeting survey but going forward the community survey results will be available in time for ADRC/TAGC organizers to use (see below). Everyone thanked Savraj and his co-organizers for all their hard work.

h) #TAGC24: Harmit Malik presented a brief report on #TAGC24 as one of its two main co-organizers. An APC (Allied Program Committee) has been assembled to represent the various constituent communities and interest groups at TAGC, including a Drosophila representative (Michelle Arbeitman has agreed to this role) and a community organizer who will help organize the Drosophila community portion of the meeting (Melissa Harrison has agreed to this role).

Three keynote speakers have already been selected and three more speakers are anticipated. The emphasis of #TAGC24 is to pick keynote speakers who are well known for their science and one other aspect of their scholarships (advocacy, mentorship etc.) which will make them inspiring speakers to listen to. However, in contrast to previous TAGC meetings where each community selected some keynotes, this year the emphasis is to pick speakers who will have broad appeal, but fewer keynotes overall to give enough time to the community programs (50% time), to mentoring workshops, and to a community- and education-facing public program taking advantage of the DC location. Harmit pointed out that the proximity to DC could attract people to attend TAGC24 with families and take advantages of the great location and opportunities to visit monuments and museums. Childcare is a huge priority as is making sure that TAGC24 is as great an experience for those attending their first GSA meeting as for those attending their 30th. A suggestion was made to make registration cheaper for undergrads or people attending from developing countries and Harmit responded this is something the committee will look into, to decide whether cheaper registration is a better alternative to registration or travel grants; the latter might be easier to help predict the fiscal health of the meeting as well. Tania Reis asked about reduced registration costs for those whose lab funding rates might have recently declined; Harmit did not have a great solution to this but again suggested that one-time awards might be easier to administer than blanket lower registration rates. Suzy Brown pointed out that members of the community could help TAGC24 organizers by helping to write grants to help cover these costs. Tania pointed out that an inclusivity committee could take this in its charge and members agreed. Daria Siekhaus suggested that the Gates Foundation might be willing to help lower or waive costs from developing countries (especially since most of these are going to involve virtual attendance). Tim Mosca asked about community outreach and Harmit responded that there are plans to have a Capitol Hill Day as well as to invite students and teachers from local high schools and HBCUs to one or two evenings focused on public outreach. Michelle encouraged members to reach out to Harmit for fundraising or other ideas, and Harmit pointed out that even small pots of money could help - $5000 could cover costs for 5 undergrads for example.

(i) Drosophila Information Services: Jim Thompson presented a report on volume 105 which is published in print and online with color figures. Most contributions were research reports but technique articles and teaching resources were also included. Volume 105 also includes profiles of Edith Wallace and J.P. Gupta. Jim would like to see more historical profiles to be submitted in future volumes. Manuscripts can be sent to James N. Thompson, jr., Department of Biology, University of Oklahoma, Norman, OK 73019; jthompson@ou.edu. DIS can be readily accessed at: www.ou.edu/journals/dis/byissue.html.

(j) Finnerty Undergraduate Travel Awards: Justin DiAngelo presented a report on behalf of the committee (Justin DiAngelo, Jennifer Bandura, Daniel Cavanaugh, Jennifer Kennell, Judith Leatherman, and Matthew Wawersik) assigned to select the travel awardees. 14 of 40 applicants were selected for funding this year. Justin pointed out that the awards do not fully accomplish the original intention of encouraging more PUI undergraduate applicants because of the timing mismatch between abstract selection and Finnerty award decision (could try to move up the timeline?). Knowing whether you have the money would encourage more folks to submit abstracts to the meeting. This is something we can adjust through GSA. Harmit mentioned that together with the education committee, we would like to arrange special sessions of the Finnerty and other undergrad travel award recipients with keynote speakers and organizers at TAGC24. Michelle thanked Justin for his efforts as this is his last year on the Fly Board.

(k) Bloomington Drosophila Stock Center: Kevin Cook presented a report on the Bloomington Stock Center, which currently houses more than 80,000 fly strains. The 2022 calendar year saw an 8% drop in shipments compared to 2021. The drop in stocks ordering could be because labs adopted their own CRISPR-mediated knockouts. However, this drop does have ramifications for the fiscal health of the Stock Center. A new grant will be submitted this year. However, since the NHGRI grant covers only about 20% of the stock center costs, this will require either raising prices or culling stocks. Most likely outcome is culling of stocks. Suggestions are invited from the community. Harmit asked if there is a list kept at Bloomington about who has ordered a stock before, so that someone may request even a culled stock from that lab. Kevin responded that all stock requests are completely confidential and not shared. A solution might be hosting a forum in which people could actively ask for previously-culled stocks that community members could respond to. Michelle commented that Twitter might be good for this but not everyone is on Twitter; it is unclear who would host this although Flybase might be one such place. Laurel pointed out that it is hard for individual labs to preserve stocks many years after they have been published. Cryopreservation could help with this and there should be a community-wide effort in this direction. Kevin mentioned that efforts are underway to explore cryopreservation for a small number of stocks. Currently this is working on a very small scale but there is a major effort to expand this to a stock center scale operation. Tania asked whether it might be still worthwhile and cheaper to sequence the stocks before culling them; Hugo pointed out that once the lesions are known, they can be recreated later using CRISPR. Justin pointed out that may PUIs use sets of stocks and they should report these to Bloomington so they are protected from culling. Finally, Daria mentioned that the Fly Jedi group is a nice way to coordinate and request stocks among Drosophila labs in Europe; having such a forum between fly labs in US and Canada might be worth exploring. This could be an action item for the Fly Board in addition to creating a full list of Drosophila labs (below).

(l) Vienna Drosophila Resource Center: Lisa Meadows presented a report on behalf of VDRC. They also reported a reduction in orders. Stocks that have not been ordered in 5 years are being culled. However, there is DNA in case RNAi lines need to be remade later. A new website for ordering will be up later this year. One way VDRC is dealing with reduced orders is by increasing fees. The new fees will be reflected on the new website. Harmit asked if there have been problems shipping to the US. Lisa replied that most of the time, there are no issues but occasionally flies sent via Memphis Customs/USDA site get held up for days without explanation. Like other stock centers, VDRC is open to integrate widely used stocks, to host private collections on a cost recovery basis and to help run large scale RNAi screens. Also working on cryopreservation. Would love to collaborate with researchers on new lines and transgenics.

(m) Drosophila Genome Resource Center, Bloomington: Andrew Zelhof reported on behalf of DGRC. He thanked the community for suggesting and submitting reagents for wide distribution. Reported that DGRC now hosts cell lines with attP sites. Urged community members to take the DGRC survey to report on needs.

(n) DRSC/TRiP at Harvard Medical School: Stephanie Mohr provided an update on DRSC. Mentioned that a number of new technologies have been developed in the last year and posters and talks at the Fly meeting will report on several of these, including a new pooled CRISPR screening approach, a nanotag technology, and new cell lines. CRISPR screen ready attP cell lines have been deposited at DGRC to facilitate wide use by the community. A number of new technologies in cell-based and in vivo screens as well as bioinformatics resources ere developed and published on. Notably CRISPR cell-based screening technologies are readily applicable to other arthropods, including most recently to ticks at DRSC. Michelle suggested

that DRSC could do a separate blog post hosted by GSA about all the exciting outreach activities.

(o) Flybase: Susan Rosso Gelbart presented on behalf of Flybase; a detailed report is included with latest updates. Flybase is physically at 4 sites. A grant renewal has been submitted. A discussion of resources for those new to flies is now on the frontpage, as are links to new website where all model organisms are linked together (*D. melanogaster, C. elegans, S. cerevisiae, D. rerio, M. musculus and R. norvegicus*). Harmit requested that the alliance pages should be heavily advertised and featured at TAGC24; Brian said that he will definitely look into this. Community members are encouraged to pay their access fees to Flybase- in response to a question about automatic renewals, it was mentioned that the fees are now being collected via a Harvard set up server. Blake thanked Flybase for the fly icon on home page. In response to a question about how much user fees have helped, it was noted that there were almost no user fees in 2020-21 likely due to the pandemic but they hope to see some more. Michelle asked if there was an email server where community members could get updates about the alliance website, and Brian said yes. This will be advertised in the next Fly Board report.

(p) Gene Disruption project and human cDNA project: This report was presented by Hugo Bellen, Shinya Yamamoto, and Oguz Kanca on systematic CRISPR-based efforts for disruption of all Drosophila genes. Additional important resources were also discussed (see written report). In addition to these ongoing efforts, a project to introduce all human cDNAs under UAS control is also underway, as are fly lines expressing all SARS-Cov2 proteins in flies. In addition, Hugo reported on a model matcher informatics tool, in which Drosophila (or any model organism) researchers studying a particular gene can query to be matched with a physician studying the human ortholog to understand the genetic and biological basis of disease.

(q) BDGP: Sue Celnicker was unable to attend the Flyboard meeting. A written report outlining all the various activities of BDGP were made available to the Fly Board ahead of the meeting. A couple of new highlights include a reference microbiome sequence, updates and expanded list of embryonic gene expression patterns, and a conserved small ORF project.

(r) Nomenclature committee: Kevin Cook presented a report on the ad hoc nomenclature committee (Kevin Cook, Scott Hawley, Michelle Arbeitman, Mariana Wolfner, Atanu Duttaroy, John Tomkiel, and Steven Marygold from Flybase as a non-voting member) that was instituted last year by the Fly Board to look into fly gene names that could be considered offensive or to disambiguate them. Although the work is likely to be ongoing, the committee has now made recommendations to alter some genes names that may be offensive, while still providing clear links to the literature and mutant alleles. There were different ways forward depending on if the gene is actively being studied or was a historical mutant allele that is no longer available to the community. Additionally, changes to gene names would consider known biochemical functions and input from colleagues that actively study the gene. In some cases where it was unclear if the gene name was inappropriate, a comment that indicates a gene name may be offensive will be added without changing the gene name. The report of the committee is now open for three months for comments and suggestions from the community. The committee itself will disband after the final report, but this work will continue at Flybase using the principles that were decided upon. The Fly Board will continue to have standing members that respond to nomenclature issues (Kevin Cook and Scott Hawley). Michelle thanked the committee for its work, commented on what a huge effort it was, and how seriously the committee took the task given the history associated with many gene names. Hugo pointed out that gene names might appear inoffensive to most fly researchers but take on a huge significance when they refer to mutations in genes that could be applied to human patients; its best to err on the side of discretion. Tania asked if

the Fly Board or the committee can come up with guidelines for new gene names, as is the case for many other model organisms. Kevin responded that Flybase does have guidelines about gene nomenclature but does not actively police gene names. Brian pointed out that there is a push to rename Flybase gene names to reflect their human gene names at NIH, especially NHGRI. Blake asked whether there was a guideline to consult before naming fly genes- the response was that it was always a good idea to consult with Flybase curators. Hugo suggested picking the human ortholog. This discussion was longer but at this point, the community's response is important before this report becomes final and the guidelines are adopted as a matter of future practice.

(s) Community survey: Michelle Arbeitman reported on the results of the survey that got a good but not as strong a response as was hoped for. Nevertheless, the survey was successful in terms of collecting some information about the community and populated a list of volunteers for various Fly Board positions, Drosophila meeting organizer positions, and meeting speakers etc. that would go a long way in diversifying such committees and ensure that there is lower bias in these in the future. To avoid survey fatigue, one year the survey could be focused on obtaining a list of emails of Drosophila Community members (see below). Brian Calvi indicated that Flybase was working towards generating an email list of faculty that run Drosophila Labs. Members of the Fly board thought that the community survey should be implemented every year, or every other year.

(t) Additional topics: Blake pointed out that as a local community rep to Fly Board, he does not have access to which Drosophila labs fall under his jurisdiction. He wanted to know if we can access names of fly labs as GSA must collect this information. In response, Suzy pointed out that GSA collects this information with the express understanding it will not be shared, so this will have to be a new effort. This could be an action item for the new Fly Board in the coming year or two to organize our community, though this is also something that may be solved by Flybase colleagues. Michelle pointed out that an author is writing about a historical account of early days of fly genetics and molecular biology and is looking for resources. Programs of fly meetings from mid-1970s to early 1980s would be especially useful. Although abstracts are preferred, even titles and authors would be very useful. The Ecdysone workshops are of special interest. This information could be shared with Linda Restifo, LLR@arizona.edu who is collecting the information on behalf of a committee (Anna Chao, Greg Guild, Marc Muskavitch, Eileen Shore, Linda Restifo, and Mariana Wolfner).

The minutes were prepared by Harmit Singh Malik, with the help of notes from Sally Horne-Badovinac, and written reports submitted ahead of the Fly Board meeting by various committees. Harmit, Michelle, and Sally edited the report to correct any factual errors.

Agenda for Fly Board meeting at Dros23 held in Chicago.
1-4 PM Central Time Zone, Wednesday, March 1, 2023

Invite Link for zoom:

https://fsu.zoom.us/j/91773120940
Passcode (Drosophila)

1. Welcome and Introductions ~5 minutes

2. Approval of 2022 Board meeting minutes. The 2022 Minutes were attached to an email. The full set of reports and minutes are on the Fly board Wiki for those that would like to review the reports (https://wiki.flybase.org/wiki/FlyBase:Fly_Board) ~5 minutes

3. Brief review of reports (all attached in email; file called 'ReportsDros23')
   a. Fly Board elections (Mariana Wolfner) ~5 minutes
   b. Treasurer report with Trainee Award (Jessica Treisman will report by Zoom) ~10 minutes
   c. Sandler Award (Tim Mosca) ~5 minutes
   d. Image Award (Julie Brill) ~5 minutes
   e. Drosophila Community Service Award (Michelle Arbeitman) ~5 minutes
   f. GSA Conferences Report (Suzy Brown) ~10 minutes
   g. ADRC Dros23 report (Savraj Grewal) ~5 minutes
   h. TAGC with Dros24 planning (Harmit Malik) ~5 minutes
   i. Drosophila Information Services (Jim Thompson) ~5 minutes
   j. Finnerty Fly Board Report (Justin DiAngelo) ~5 minutes

10 minute Break will occur at ~2:00 PM

4. Resource Center Reports (~5-10 minutes for each Center)
   a. Bloomington Drosophila Stock Center (Kevin Cook)
   b. Vienna Drosophila Stock Center (Lisa Meadows)
   c. Drosophila Genomics Resource Center (Andrew Zelhof)
   d. DRSC/TRiP (Stephanie Mohr)
   e. Flybase (Susan Gelbart)
   f. Gene Disruption project and human cDNA project (Hugo Bellen, Shinya Yamamoto, Oguz Kanca)
   g. BDGP Fly Board Report (from Sue Celniker, Michelle will summarize)

5. Additional items
   a. Ad hoc committee on nomenclature (Kevin Cook) ~10 minutes
   b. Updates on Community Surveys (Michelle Arbeitman) ~5 minutes

c. Open Discussion for additional topics (for example, colleagues wrote Flyboard president about Flypapers Twitter bot not working; European Drosophila Society)

Report of the 2022-2023 FlyBoard Nominations/Elections Committee
Respectfully submitted by Mariana Wolfner on Feb. 8, 2023

The committee (constituted in October 2022) was: Alissa Armstrong, Erika Bach, Lydia Grmai, Ana-Maria Raicu, Michael Welte, and Mariana Wolfner (Chair).

Alissa had been on the nominating committee last year, and provided continuity as well as advice about what worked best then.

We had 8 positions up for election:
VP
Treasurer
Northeast Rep
Mountain Rep
Australia/Oceania Rep
PUI Rep
Graduate student Rep
Postdoc Rep

We began the process in early November 2022.
<u>For VP and Treasurer:</u>
All committee members generated names of potential candidates.

<u>Regional, PUI, Trainee Reps:</u>
Each committee member took charge of identifying (and giving an initial ranking of) ~4 potential nominees for one rep position. The trainees focused on the trainee reps. The faculty each focused on one regional or PUI Rep position, choosing constituencies with which they had the most familiarity, when possible.

Potential nominees for all positions were identified by: (1) Mariana asked the outgoing regional and PUI Reps for suggestions of potential nominees for their replacement. (2) We mined the list of community members interested in service positions (obtained from GSA). (3) We obtained nominations (including self-nominations) from the community following an email solicitation, and Twitter solicitations for the Trainee Reps. (4) In some cases, the previous unsuccessful candidates for these positions were considered. (5) Committee members came up with names themselves.

Lists of potential nominees were submitted to Mariana and circulated among the committee. We then met by Zoom to discuss the nominees for each position and put them in a rank-order. Attention was paid to nominees' career stage; diversity was also considered. In general, we avoided selecting non-tenured people as candidate for regional or PUI Reps, because of the workload and concern for effects on their tenure cases if potential promotion-referees might've been unhappy with a Board decision. We also avoided nominating relatively junior people to be candidates for officer positions. For officers, we also considered that experience/familiarity

with NIH/NSF to be very important. For Reps, we avoided nominating people who had previously been Rep for the same constituency, or had recently been a Rep (for any constituency). [One nominee had been a Rep for a different constituency, 2 decades ago. The committee decided that that was not disqualifying.]

We then contacted the top two nominees for each position. Each committee member contacted the top two nominees for their assigned Rep position; Mariana also ontacted the VP and Treasurer nominees. Potential nominees were referred to the FlyBoard Wiki site for more information, and we also answered their questions about the position.
[We were asked whether their travel costs to the ADRC/Board meeting would be covered, and replied "no". After checking with Michelle we assured those who could not travel that they could Zoom into the Board meeting if necessary.]

For six of the positions, the first two people we contacted agreed to run. For the other two position, one person declined to run, so we asked the next person on our ranked list, and they accepted.

Candidates were then asked for a statement and photo. Those were passed along to GSA by mid-December. [We asked GSA for assistance based on discussions with Mary and with Suzy Brown at GSA, with Brian Calvi, because they have the version of Survey Monkey software that prevents multiple voting (an open version had been used in the previous election).] Mary van Tyne at GSA kindly set up the ballot, sent out the emails alerting, and then reminding, the community to vote, and tabulated the results. We are very grateful for all her time and effort. The ballot (included at the end of this report) was sent out to the Fly community on January 9, 2023, with voting open for 2 weeks; a reminder was sent after 1 week; I believe we kept it open for a few additional days to be sure everyone had a chance to vote.

Results are on the next page. Mariana notified the committee of the results, and notified each candidate of the outcome on Feb. 5, 2023. She also notified Michelle Arbeitman (Board Prez), who then extended an invitation to the winners to attend the March 1, 2023 Board meeting.

For every position, the person who did not win the election was also considered outstanding by the committee. Upon hearing that they were not elected, all those individuals noted that they would be happy to run again for the position in a future election. The committee has passed along their names to the next committee Chairs to be considered for future election slates. We included on the list the names of alternate-nominees whom we also considered outstanding and appropriate for the position (and who did not decline when invited). [However, we did not pass along potential nominees for graduate student or postdoc rep as the people on our list will likely have moved out of their trainee positions by the time of the next election for those Rep positions.]

Results (winner in bold):

Vice President
Sally Horne-Badinovac: 189 votes
Marc Halfon: 142 votes
Blank: 118 votes

Treasurer
Jessica Treisman: 170 votes
Tina Tootle: 168 votes
Blank: 114 votes

Northeast
Barbara Mellone: 233 votes
James Walker: 78 votes
Blank: 139 votes

Mountain
Laurel Raftery: 196 votes
Marc Freeman: 125 votes
Blank: 130 votes

Australia/Oceania
Louise Cheng: 196 votes
Travis Johnson: 106 votes
Blank: 148 votes

PUI
Ruth Johnson: 205 votes
Matthew Wawersik: 109 votes
Blank: 136 votes

Postdoc
Shyama Nandakumar: 168 votes
Gavin Rice: 138 votes
Blank: 144 votes

Trainee
Shefali Shefali: 169 votes
Maria Porter: 158 votes
Blank: 123 votes

[There were approximately 450 votes; the numbers don't add up perfectly because not all fields were required (people could choose whether or not to vote for a particular position or to leave the ballot blank for it). This total is within range of most previous FlyBoard elections, except for last year's where the total was >700, but multiple-voting was possible (not that we would ever suggest that it happened).]

2023 Fly Board Election Candidates and Ballot

To cast your vote, you will need to create an account or log in at the link below using an email address and password. This helps the Fly Board ensure a fair election. You do not need to have an active GSA membership to vote in the election.

1. View the Candidates' statements
2. Click Access Ballot below
3. Click Login in the upper right corner to log into your account
4. Click on More under the heading "2023 Fly Board Election"
5. Click Apply
6. Vote
7. Click Mark as Complete

You will receive an email confirming your ballot has been submitted (please check the spam folder). If you have technical difficulties, email society@genetics-gsa.org.

Deadline to vote: January 23, 2023, 11:59 p.m. EST.

ACCESS BALLOT

Candidate Statements and Biographical Information

Read each candidate's statement and biographical information at the links below. Return to this list using the "Return to Top" links.

Vice President

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Marc Halfon

Professor, University at Buffalo Jacobs School of Medicine & Biomedical Sciences

Candidacy Statement

I've worked with *Drosophila* for over 30 years. My experiences as an undergraduate in Fotis Kafatos's lab at Harvard introduced me to the incredible power of *Drosophila* as a research organism and to the welcoming community of fly researchers. Over the years my conviction has grown that there is no better confluence of organism, community, resources, and breadth of research questions than what we find with *Drosophila*.

I am continually struck by the diversity of scientific questions addressed by the fly community. My own work has spanned the study of transcriptional mechanisms during oogenesis (undergraduate), to neuromuscular development (Ph.D. with Haig Keshishian at Yale), and to cell fate specification during muscle development (postdoc with Alan Michelson at Harvard). When the *Drosophila* genome was sequenced in 2000, I retrained in bioinformatics so I could take advantage of this powerful new resource. My laboratory at the University at Buffalo has helped pioneer methods for the computational identification of enhancers, and we use these methods to study questions of gene regulatory network evolution in flies and other insects, as well as continuing our studies of enhancer function and signal integration during *Drosophila* embryogenesis.

The fly community's century-old tradition of openness, collegiality, and inclusiveness is unparalleled. It's important that we maintain these values and continue our efforts to include marginalized groups. Our values are directly reflected in the extensive and freely-shared resources—the Bloomington stock center, FlyBase, the Gene Disruption Project, the DGRC, etc.—that boost the ability of the entire community to conduct ground-breaking research. I developed and maintain REDfly, a database of *Drosophila* enhancers. Through this effort we have annotated almost 40,000 validated enhancers and have contributed the bulk of the regulatory data contained in the FlyBase-maintained genome annotation.

My experiences as both a user and developer of community resources have taught me how difficult it is to keep these tools well-funded. FlyBase and other resources are experiencing steep funding cuts, imperiling their ability to remain current and provide the services on which we all rely. It's essential that we advocate for robust

support of these critical resources and to make the case for the huge return-on-investment provided by model-organism research. My experience with a broad array of funding bodies, including NIH, NSF, and USDA, positions me well to aid in this effort.

The past several years have been a time of changes and challenges for scientists. We celebrated the triumphs of both basic and applied research in the response to the COVID19 pandemic, but also witnessed deep denialism of scientific facts among segments of the population. Education and public outreach must remain an important part of our collective mission.

When the Fly Meeting resumed in person last spring after a two-year hiatus, the sense of joy was palpable. This is truly a special community, and I can think of no better way to contribute and to give back than to represent all of you as President of the Fly Board. It would be a privilege and an honor to serve.

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Sally Horne-Badinovac

Professor, University of Chicago

Candidacy Statement

My scientific journey began in the zebrafish community, first as an undergraduate researcher with John Postlethwait at the University of Oregon and then as a graduate student with Didier Stainier at University of California, San Francisco. In the Stainier lab, I became fascinated with how the collective behaviors of epithelial cells shape tissues and organs during development. Consequently, I spent much of my time reading papers from fly labs where the best epithelial work was (and still is) being done. I marveled at the tools and resources that had been built by fly researchers and the deep scientific insights they revealed. When it came time to choose a postdoctoral lab, I knew that this was the type of work I wanted to do. I joined David Bilder's lab at UC Berkeley and became an active and highly enthusiastic member of the vibrant fly community I had admired from afar. Since starting my lab at the University of Chicago in 2008, my team has studied how epithelial cells coordinate their movements for collective migration and how this motion synergizes with new protein secretion to build a highly structured extracellular matrix that directs organ morphogenesis.

Science is a social endeavor, and the impact of the work from our individual labs depends heavily on the resources that the wider community provides. I have worked to support and strengthen our scientific community on multiple fronts. I co-organized both the Fly Meeting and the Santa Cruz Developmental Biology Meeting in 2022, and I was elected to be Chair of the Directed Cell Migration Gordon Conference in 2025. I am on the Editorial Board for *Development* and work as an Associate Editor for *Cells & Development*. Finally, I have been a faculty member in the Embryology Course at the Marine Biological Laboratory, and I am co-director of University of Chicago's T32 Training Program in Developmental Biology. As Fly Board President, I would advocate for increased funding for model organism databases and labs, seek to recruit young researchers to the field, and strive to make the fly community an even more inclusive and welcoming place to do research.

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Tina Tootle

Professor, University of Iowa Carver College of Medicine

Candidacy Statement

Tina Tootle received her BS in Microbiology from the University of Maryland, College Park (1998), where she earned High Honors for her thesis studying plant-pathogen interactions in *Arabidopsis thaliana*. She then served as a research assistant in the laboratory of Soichi Tanda, where she fell in love with *Drosophila* as a model system. Tina studied Ras/MAPK signaling and the Retinal Determination Network in *Drosophila* during her graduate studies with Ilaria Rebay at the Massachusetts Institute of Technology (1999-2004). As a postdoctoral fellow with Allan Spradling at the Carnegie Institution for Science in Baltimore, she began her studies on prostaglandin signaling (2004-2009). Since starting her own lab at the University of Iowa in 2009, Tina has focused on understanding how prostaglandins regulate the actin cytoskeleton to control *Drosophila* follicle or egg chamber morphogenesis. These studies have led her to exam the roles of actin and actin binding proteins in the nucleus.

Tina has been active in graduate training and diversity, equity, and inclusivity work. She co-developed and served as the Director of the Cell and Developmental Biology Graduate Program from 2017-2022. She teaches graduate level Principles in

Molecular and Cellular Biology and. Tina also served as the departmental Director of Diversity and the Chair of the Basic Sciences Diversity Taskforce from 2014-2021. She is active in outreach and uses these programs to both increase the diversity of individual pursuing biology-related creases and increase appreciation for the value of using *Drosophila* for biomedical research.

Tina has also been an active participant in the scientific community. She has served as part of the organizing committee for the Midwest Drosophila Research Conference, the Midwest Representative to the FlyBoard from 2018-2021, and numerous FlyBoard Committees including the Election Committee and the Trainee Awards Committee. She is currently on the *Drosophila* Image Awards Committee. Tina is an associate editor at Genetics and serves on the GSA Publications Committee. She is the co-editor of the Springer Nature, Methods in Molecular Biology: *Drosophila* oogenesis book that will be published in early 2023. She also serves on both NSF (MCB) and NIH study sections. Tina is dedicated to improving biological education to better prepare students for the array of career options, increasing the diversity of students pursuing degrees and careers in biological sciences, and being an advocate for model organism research.

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Jessica Treisman

Professor, New York University Grossman School of Medicine

Candidacy Statement

Jessica Treisman was born in Oxford, England, and grew up there and in Vancouver, Canada before returning to Oxford University for her BA, where she fell in love with flies after reading early papers by Lawrence, Morata and Garcia-Bellido about clonal analysis. She moved to New York in 1985 to do her PhD in Claude Desplan's lab at Rockefeller University, where she studied how transcription factors pattern the *Drosophila* embryo. She continued in flies for her postdoctoral research in Gerry Rubin's lab at UC Berkeley, where she studied genes that affect patterning, cell division and cell shape in eye development. In 1996 she started her own lab in the Skirball Institute and Department of Cell Biology at NYU School of Medicine, where she is now a Professor and director of the graduate program in Developmental Genetics. Her lab has used the eye and wing imaginal discs and the visual system to study the molecular mechanisms of cell-cell signaling, cell fate determination, and synapse formation. Fly genetic screens have taken her into many interesting areas of biology, and she enjoys the challenge of constantly learning about new fields. Jessica was a co-organizer of the 2007 fly meeting in Philadelphia, and served on the organizing committee for the Crete meeting from 2012-2016 and as mid-Atlantic representative on the *Drosophila* Board from 2013-2016. She was Treasurer for the Harvey Society from 2010-2013, and has been the Fly Board Treasurer for the last three years. During this time, a new outreach award to promote diversity, equity and inclusion among *Drosophila* trainees was approved by the Board, and Jessica chaired a committee to oversee its distribution. She would be happy to serve another term in this role.

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Barbara Mellone

Professor, University of Connecticut, Storrs

Candidacy Statement

I am a Professor in the Genetics and Genomics division of the Molecular and Cell Biology Department at the University of Connecticut, Storrs. The goal of my research program is to understand the molecular mechanisms underlying genome organization and inheritance. We focus primarily on the centromere, an essential chromosomal locus that mediates accurate chromosome segregation during mitosis and meiosis. Since its inception in 2009, my laboratory has elucidated key aspects of centromere assembly, DNA sequence composition, and evolution, while further enhancing *D. melanogaster* as a powerful model system for centromere biology.

My passion for chromosomes and genome inheritance started when I was an undergraduate student at the University of Milano, Italy, where I worked on budding yeast DNA replication. I left my home country to pursue a PhD with Robin Allshire at the MRC Human Genetics Unit in Edinburgh, Scotland, studying pericentric and centromeric chromatin in fission yeast. After completing my PhD, I became very interested in how centromeres are specified and decided to pursue this exciting question in *Drosophila*, because of its complex chromosomes and myriad of molecular tools. As a postdoc with Gary Karpen at University of California, Berkeley, I identified key centromere chromatin effectors at a time when

little was known about the mechanisms of centromere chromatin formation in any organism. Since starting my position as an independent investigator, my lab's efforts resulted in several discoveries, including the identification of the chaperone that recognizes and deposits the essential centromeric histone CENP-A. My early independent work was recognized by the American Society of Cell Biology Women in Cell Biology "Junior Award for Excellence in Research". A recent contribution I would like to highlight is the discovery, through a collaborative effort, of the sequences and chromatin organization of all *Drosophila* centromeres. This work fundamentally shifted previous assumptions about the sequence composition of centromeres and generated the first reference to include annotated centromeres.

Since adopting *Drosophila* as my model organism of choice, I have been a regular attendee of the *Drosophila* Research Conference and was an invited plenary speaker in 2019. I was also a member of the GSA Larry Sandler Award committee in 2018 and 2019 and the chair in 2020. As chair, I introduced a new format for the letter of nomination for this award to the board in an effort to reduce bias, which was adopted and has been used since. During the height of the pandemic, I organized multiple virtual meetings in an effort to provide presentation opportunities for trainees.

In all of my professional endeavors, I strive to improve diversity and equity in science and academia and make every effort to combat discrimination and bias. I am passionate about mentoring students from historically underrepresented groups and have hosted several high school and undergraduate scholars through programs at my university for students from historically excluded groups in STEM fields. I am an ASCB MOSAIC mentor, I am very active in my department's diversity, equity, and inclusion committee, and other organizations and task forces at my institution.

Over the years, I have greatly benefited from the generosity and collegiality of the fly community. I am excited at the prospect to serve the community as Northeast regional representative to the Fly Board.

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James Walker

Assistant Professor, Harvard Medical School

Candidacy Statement

I am dedicated to harnessing the potential of *Drosophila* models to improve patient outcomes associated with neurological disease. I am an Assistant Professor in the Center for Genomic Medicine, Massachusetts General Hospital (MGH) and Harvard Medical School. My lab utilizes *Drosophila* as a model system to study neurological diseases, both to elucidate pathogenic mechanisms and to develop potential therapeutic strategies. I adopted *Drosophila* as my model organism of choice, after my PhD at Cambridge University. While studying the regulation of the cell cycle in the eggs of *Xenopus* and marine organism gave me a solid foundation in biochemistry and molecular biology, I recognized the immense power of fly genetics while attending seminars in the neighboring Department of Genetics. For my postdoc, I worked with both Iswar Hariharan and Andre Bernards at MGH to develop fly models of neurofibromatosis (NF). I had the opportunity to lead my own lab at MGH in 2016, and continue to use flies to study NF, in addition to other neurological disorders. I have been particularly grateful for the successful and productive interdisciplinary collaborations my lab has with clinicians, chemists, and human geneticists, using fly biology to add new dimensions to other biomedical projects.

I have incorporated *Drosophila* into my practical classes while teaching at Harvard College and am always heartened by how readily students see the advantages of using flies in research. As a faculty member, I seek to enhance diversity, equity and inclusion in both the classroom and the laboratory. I am passionate about mentoring the next generation of researchers and several Research Technicians who have worked in my lab have gone on to graduate studies and joined *Drosophila* labs. My lab has an active outreach program, organizing educational programs for local disease foundations in which lab members explain the usefulness of *Drosophila* as a model for studying human diseases, as well as participating in hospital open days when we welcome patients and families into our Fly Room to view first-hand our model system.

I am one of the founding members of the Boston Area Drosophila Meeting. Since 2016 we have organized an annual event at different universities and colleges in the greater Boston area, bringing together *Drosophila* researchers from different institutions to share their latest findings and expertise. We focus on encouraging post-docs, students, and technicians to give presentations in a friendly atmosphere to highlight their research. The all-day programs include poster sessions and breakout groups during which junior researchers meet with faculty and the meetings have resulted in multiple collaborations between different labs and institutions. This has been particularly instrumental in enabling new faculty from smaller teaching colleges in Massachusetts to connect with established investigators in and around Boston. The most recent meetings have attracted participants from across New England, including New Hampshire, Connecticut, and even New York.

As a member of the Fly Board, I would be able to draw upon my networking skills and connections in the *Drosophila* community of the Northeast states. My goals would be to encourage greater inclusion of all institutions and viewpoints, to continue to advocate for the importance of fly research in biomedical research to disease foundations and the public and seek new ways of attracting young investigators to the field.

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Marc Freeman

Director and Senior Scientist, Vollum Institute, Oregon Health and Sciences University

Candidacy Statement

I have worked with Drosophila my entire career, beginning in John Carlson's laboratory (olfaction), then in Chris Doe's (embryonic neurogenesis) and on my own since 2003. We study glial cell development and function, and neuron-glia interactions in the developing and mature nervous system. In 2008 we started working with mouse models also, but quickly realized that was silly—they are too slow, too expensive, questions are answered there with far less precision, and there are countless exciting questions left to answer in flies, so we abandoned that idea. Now we just try to make friends with good mouse colleagues and synergize with them. Our group combines classical forward genetic screens and genetic mosaic approaches with all the wonderful cutting-edge tools the fly community generates.

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Laurel Raftery

Professor, University of Nevada, Las Vegas

Candidacy Statement

I became convinced of the power of flies as system to discover the unknown, when I read Nüsslein-Volhard and Wieschaus's seminal 1980 paper describing the classes of genes that control segmentation. I was a graduate student at the University of Colorado, Boulder, using bacterial genetics to study translational accuracy at that time, and switched to *Drosophila* genetics as a postdoctoral fellow with William Gelbart at Harvard. There we used maternal effect modifier screens to identify genes required for signal transduction by a fly Bone Morphogenetic Protein, most notably identifying the founding member of the Smad protein family, Mad. Surprisingly, my work on *Drosophila* BMP signaling led to my first faculty position at the Cutaneous Biology Research Center of Massachusetts General Hospital/Harvard Medical School. Working with flies, my lab could follow the surprises we uncovered, moving ultimately to investigate BMP signaling in morphogenesis of the fly ovarian follicular epithelium. During the years my lab was in a teaching hospital, I became convinced in the importance of undergraduate education as providing foundational knowledge for our future healthcare providers and for all voters in the US. I left Boston to return to the US intermountain West, where I had spent my youth and years of graduate education. I am now a Professor at the University of Nevada, Las Vegas, where I teach Developmental Biology to first generation college students, train undergraduate research volunteers in my lab,

and mentor graduate students who were themselves first generation college students. I was a founder of Science Café Las Vegas, which brings local scientists to discuss science with members of the broader Las Vegas community. I have attended the *Drosophila* Research Conference nearly every year since beginning my post-doc, and I was co-Organizer for the 39th ADRC in 1998. I have also organized a regional Society for Developmental Biology in 2002, and I served on the FASEB Scientific Advisory Committee for the Summer Research Conferences from 2010–2021.

As funding for model system community resources has dwindled, the role of the Fly Board has grown as a voice for the *Drosophila* community, particularly in defining community-wide priorities for resources such as Flybase. If I am elected to the Fly Board, my role of representing a segment of the fly community would be central. I will advocate for affordable and accessible locations for the fly meeting, so that we can continue to attract international attendees from all continents and to send undergraduate and graduate students to present their research to an international audience. With new methodologies, there will come opportunities for new genome-wide resource development, again challenging the Fly Board to fairly represent the wishes of the research community. I would be proud to serve as regional representative.

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Louise Cheng

Associate Professor, Peter MacCallum Cancer Center

Candidacy Statement

I grew up in Nanjing, China, and received my undergraduate degree in Sydney, Australia. I fell in love with Developmental Biology during an exchange year at Kings College London. This prompted me to first work as a research assistant in the lab of Patrick Tam at the Children's Medical Research Institute in Sydney in the field of mouse gastrulation and then to work on chick somite development during my PhD studies at Kings College London in the lab of Suzanne Dietrich. For my postdoctoral studies, I changed model organisms, and worked on *Drosophila* neuroblast proliferation in the lab of Alex Gould at the National Institute for Medical Research. *Drosophila* really suited my temperament, as it allowed me to test multiple ideas simultaneously and quickly.

I moved back to Australia to set up my independent laboratory at the Peter MacCallum Cancer Center in 2012, a research institute embedded within a cancer hospital. My lab studies growth, nutrition, and organ size control using *Drosophila* and patient samples. We are interested in understanding how the microenvironment influences the growth of tumors and how neuronal cell identity is maintained in the developing CNS to inhibit dedifferentiation, a process implicated both in regeneration and in cancer. More recently, we have become interested in cancer cachexia, a metabolic syndrome affecting around 30 percent of

cancer patients and 80 percent of late cancer patients, where tumors induce the wasting of muscle and fat. We have coupled genetic studies in flies with validation studies in matched tumor/adipose/muscle samples from cancer patients, to discover conserved mediators of this disease.

I have served on the board of the Asia-Pacific Drosophila Research Conference since 2019. Along with my co-organisers, we are putting together an exciting program for APDRC6 in Cairns, Australia (July 23-27, 2023), which involves a great scientific program, as well as an outreach program for school students. I am the co-program head for the Australian Transgenic Drosophila Center, and I have co-organised the Australian Fly Meeting from 2018 to 2020. I serve on the editorial board of four scientific journals. I am passionate about science outreach, and I have been involved in advocating for basic research and increasing science education in general (to school students and the general public). As a Fly Board member, I will continue to advocate for these causes close to my heart, both through my connections within the *Drosophila* community in Australia, as well as through my contact with patients through my clinical links.

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Travis Johnson

Lecturer and Group Leader, Monash University

Candidacy Statement

I am excited to have this opportunity to serve the international *Drosophila* community. Despite being a junior group leader, I have been involved in *Drosophila* research for over 20 years – from humble beginnings as a fly bottle washer to recently starting my own group in 2018 at Monash University in Melbourne, Australia. I obtained a PhD in 2010 studying the molecular and population genetics of thermotolerance adaptation in wild *Drosophila*, then moved into developmental genetics and cell signalling as a postdoc with Coral Warr. We investigated spatial control mechanisms in embryonic patterning and chased several genes across a variety of other tissues and life-stages. My lab now continues this work and has further expanded to studying cell signalling in blood cell fate, as well as applying *Drosophila* as a disease model for both treatment exploration and understanding pathogenesis.

Down here in Oceania and Australia, we face many diverse challenges in our fly research, such as the large distances between our groups and difficulties importing strains, among others. With this role I am determined to find ways to minimise the burden of these issues, in part by connecting and working with other continents with similar challenges. I will also seek to further galvanise our region's growing and changing fly community – which I believe is particularly important as we emerge post-Covid. Using the close ties I have with many of the fly groups in our region and with my enthusiasm for fly advocacy, I hope to give back to the community that has been so kind to me over the years.

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Ruth Johnson

Associate Professor, Wesleyan University

Candidacy Statement

After completing an undergraduate degree at a 27,000 student PUI in South Africa, a PhD at an R-1 equivalent institution in the UK and postdocs at two medical schools in the US, I chose to establish a research group at a PUI and embrace a 'teacher-scholar' PI model because I adore the vibrancy and 'potential energy' of undergraduate students. I am an Associate Professor of Biology at Wesleyan University in Connecticut, and my research group uses the fly eye as a model to elucidate the conserved mechanisms that organize cells to correctly shape an organ. I couldn't imagine doing this work with another model organism: the genetic tools and reagents developed by our fly community, coupled with the sharing-philosophy of our community, make the fly an accessible model, especially to scientists with limited resources. Like many of my fly-pushing peers at PUIs, I find that there are few biology concepts that we teach in our classrooms that we cannot bring alive with examples from *Drosophila* research, and the research experience undergraduates gain in our PUI labs provides them with inspiration, confidence, and foundational tools that can be applied to multiple science (and other) career tracks. I'm always delighted by what I learn from undergraduate students. They can be our 'fingers on the pulse' on societal issues that our *Drosophila* community should take note of. For example, my undergrads challenged my complacency on diversity, and challenged my notion of gender, many years before these became

mainstream topics of discussion. Further, our undergrads remind us to use our taxpayer-backed funding effectively and with the future and their generation in mind. The rewards of teaching and training undergraduates at non-R1 institutions can, however, be coupled with challenges: lower funding, less sophisticated equipment, shorter-term research teams, and varied demands on our time can dampen our publication metrics, and these challenges require PIs at RUIs to be resourceful and bold. As PUI representative to the Fly Board my goal will be to represent these challenges and promote the joy and success of our undergraduates and PUI-PIs within our *Drosophila* community.

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Matthew Wawersik

Associate Professor, College of William and Mary

Candidacy Statement

It is an honor to be nominated as Fly Board representative for Primarily Undergraduate Institutions. I am an Associate Professor of Biology at the College of William & Mary, a public liberal arts research college in Williamsburg, Virginia. I have been an active member of the *Drosophila* research community for >20 years beginning with a post-doc in Mark Van Doren's lab at Johns Hopkins University. My

lab's current research focuses on understanding mechanisms of stem cell development and homeostasis, using *Drosophila* testes as a model system. This work is conducted by teams of undergraduate and master's students, who have greatly benefited from thoughtful advice from our nurturing community over the years. In addition to conducting research that provides a training-ground for our next generation of scientists, I am also engaged in science education research through the Genomics Education Partnership that is focused on understanding best practices for implementation of course-based undergraduate research experiences (CUREs), as well as expanding the network of students gaining research exposure through these genomics CUREs.

I am indebted to the *Drosophila* research community for providing so many experiences that have benefited my career and the careers of the many undergraduate and master's students that I teach and mentor. These opportunities include oral presentations given by my undergraduate students at PUI platform sessions, the ability to network with other PUI faculty engaged in science education research, and of course, the opportunity to share our lab's research findings with the broader scientific community. For many of my undergraduates, the Fly Meeting has provided the first opportunity to discuss their work on a national stage, and the fly community never fails to provide rigorous, yet supportive, feedback.

As PUI representative to the Fly Board, I would be committed to ensuring continuance of the opportunities that have been so beneficial to me and my students. In particular, I would work to support and highlight opportunities for undergraduate researchers to present and gain feedback from a range of faculty in our community. Maintaining opportunities for faculty and aspiring teacher-scholars to share their research and experiences in science education would also be a focus. Finally, it is critical that students with more limited means have knowledge of and access to travel grants necessary for them to gain exposure to research as a career.

I look forward to the chance to give back to our community as a member of the Fly Board!

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Shyama Nandakumar

Postdoc, Cornell University

Candidacy Statement

I am writing to express my interest in serving as the postdoctoral trainee representative on the Fly Board. I am currently a postdoctoral associate in the lab of Nicolas Buchon at Cornell University. I graduated with a PhD from the University of Michigan in 2020, where I was advised by Laura Buttitta in the department of Molecular, Cellular and Developmental biology (MCDB)—a vibrant department which focuses strongly on basic biology research using model organisms where I was first introduced to *Drosophila melanogaster* as a model organism. I completed my undergraduate education in India at SRM university, during which I spent two semesters abroad to gain research experience: one in Sweden at Umea University and another (my Bachelor thesis work) at Brigham and Women's Hospital in Boston. My long term career goal is to return to India to run an independent research program at an academic research institution, using primarily *Drosophila.*

In addition to my broad interest in science, throughout my education, I have taken service seriously and have always taken an active role in engaging with the wider

scientific community. In my years as a junior graduate student, I became involved with the departmental student council, and I was instrumental in organizing a peer mentorship program named GradGab which paired incoming graduate students with a more experienced student mentor to ensure that incoming students have a support system while they navigate the transition into graduate school. I also served as the International student representative on MCDB's Admissions committee for two years. As the Vice President and later President of the MCDB student council, I organized several years of the departmental recruitment events for both the traditional PhD program and the Pathways Masters program. I also served as the graduate student representative on the MCDB Faculty search committee for the 2018-2019 academic year. In addition to departmental service, as a Barbour Scholar, I served on several panels for Rackham Graduate School's outreach initiatives. I have also organized and participated in scientific outreach initiatives such as University of Michigan's FEMMES (Females Excelling More in Mathematics Engineering and the Sciences) and events at the Ann Arbor Hands On Museum where I have taught children basic cell biology and fruit fly genetics. More recently I have participated in organizing Cornell's department of entomology's annual event 'Insectapalooza'—an event which showcases arthropod research to the public. I strongly believe that outreach activities like these are crucial to shaping and influencing the public perception of science, and current times highlight the importance of this more than ever. I have also become engaged with the broader scientific community by organizing conferences and meetings. As a graduate student, I was elected to chair the Gordon Research Seminar on cell growth and regulation for 2021 (delayed due to pandemic to 2023). As a postdoc, I am also part of the organizing committee for the first international conference on polyploidy across the tree of life—a conference intended to bring together researchers using diverse model and non-model organisms to study whole genome duplication, which will also be held in 2023. At Cornell, I have also helped organize the monthly intra-mural meeting of *Drosophila* researchers named 'Superfly'.

Throughout my higher education, and particularly since I began working with flies, I have found that having a supportive network of colleagues is crucial to trainees' success, and I strongly believe in contributing to this by building a sense of community at multiple levels. *Drosophila* are one of the most accessible and

successfully used model organisms for many reasons, including the tight-knit body of scientists who build resources that the entire community can benefit from. The ramifications of the COVID-19 pandemic and many other ongoing issues that directly impact the lives and careers of graduate students and postdocs have made it clear that advocating for trainees' needs are critical for the career development and ultimate success of future generations of scientists. As an international trainee with scientific experience across three continents, as well as my commitment to service, I believe I am uniquely qualified for this position. I will strive to be a vocal and effective representative for postdoctoral trainees on the Fly Board.

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Gavin Rice

Postdoc, University of Pittsburgh

Candidacy Statement

I am a postdoc at the University of Pittsburgh studying the evolution of genetic networks and its role in the generation of novel traits in *Drosophila*. I am honored to be nominated to be a postdoctoral representative for the Fly Board. I deeply care for our community of *Drosophila* researchers and advocate for early career researchers.

My love of *Drosophila* has always been tied to the amazing scientists that make up the fly community. My first scientific conference was the *Drosophila* Research Conference. As a second-year graduate student I was captivated by how every talk, even in fields well outside my own, felt connected to my work through the genetic techniques that we use. Beyond that I was astonished by how friendly everyone was and how willing they were to share insights and resources. This friendly community was especially important to me as I have a speech disability known as a stutter. My disability has made it difficult for me to both share my research and engage others about theirs during my early career in graduate school. The Drosophila community has been relentlessly encouraging in my career, giving me opportunities to present my work and find collaborators that share a passion for building shared resources.

I have taken this community mindset to my work with the Genetics Society of America. I have served as an early career representative to the GSA Board of Directors as well as co-chair of the Steering Committee of the GSA's Early Career Leadership Program. As a co-chair I heard members say that they felt disconnected from the larger GSA organization. To address this, I worked with Dr. Jessica Vélez, our program manager, to set up short zoom meetings between Early Career Leadership Program members and the GSA Board. During these meetings Board members shared career advice on specific topics requested by the Early Career Leadership Program members. These meetings allowed ECLP members to feel seen by the Board and gave them a connection to those running the organization.

I have also worked locally at the University of Pittsburgh to connect postdocs to our faculty members. One initiative that I organized was to help postdocs receive feedback on their faculty applications. Postdocs, especially those that feel disconnected from a departmental community, can feel reluctant to ask for feedback from faculty they do not know personally. However, feedback from faculty outside of their immediate expertise can be vital in crafting a clear and engaging application. I also understood that faculty have heavy restraints on their time and that those that seem more approachable can be overwhelmed with requests for help. I organized a workshop where faculty volunteer to review job packets and are matched with postdocs in the department. This allowed faculty to

volunteer to review the number of applications that they felt they had time for and allowed postdocs to receive feedback from, on average, three faculty members without feeling that they were burdening faculty. This program is in its second year and has received great feedback from both postdocs and faculty. I would be excited to support venues for early career researchers to feel valued and supported by senior members of our community as a postdoctoral representative to the Fly Board.

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Maria Porter

Graduate Student, University of Mississippi

Candidacy Statement

I received my undergraduate degrees (B.S. in Biology and B.A. in Psychology) from Converse College in South Carolina. My interest in working on a model system led
me to Gregg Roman's lab at the University of Mississippi, where I am working on understanding the role of circadian modulation of short-term olfactory learning in *Drosophila melanogaster*. My leadership roles have included serving in the Biology Graduate Student Society at the University of Mississippi starting in 2019. I started

as the Activities Coordinator because I enjoy brainstorming events and seeing them come to fruition to unite members in essential discussions or fun events for everyone to enjoy. I was elected President in 2021, where I budgeted and was awarded over $2,500 for student activities, including an invited seminar speaker. I also spearheaded the revision and addition of several positions into the constitution to better serve the Biology Graduate Student members. This year, I decided to take a step back and run for Vice President to aid the new President and new officers in their positions while providing open communication between officers and members. My goal is to determine if there are any other modifications to current roles that may be needed and continue to listen to the biology graduate students in their needs to be successful in the graduate program. Furthermore, I have served as a University of Mississippi Graduate School Ambassador, where I had several duties to increase recruitment, including serving as an ambassador of the Biology Graduate Program. I have also participated in three hiring committees to assist in finding the best candidate for the position.

My involvement in the *Drosophila* community has involved sharing essential topics, papers, and methods through Twitter and making connections through this platform since the pandemic prevented travel or in-person gatherings for the last few years. I have connected with several Drosophilists this way and have enjoyed problem-solving collaboratively online. I have found that the *Drosophila* community is very welcoming and eager to help. Because of this, I felt confident to reach out to Drosophilists whenever I had a question and received timely and helpful suggestions. I am deeply thankful to Daniel Ranson, who helped me with my *Drosophila* brain imaging issues during the pandemic. I also met one of my collaborators, Chris Vecsey, this way and recently collaborated to have two protocols submitted to the Cold Spring Harbor's second edition of *Neurobiology: A Laboratory Manual*. These protocols are for anyone interested in analyzing positional preference, sleep, and circadian parameters, using the *Drosophila* Activity Monitors (DAM) System. I hope the *Drosophila* community will find these protocols helpful.

I am interested in becoming the graduate student representative because I believe this position will further allow me to connect with Drosophilists worldwide. As I

near the end of my PhD program, I would like to foster more connections since I enjoy collaborating and learning about other researchers' projects. In this position, I hope to address and improve any graduate student concerns in the *Drosophila* community while fostering communication between all Drosophilists, from high school students to retired researchers. In this way, I hope to make a change for the better in our community and provide everyone with lasting connections. Thank you for the opportunity.

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Shefali Shefali

Graduate Student, University of Indiana

Candidacy Statement

I grew up in Patna, a small city in India. I moved to Kolkata to pursue my undergraduate degree in Biochemical Engineering (2016-2020) from Jadavpur University, which is one of the premier universities in India. My first-year coursework initiated my fascination towards biological research. Acting on my nascent interests, I did a few summer projects in some
labs at InStem, a premier Indian biological research institute. These experiences enhanced my

interests in the areas of developmental biology and inspired me to pursue graduate studies. Then, I applied for graduate school and moved to the US for my graduate studies at Indiana University, Bloomington. Currently, I am a third year PhD student in Jason Tennessen's lab. I am working on understanding how the cross-talk between glucose metabolism and growth signaling affects fly development.

During my undergraduate days, I was strongly involved in several aspects of community building at my engineering school. I served as a member of organizing committees for various technical-fests and cultural events. Moreover, I was an active member of educational groups which provide curiosity-driven education in Indian rural areas. While I was pursuing these roles, I began to understand the strengths of creating collaborative platforms for scientific problem solving. When I started my graduate school at University of Indiana, I acted on these ideas and discovered my interests toward creating a diverse and inclusive environment. During my graduate studies at the Tennessen lab, I have tried to integrate equity in all aspects of my work—from research training to teaching assignments. In my department, I have worked toward starting a Biology International student organization to create a welcoming workplace for international graduate students by organizing orientation events and other community building events like picnics.

It would be a great honor to serve as the graduate student representative for the Fly Board. I am excited for the opportunity to contribute toward creating an impactful platform to instill integrity and inclusion in fly science. To begin with, I would be interested in working toward equity in availability of fly-resources to trainees from diverse backgrounds and communities. I would also affirm my commitment toward equity by promoting transparent discussions on issues like lack of fellowships for international students, hiring biases, etc., to strengthen the intellectual diversity and core goals we have as scientists and educators. Since I am a graduate student from the COVID era, I have had limited opportunities for interacting with graduate students and professors from other universities. If selected, I would wish to focus on building strong connections among fly graduate students, so we can all communicate with each other—not only regarding research, but also other grad-life issues. I want to contribute to fostering engagement within

the fly community by organizing grad-student monthly or bimonthly virtual hangouts. I hope these steps shall improve quality and application of research science. I strongly believe this position will serve as an important learning experience for me. I want to use this opportunity to learn about existing initiatives, work on new ideas with the global fly community and work toward creating a better scientific culture. I believe my experiences from my undergrad time and grad school have strongly prepared me for a shared vision for change.

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Treasurer's Report 2023 (Jessica Treisman)

Activity and balances for the *Drosophila* Reserve Fund, Larry Sandler Fund and Victoria Finnerty Fund

Drosophila Custodial Reserve Investment Activity (Life Strategy Moderate Growth Fund)

Date	Description	Reserve Funds Invested	Dividends & Capital Gains	Awards	Withdrawals & Fees	Fair Market Value Adjustments	Balance
7/1/18	initial investment	161,427.07					161,427.07
7/1/18	custodial fee 2018-2019				(2,421.41)		159,005.66
12/31/18	dividends and capital gains		4,553.40				163,559.06
12/31/18	market value adjustment					(12,191.68)	151,367.38
2/12/19	balance of reserves invested	3,048.00					154,415.38
6/28/19	dividends		1,831.37				156,246.75
6/28/19	custodial fee 2019-2020				(2,343.70)		153,903.05
12/27/19	dividends		2,666.47				156,569.52
12/27/19	capital gains		116.82				156,686.34
12/31/19	market value adjustment					25,558.84	182,245.18
6/30/20	dividends		1,488.44				183,733.62
6/30/20	custodial fee 2020-21				(2,766.54)		180,967.08
12/31/20	dividends		3,512.47				184,479.55
12/31/20	capital gains		3,620.12				188,099.67
12/31/20	market value adjustment					16,801.96	204,901.63
1/2021	Fly Board Awards			(6,483.50)			198,418.13
6/30/21	dividends		1,526.30				199,944.33
6/30/21	custodial fee 2021-22				(2,999.17)		196,945.26
12/31/21	dividends and capital gains		8,732.98				205,678.24
12/31/21	market value adjustment					11,150.00	216,828.24
1/2022	Fly Board Awards			(10,379)			206,449.24
6/30/22	Custodial fee 2022-23				(2,923)		203,526
12/31/22	Dividends and capital gains		3,319				206,845
12/31/22	Market value adjustment					(42,833)	164,013
1/1/23	Return of unused award - Williams			1,460			165,473
As of 2/3/2023	Market value adjustment					10,332	175,804

2022 award amount was for 5 awards of ~$2000 each, funded jointly from the Larry Sandler Fund and the *Drosophila* Reserve Fund. Following the new Trainee Awards Policy, we used approximately 5% of the value of the Reserve Fund. It should be possible to make 5 awards again in 2023, using 5% of the value of the Reserve Fund ($8,790) and $1210 from the Sandler Fund.

Larry Sandler Fund (Wellesley Income and Wellington Funds)						
	Investment Gain/(Loss)	Awards	Travel Expenses	Other Expenses	Net Surplus/(Deficit)	Fund Balance
2003					(2,431)	28,377
2004					432	28,809
2005	1,076		1,208	37	(169)	28,640
2006	1,963		469	15	1,479	30,119
2007	2,187		501	15	1,671	31,790
2008	(859)		441	20	(1,320)	30,470
2009	1,198		768		430	30,900
2010	947		1,482		(535)	30,365
2011	555		420		135	30,500
2012*	23,821		826		22,995	53,495
2013	6,847		1,171		5,676	59,171
2014	4,865		580		4,285	63,456
2015	369		428		(59)	63,397
2016	5,716		709		5,007	68,404
2017	8,201		1,014	112	7,075	75,479
2018	(2,212)		753	107	(3,072)	72,407
2019	14,009		573	107	13,329	85,736
2020	8,206		-	113	8,094	93,829
2021	13,456	1,500	-	113	11,843	105,673
2022	(12,910)	1,500	1,080	113	(15,603)	90,070
As of 2/7/2023	3,265				3,265	93,335

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

2021 and 2022 Fly Board Awards funded jointly with the Drosophila Reserve Fund.
No travel expenses for 2020 or 2021

	Vicky Finnerty Memorial Fund (Wellington Fund)					
	Contributions	Investment Income	Fees	Transfers from Meetings	Awards	Fund Balance
2011	3,726			-		3,726
2012	4,102			6,000	5,178	8,650
2013	-			6,000	7,150	7,500
2014	3,960			6,000	8,940	8,520
2015	1,324			6,000	4,705	11,139
2016	886			6,000	3,795	14,230
2017	1,500			6,000	3,844	17,886
2018	2,560			6,000	4,945	21,501
2019	2,121			6,000	4,800	24,822
2020	1,730	1,562	323	-	-	28,114
2021	500	4,099	385	6,000	941	37,063
2022	400	(3,744)	329	6,000	5,989	33,401
As of 2/3/2023		934		6,000	5,999	34,336

Investment account established October 2020
2023 Awards: 14, totaling $5,999

Use of the Reserve and Sandler Funds for Awards

A new policy was adopted in 2020 stating that the *Drosophila* Reserve Fund will be used to support efforts to increase trainee participation, equity and diversity in our community, with the goal of generating and maintaining a vibrant *Drosophila* research community. The plan was to use approximately 5% of the total fund balance each year based on a three-year average return rate, with the amount being approved at the Board meeting. Suggestions for use of the funds included travel support to attend the GSA *Drosophila* Research Conference (DRC), or programs for pre-high school, high school, and college students to gain knowledge of *Drosophila* research. After discussion by the Board and consultation between Mariana Wolfner and Scott Hawley, it was decided that up to $1500 per year from the Sandler fund could also be used for this purpose.

A Trainee Awards Committee to oversee these awards is chaired by the *Drosophila* Board Treasurer and includes three Fly Board Regional Representatives that are appointed by the President, with one representative serving two consecutive terms for continuity. Starting in 2021, we added a trainee representative. This year, the representatives were Brian Lazzaro (for a second year), Rachel Smith-Bolton (for a second year), Blake Riggs, and Ana-Maria Raicu (trainee representative). At the first meeting, the committee decided on what type of awards to make. It was felt that the awards made in 2021 and 2022 for outreach efforts to get students, including those from under-represented groups, involved in fly research, had been successful, and could potentially be more transformative than travel awards. The committee favored repeating this approach to gain additional data and

experience. However, there was some concern that 16 applications had been received in 2021 and only 7 in 2022. In order to reach more potential applicants, the committee decided to delay the application deadline till March 31st so that the opportunity could be advertised at the fly meeting as well as online. Ana-Maria generated a flyer that was posted on Flybase in mid-December and will be shown at the fly meeting between talks. The winners will be selected in April and included in next year's Treasurer's Report.

Funding Opportunity for Outreach Efforts

The Drosophila Board invites applications for funding to support efforts to **increase trainee participation**, **equity** and **diversity** in the Drosophila research community.

Non-profit programs **anywhere in the world** that introduce middle school, high school, or college students to Drosophila research are eligible to apply! The number of students that this funding would impact and financial need will be considered.

Please provide the following to Jessica.Treisman@med.nyu.edu:

1. Name and contact information
2. A 1-page summary of the program, including an explanation of how the program would promote diversity, equity, and inclusion among Drosophila scientists
3. Budget justification of up to $2000

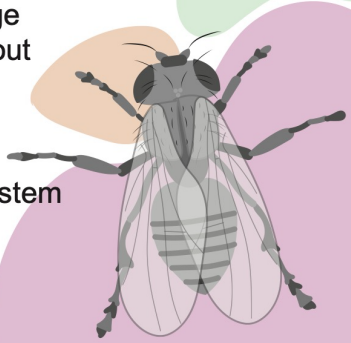
Deadline: **March 31st, 2023**

Past awards have been used to fund:

>Outreach events to educate high school/college students in under-represented communities about Drosophila research

>Summer research opportunities to introduce high school/college students to the fly model system

>Making educational material accessible to under-represented groups online



The 2022 winners were asked to provide a progress report:

Derek Dean and David Deitcher for materials for a summer teachers' workshop held at Williams College to train college and high school teachers in implementing a lesson plan that gives students experience in primary research by having them map unannotated *Drosophila* genes.

A one-day conference was held in July 2022. Five teachers participated and were exposed to successful genetics lesson plans as well as discussing their own teaching ideas. The expenses were only $540, so the remaining money was returned to the *Drosophila* Reserve Fund.

Priscilla Lumbreras for her plan to attract under-represented students to the AP Research course at Granbury High School, Texas, by enabling them to construct their own treadmills to carry out behavioral experiments on *Drosophila*. The equipment will also be used for a science research camp for middle school students in the area.

The report has not yet been received.

Drosophila Research and Training Center for a three-day intensive training program in techniques and concepts of *Drosophila* research for 20 undergraduates from different institutions in Nigeria. This organization had also been funded in 2020 for a different program of outreach to high school students.

The three-day program took place in September 2022 and included both in-person and virtual lectures from senior *Drosophila* scientists in the UK, as well as lab exercises. Twenty participants from the six regions of Nigeria were selected from a total of 153 applicants, and the other applicants were also able to join the virtual lectures. Some of the participants are now planning to begin working on *Drosophila* at their home universities.

Kenan Krakovic to develop an interactive virtual course for college and high school students in Bosnia and Herzegovina to teach them the history, current importance and practice of *Drosophila* research.

The report has not yet been received.

Karla Yotoko received an award for a course to train undergraduates at the Federal University of Viçosa, Brazil, to collect and molecularly characterize wild *Drosophila* strains, and for the students to visit local high schools to discuss *Drosophila* species diversity and its relevance to genetics, ecology and evolution.

The course was taught by a taxonomist, Camilo Guzman, in February 2022 to 5 female students, who then collected strains of both *Drosophila* and related *Zaprionus* species, one of which had not previously been reported in the region. A second course on molecular taxonomy was taught in September 2022 to train the students to identify species from the sequence of a mitochondrial gene. The students also visited two public schools with many low-income students and set up four workstations to introduce different aspects of *Drosophila* biology and research.

A couple of the reports included photos, which we should consider using in the publicity material when applications are solicited in future years.

2023 Larry Sandler Award (for a PhD completed between July 2021 and December 2022)

2023 LARRY SANDLER COMMITTEE

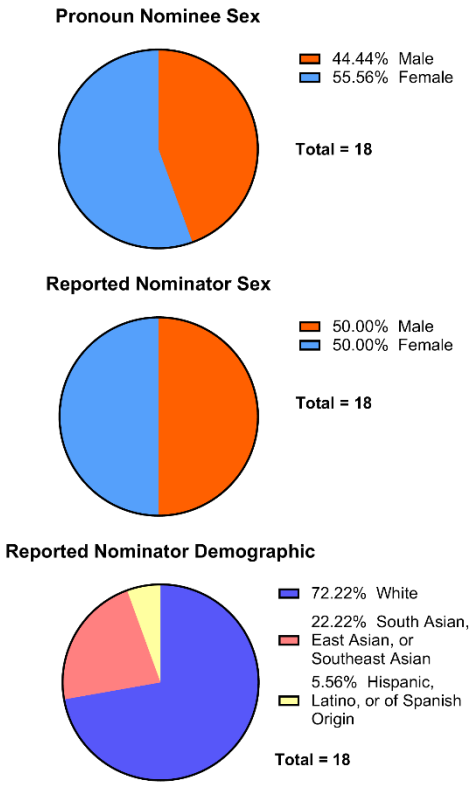
Tim Mosca	(*Chair*, Thomas Jefferson University, Philadelphia, PA)
Beverly Piggott	(*Member*, University of Montana, Missoula, MT)
Filip Port	(*Member*, DKFZ, Heidelberg, Germany)
Sarah Signor	(*Member*, North Dakota State University, Fargo, ND)
Deepika Vasudevan	(*Member*, University of Pittsburgh, Pittsburgh, PA)

TIMELINE

15 December 2022	Nomination Deadline
16 December 2022	Nominee Packages Sent to Committee
5 January 2023	Meeting to Identify Finalists
6 January 2023	Finalist Theses Requested
11 January 2023	Finalist Theses Distributed to Committee
2 February 2023	Meeting to Determine Winner and Runner-Up
3 February 2023	Winners, Runner-Up, Finalists, and Nominators Notified of Results

NOMINATOR / NOMINEE DEMOGRAPHICS

We received **18 nominations** this year for the Larry Sandler Award. Of those 18 nominations, there was an equal representation in male (9) and female (9) nominators (entered in the nomination form by the nominator) and a similar male (8) and female (10) distribution for the nominees (inferred from the use of individual pronouns referring to the candidate by the nominator). Statistics are only collected by the GSA based on the nominator and not the nominee. Demographics were predominantly white (13, 72.22%) with 22% (4) indicating "South Asian, East Asian, or Southeast Asian" as a category and 5.56% (1) indicating "Hispanic, Latino, or of Spanish origin." Nominations came from 5 countries (US – 13, France – 2, Germany – 1, Austria – 1, Netherlands – 1). In the United States, mostly East Coast institutions and cities were represented with a single West Coast institution (UC Santa Barbara) represented. There were no nominations from any schools located between New Orleans, LA (Tulane) and Santa Barbara, CA (UCSB).



Distributions of Nominee Sex (inferred via pronoun), Nominator Sex, and Nominator Demographic as reported on the GSA nomination form.

DECISION PROCESS

The committee deliberated amongst **18 nominations** that were submitted through the GSA website. For each nomination, there was a brief form, a nomination letter from the PhD advisor / nominator, and the PhD thesis abstract (2 page maximum). To identify a shortlist of thesis options, each committee member scored each of the 18 applicants according to 3 criteria: **Significance** (a clear description of what the thesis entailed, why the work is important to the field at large, and how it advanced the field); **Originality** (how 'groundbreaking' was the thesis – did the project use

a new technique or develop a new method? – did the thesis use an old approach but applied in a new way or with new attributes to ask a different question? – did the thesis ask a completely novel question or one that hadn't been tackled before? – did the thesis address assumptions in the field that had been previously made but never experimentally tested?); and **Clarity of Abstract** (were the findings of the thesis and the significance of those findings adequately explained in a way that was informative to experts and non-experts alike? – was the abstract and the question it sought to answer understandable to a diverse audience of *Drosophila* researchers?). Each committee member scored these aspects on a scale of 1 – 10 (poor to outstanding) along with a confidence score of 1 – 5 (where 5 indicates absolute confidence and 1 indicates an educated guess). The committee chair compiled the scores and calculated an average score where **Significance** and **Originality** were weighted twice and **Clarity** once. The scores were ranked and the top 9 discussed (with an opportunity to "rescue" bottom 9 candidates if desired) in the first meeting.

Within the top 9 candidates, 5 scholars emerged as the top options. Three of the candidates were consistently ranked above an 8.0 score by all committee members while two candidates were ranked at 7.5 and 7.3 respectively, but discussion raised their scores. The committee decided to invite all 5 as finalists and to submit their full thesis for the committee to consider. Following the complete reading of the thesis candidates, each committee member submitted a rank order of the candidates from 1 – 5 (best to worst). The committee chair compiled the rankings and provided an additive score. During the final meeting, two theses quickly emerged as the top ranked. Following a spirited 40-minute debate, a vote was taken and a winner declared. It was subsequently decided to offer only 1 "runner-up" position to the other top candidate (as the work was resoundingly impressive and the margin of decision thin) and the status of "finalist" to the remaining three scholars.

RESULTS

2023 Winner:	James O'Connor, PhD. Vanderbilt University (Mentor: Dr. Andrea Page-McCaw)
2023 Runner-Up:	Xiaoran Guo, PhD. University of California at Santa Barbara (Mentor: Dr. Denise Montell).
2023 Finalists:	Lisa Baumgartner, PhD. Institute of Molecular Biotechnology, Vienna (Mentor: Dr. Julius Brennecke)
	Mireia Coll-Tané, PhD. Radboud University Medical Center, Netherlands (Mentor: Dr. Annette Schenck)
	Zinan Wang, PhD. Michigan State University (Mentor: Dr. Henry Chung)

COMMENTARY ON SELECTION PROCESS

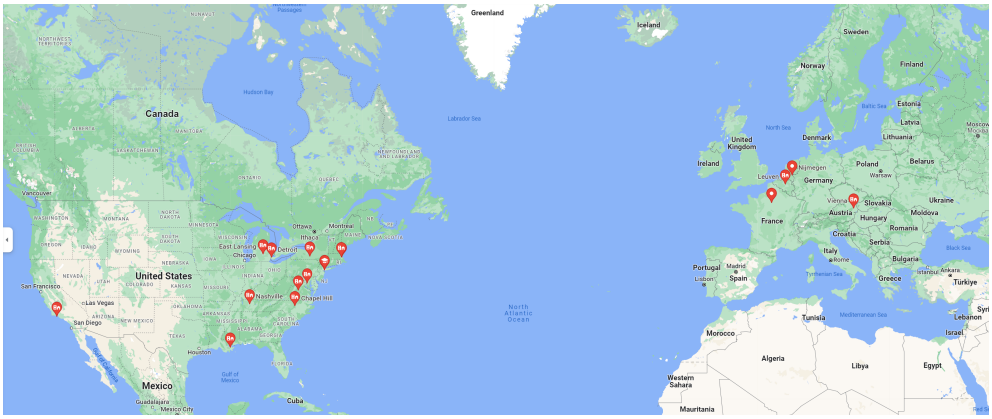
The process ran similarly to previous years, though there was a slightly compressed timeline this year due to a mid-December deadline and the request to have a decision by 2 February 2023 to accommodate the 1-5 March 2023 meeting. The Committee all felt the process ran smoothly and was even an enjoyable committee and though it was a challenge to identify the final winner, this was viewed positively as a reflection that there is a considerable amount of excellent science being done in the field. Prior to meeting, we discussed thoroughly the ranking system used, the definition of criteria, and how each committee member would engage scoring. This was helpful as it made the charge clear to committee members. Though a numerical system was used and a rank order determined, this was designed to guide the committee. Consensus, discussion, and debate finalized the decisions and this process worked well with no major difficulties.

The biggest challenge noted by the committed was regarding the topic of diversity, equity, and inclusion. We lack any demographic information for the nominee themselves; nominators enter their Gender and Ethnicity into a web form but we do not receive any of that information for the nominees. The committee chair provided an inferred gender (taken from the pronouns used to refer to the nominee by the nominator) for each candidate. We were unable to make any inferences regarding any nominees' status as PEERs (persons typically excluded due to ethnicity or race) or as belonging to any additional historically excluded groups. **It was universally indicated by committee members that to ensure Best Practices for DEI are engaged with this committee, more information should be solicited from candidates in the future regarding gender, ethnicity, protected group, or any other relevant information.** Information supplied by the candidate themselves would ideally solve this situation and not add notable work to the nomination process. However, potential gains from such information would be significant.

NOMINEES

The nominees for the 2023 competition and their nominator are listed below. Finalists are indicated in bold. A world map with indicated geographical nominee distribution (red map pins) is below.

Nominee	*Nominator*
Baumgartner, Lisa	Brennecke, Julius
Chatterjee, Deeptiman	Deng, Wu-Min
Coll-Tané, Mireia	Schenck, Annette
Cunningham, Karen	Littleton, J. Troy
Fischer, Matthew	Pick, Leslie
Guo, Xiaoran	Montell, Denise
Hatch, Hayden	Secombe, Julie
Janssens, Jasper	Aerts, Stein
Ji, Hui	Han, Chun
Mallart, Charlotte	Malartre, Marianne
O'Connor, James	Page-McCaw, Andrea
Perez-Vale, Kia	Peifer, Mark
Santiago, Ivan	Palavicino-Maggio, Caroline
Sood, Chhavi	Siegrist, Sarah
Sujkowski, Alyson	Todi, Sokol
Wang, Zinan	Chung, Henry
Witt, Evan	Zhao, Li
Zane, Flaminia	Rera, Michael



WINNER ABSTRACT

Supplied by Dr. James O'Connor
A Protease-initiated Model of Wound Detection

When an organism is injured, the damaged tissue recognizes the presence and severity of the wound and rapidly responds to repair the injury and restore proper tissue functionality. But how do cells first detect the presence of a wound? In epithelial cells, the earliest known wound response, occurring within seconds, is a dramatic increase in cytosolic calcium. After wounding in Drosophila pupae, two mechanistically distinct calcium responses are observed. Extracellular calcium rushes into damaged cells within seconds, before diffusing the neighboring cells through gap junctions. Then, about one minute after wounding, distal cells far from the wound begin to have an increase in cytosolic calcium through an independent mechanism. This dissertation presents evidence that wounds in Drosophila epithelia trigger a cytosolic calcium increase by activating extracellular cytokines, Growth-blocking peptides (Gbps), which initiate signaling in surrounding epithelial cells through the G-protein coupled receptor, Methuselah-like 10 (Mthl10). Latent Gbps are present in unwounded tissue and are activated by proteolytic cleavage. Further, multiple different protease families can activate Gbps in imaginal wing discs suggesting Gbps act as a generalized protease-detector system. In this way, this project has characterized a protease-initiated wound detection system, whereby proteases released during wound-induced cell lysis serve as the instructive signal, activating Gbp ligands, which bind to Mthl10 receptors on epithelial cells distal from the wound to elicit an increase in cytosolic calcium that initiates cellular wound responses.

EMAIL TO WINNER

Dear Dr. O'Connor:

On behalf of the 2023 Sandler Award Committee, I am delighted to inform you that you have been selected as the recipient of the 2023 Larry Sandler Memorial Award!

As you no doubt know, the goal for this award is to identify the "best" Ph.D. thesis in *Drosophila* research from the previous year. In this round we had 18 nominations of outstanding science and the competition was fierce! The committee (composed of Drs. Beverly Piggott, Fillip Port, Sarah Signor, Deepika Vasudevan, and myself) felt that your truly outstanding work investigating the mechanisms of wound detection, calcium responses, and the roles of proteolysis and growth peptides in driving this system stood out as significant, complete work and deserving of this recognition. The coherence of your thesis was especially noted as representing a body of work that advanced the field. It also helped that we received a very supportive letter from your advisor, Dr. Andrea Page-McCaw. Many congratulations on executing this spectacular set of experiments and on a superb thesis.

As the recipient of this award, you will have the honor of presenting your thesis work in the Larry Sandler Memorial Lecture on Wednesday, March 1st, 2023 at the opening night of the 64th Annual Drosophila Research Conference in Chicago, IL. You will give your plenary lecture in front of the entire fly community present at the meeting. In addition to sharing your work with the field, we hope that your talk will help to inspire other students just starting or in the midst of their PhDs (and perhaps even a few postdocs and faculty as well!). Ms. Suzy Brown (cc'ed on this email) of the GSA will be in touch to make (and pay for) your travel arrangements to Chicago.

Again, please accept my heartiest congratulations. You now join a long list of excellent scientists who have gone on to have successful careers (https://en.wikipedia.org/wiki/Larry_Sandler_Memorial_Award).

Please don't hesitate to let me know if you have any questions as you prepare for your talk in Chicago. I really look forward to meeting you in person in March and to hearing you present your beautiful work. Congratulations!

Best,
Tim Mosca

RUNNER-UP ABSTRACT

Supplied by Dr. Xiaoran Guo
CELLS ON THE MOVE: Intra- and Extra-cellular Mechanisms of In Vivo Cell Migration

My thesis investigated collective cell migration, a cell biological process critical for development, wound healing, and tumor metastasis. Moving cells can sense and respond to physical features of the microenvironment; however, in vivo, the significance of tissue topography was mostly unknown. My research used the Drosophila border cells in the ovarian egg chamber to study how chemical and physical information influence in vivo cell migration path selection.

Border cells are the 6-10 follicle cells that delaminate from the anterior and migrate posteriorly and collectively within the egg chamber, each chamber composed of 15 nurse cells and one oocyte all encased within ~850 epithelial follicle cells. Despite the presence of ~40 possible paths between nurse cells, wild type border cells always choose the middle path. Using live imaging, genetics, and in collaboration with physicists who did modeling and simulations, we showed that tissue microtopography is the reason why border cells migrate along the middle path.

Border cell migration is chemotactic. The oocyte secretes chemoattractants that activate receptor tyrosine kinases (RTKs) on border cells. I measured the chemoattractant concentration along the potential migration paths and found an anterior to posterior gradient but no difference in the chemical along the medial-lateral axis. I manipulated the location of chemical sources and discovered that even when cells were redirected by a high concentration of ectopic chemoattractant, they nevertheless found their way back to the egg chamer center. Genome wide screens have only identified E-cadherin (Ecad) on nurse cells as responsible for central path selection. Through genetic manipulation and live imaging analysis of migrating border cells in normal and Ecad mutant egg chambers, my thesis showed that the key function of nurse-cell Ecad is to provide traction. Surprisingly, differential adhesion does not provide directional information to steer the cells.

Three-dimensional reconstruction of egg chambers revealed unique medial path tissue topography. Mathematical modeling and simulations by our physicist collaborators suggested that the organization of the nurse cells might be the instructive cue for choosing the central path. At the junctures where multiple nurse cells meet, they do not quite touch due to geometry, leaving tiny openings where protrusions need not break as many adhesive bonds between nurse cells. Thus, the presence of multiple-cell junctions near the egg-chamber center provides an energetically favorable path, at lease theoretically. I designed genetic manipulations that created altered nurse cell organization that uncoupled the geometric center of egg chamber from the effect of multiple-cell junctions. These experiments provided compelling evidence for tissue topography as a guidance cue.

In these experiments, I measured and manipulated chemical, adhesive, and topographical cues and elucidated their relative contributions to selection of the migration path. Prior to our studies, chemical cues were thought to be sufficient for explaining border cell migration. My graduate research transformed and shifted the focus of in vivo cell migration studies: tissue microtopography is now viewed as equally important as chemical cues in determining migration direction. The results provide comprehensive insight into how cells integrate and prioritize topographical, adhesive, and chemoattractant cues to choose a specific path among many. This work was published in Science.

An advantage of the border cell model is that it is amenable to large-scale genetic screens. In a screen for mutations that cause border cell migration defects in mosaic clones, the gene Catsup was identified. Catsup, the Drosophila ortholog of ZIP7 (SLC39A7), encodes a multifunctional endoplasmic reticulum (ER) transmembrane protein reported to negatively regulate catecholamine biosynthesis, to be required for Notch and EGFR trafficking, to function as a Zn2+ transporter, and to reduce ER stress. However, the relationship between these functions was unclear. I used genetics, immunostaining and confocal imaging to show that Catsup knockdown caused abnormal accumulation of Notch and EGFR proteins and induced ER stress in border cells. Ectopic expression of an unfolded rhodopsin mutant protein, Rh1G69D, also induced ER stress, inhibited Notch transcriptional responses, and blocked border cell migration, even in the absence of abnormal Notch or EGFR accumulation in the ER. Remarkably, simultaneous overexpression of Catsup/ZIP7 and Rh1G69D was sufficient to degrade Rh1G69D, resolve ER stress, and rescue border cell migration. Mutant forms of Catsup predicted to disrupt the Zn2+ transport were nonfunctional, indicating a requirement for Zn2+ transport in resolving ER stress.

The ability of Catsup overexpression to alleviate ER stress and cellular defects due to Rh1G69D expression has general biomedical implications. Dominant mutations in rhodopsin that impair folding and cause accumulation in the ER cause retinal degeneration in human patients, for which there is no effective prevention or therapy. In response to misfolded proteins in the ER, cells initially adapt by activating the ER stress response, including ER- associated protein degradation (ERAD). In collaborating with another graduate student in the lab, our work shows that overexpression of the Catsup/ZIP7 enhances ERAD and rescues retinal degeneration caused by Rh1G69D in Drosophila photoreceptor cells. Proteotoxic stress also drives the progression of other degenerative diseases including Huntington's, Alzheimer’s, and Parkinson’s Diseases. My work proposes that Zn2+ is limiting for ERAD, and that ZIP7 overexpression could alleviate the proteotoxic stress caused diseases like Retinitis pigmentosa. Preliminary data suggest that ZIP7 overexpression rescues retinal degeneration caused by overexpression of Ab42, a major constituent of amyloid plaques in Alzheimer’s Disease and due to Vap33, a gene associated with familial amyotropic lateral sclerosis. Follow up experiments are planned to uncover how generally ZIP7 overexpression will suppress neurodegeneration due to toxic misfolded proteins.

Moreover, recent work by the student who is carrying this project forward suggests that the precise mechanism by which ZIP7 enhances ERAD is by enhancing the activity of a Zn2+-dependent metalloproteinase that removes polyubiquitin chains from proteins as they are moved into the proteasome core for degradation. This work is available as a preprint in BioRxiv and will be submitted for publication soon. The ZIP7 work has also produced a patent application.

My graduate research added a new concept to the field of in vivo cell migration - that the physical tissue architecture of the microenvironment participates together with chemoattractants and adhesion molecules in steering migrating cells. Additionally, characterizing the role of ZIP7 in border cell migration uncovered an unknown molecular player in ERAD and a new approach to suppressing neurodegeneration. This work raises therapeutic possibilities for diseases like retinitis pigmentosa and possibly other neurodegenerative diseases.

EMAIL TO RUNNER-UP

Dear Dr. Guo:

On behalf of the 2023 Sandler Award Committee, I am writing to inform you that you have been selected as the runner-up for this year's Larry Sandler Memorial Award.

Although you are not the winner for this year's award, I nevertheless want to congratulate you for executing a spectacular thesis. The committee (composed of Drs. Beverly Piggott, Fillip Port, Sarah Signor, Deepika Vasudevan, and myself) felt that your truly outstanding work investigating

the mechanisms of border cell migration, how it is influenced by tissue topography, and the fascinating role Catsup plays in this process were truly groundbreaking and innovative.

This year's competition was fierce! We received 18 nominations, many of which were truly outstanding and deserving of the Larry Sandler Award. The committee struggled to narrow this down to even a top 5 and harder still to decide a winner. We truly enjoyed reading about your work and accomplishments and have no doubt that you will continue to do superb research in the future. I should add that is evident how supportive Dr. Montell was of your work by their nomination.

On behalf of this year's Sandler Award Committee, we congratulate you on being selected as a runner-up, and wish you the very best of luck for continuing success.

Best,
Tim Mosca

EMAIL TO FINALISTS

Dear Dr. ########:

On behalf of the 2023 Sandler Award Committee, I am writing to inform you that you have not been selected as the winner for this year's Larry Sandler Memorial Award.

Although you are not the winner for this year's award, I nevertheless want to congratulate you for executing a spectacular thesis. This year's competition was truly fierce: we received 18 nominations, many of which were truly outstanding and deserving of the Larry Sandler Award. The committee (composed of Drs. Beverly Piggott, Fillip Port, Sarah Signor, Deepika Vasudevan, and myself) struggled to narrow this down to the five finalists! We truly enjoyed reading about your work and accomplishments and have no doubt that you will continue to do superb research in the future. I should add that is evident how supportive your advisor was of your work by their nomination. We will, however, acknowledge you and your thesis as one of the finalists in the opening plenary session at the 64th Annual Drosophila Research Conference next month in Chicago.

On behalf of this year's Sandler Award Committee, we congratulate you on being a finalist, and wish you the very best of luck for continuing success.

Best,
Tim Mosca

Image Award Report (Julie Brill)

This year, Leanne Jones, Rachel Smith-Bolton and former Chair Nasser Rusan rotated off the Image Award committee and three new members were added – **Tina Tootle** (University of Iowa), **Clemens Cabernard** (University of Washington,) and **Jose Pastor-Paréja** (Universidad Miguel Hernández, Alicante, Spain), maintaining the total committee membership at six (including Julie Brill, Amy Kiger and Dan Bergstralh). Amy and Dan will rotate off this year and two new members will be added. Regular committee members will serve 2-year terms, allowing for steady turnover.

New chair

This is the first year that I (Julie Brill) am serving as Chair of the Drosophila Image Award committee, taking over from Nasser Rusan, who served as Chair for 5 years. Nasser did a fantastic job and has continued in an advisory capacity while I learned the ropes. Prior to Nasser, the committee was chaired for 13 years by David Bilder, who started the Drosophila Image Award competition.

Results of the 2022 competition

For the current competition, we maintained our Twitter presence and added Facebook postings, especially leading up to the submission deadline.

80 total submissions: 51 images and 29 videos. Of these, 3 images and 1 video were ineligible, as these were published online or in preprint form in 2022 but were not officially published in the corresponding journal until 2023 (publication dates are listed as 2023 in PubMed). Thus, the total number of eligible submissions was 76, which is a 50% increase from last year.

Points for discussion

- Currently, new committee members are chosen by the Chair in consultation with other committee members. Do we need a mechanism to ensure more diversity on the committee, for example by encouraging newer faculty to volunteer?
- In the current competition, authors often did not follow the Rules or read the FAQ on the DIA website and sent incomplete submissions that lacked important information. Would providing a downloadable Powerpoint template help?

The winners

Image award: Bryce Bajar and Orkun Akin

A discrete neuronal population coordinates brain-wide developmental activity. **Bajar BT**, Phi NT, Isaacman-Beck J, Reichl J, Randhawa H, Akin O. Nature. 2022 Feb;602(7898):639-646. doi: 10.1038/s41586-022-04406-9. Epub 2022 Feb 9.PMID: 35140397

Video award: Regan Moore, U. Serdar Tulu and Dong Li

Superresolution microscopy reveals actomyosin dynamics in medioapical arrays. **Moore RP**, Fogerson SM, Tulu US, Yu JW, Cox AH, Sican MA, Li D, Legant WR, Weigel AV, Crawford JM, Betzig E, Kiehart DP. Mol Biol Cell. 2022 Sep 15;33(11):ar94. doi: 10.1091/mbc.E21-11-0537. Epub 2022 May 11.PMID: 35544300

Drosophila Community Service Award Report for ADRC 2023

The committee is:
Michelle Arbeitman (chair)
Kevin Cook (co-chair)
Amy Kiger (member)
Nadia Singh (member)
Nasser Rusan (member)

The award committee was formed in the Fall of 2022 by FlyBoard President Michelle Arbeitman. The committee wrote an announcement and call for nominations that was sent out by GSA late 2022. The announcement was also posted on Twitter by Flybase and by colleagues on the committee.

The committee received a great set of nomination letters for our colleagues. We reviewed the letters and met by zoom to discuss and decide. The decision was unanimous, though everyone agreed that there were many additional nominees deserving of the award.

In the inaugural year of the Award, we decided to give a group of colleagues the award for contributions to:

Gathering and organizing information that drives Drosophila research

The awardees are: Dr. James Thompson (Drosophila Information Services), Dr. Thomas Brody (Interactive Fly), Flybase Curatorial Team (FlyBase).

The awardees were contacted and told that the award will be presented by Dr. Kevin Cook before the Thursday morning Plenary Session.

After ADRC 2023 Michelle will contact the letter writers for colleagues that did not receive the award and let them know that their nominations will be held, so they can be reconsidered by the committee next year. She will also work with GSA to have the names of awardees on a GSA maintained Webpage, similar to what is done for the Sandler Award.

Next year, it is requested that the call for the Community Service Award be listed on the meeting website with the Sandler Award and Image Award.

The policy for the award states that committee members serve for two-years minimally. The committee is aware of this and has agreed to serve for another term.

Report to FlyBoard

GSA appreciates the opportunity to provide a brief snapshot of goings-on, and we look forward to discussing ways to continue to support FlyBoard and the community. And GSA *is* the community! In fact, fly researchers represent a substantial portion of GSA's membership, Board of Directors, Committees, journal authors, readers, and editors.

GSA and FlyBoard have maintained a close relationship collaborating on a variety of projects. In addition to the annual conference, some of these projects GSA carries out include:

- Managing the *Drosophila* reserves to ensure sustainable returns
- Providing professional development programs at the conference, such as the New Faculty Forum, Peer Review Training workshops, Community and Connections event, Mentor-Mentee lunch, Networking Hotspots, and others
- At the FlyBoard's request, establishing and administering the Victoria Finnerty Fund
- Creating and maintaining the Image Award website and creating the framed Award Image
- Managing the Larry Sandler Award Fund, making speaker arrangements (travel, registration, award presentation, lifetime GSA membership), producing the award plaque, and other tasks as needed
- Emailing the FlyNews and other special FlyBoard announcements to the community
- Managing and publishing FlyBook
- Managing the Victoria Finnerty fund and award process
- FlyBoard elections
- FlyBoard surveys (volunteer survey, demographics survey)
- Promoting the new community service award.

Code of Conduct for GSA Conferences

All participants are required to agree to abide by the GSA Code of Conduct. Additionally, participants will be reminded at the beginning of each session that adherence to the Code of Conduct is expected. GSA has a reporting system that can be utilized anonymously if necessary. Thus far, no reports of misconduct have been reported at *Drosophila* events.

Professional Development & Other Special Programming

Conference professional development programming

The Engagement department also offers a series of professional development events for both virtual and in-person registrants. These activities include:

Getting Involved in GSA's Early Career Professional Development Programs: GSA Early Career Leadership Program (ECLP) members share how to get involved in GSA's professional development programming for early career scientists.

Conference Success Tips and Welcome from the Early Career Leadership Program: This event designed to help first-time conference attendees and early career scientists make the most of the conference. Topics covered may include introductions to organizers of the meeting, advice on having meaningful interactions in a virtual space, a chance to meet other attendees in an informal setting, and an introduction to scientific events and other conference programming.

Career Exploration Panel: This event showcases the broad options available to those with a PhD by hosting a panel of individuals from multiple career paths. Career sectors highlighted may include academic research, industry research, biotech, science writing, science teaching, and academic administration.

Careers in Academia: This discussion panel features department heads and academic faculty who discuss applying and hiring in academia from both sides of the process, as well as provide insight into an academic career.

Multilingual Networking: At this multilingual networking event, conference participants who speak languages other than English have a chance to network and talk about science in their native

language or language of choice with other participants.

Virtual Networking: These virtual networking sessions include a series of moderator-led discussions featuring breakout rooms focused on specific topics. Topics include scientific discussions, professional development, academic applications, and community topics.

Networking Hotspots (In-Person only): GSA will host themed virtual discussion sessions on scientific, professional development, and community topics. Come join the conversations! All career stages are welcome.

Come Fly With Me: Career Advice and Connections: GSA will host topic-based moderated discussions during lunch with the goal of providing an opportunity for early- and mid-career scientists to ask scientific career questions and connect with fellow researchers, including established *Drosophila* community members. Topics include professional development, academic applications, and community topics.

GSA Equity and Inclusion Committee

Drosophilists have always been strongly represented on GSA's Equity and Inclusion Committee, and we're pleased to continue working together in the effort to advance equity in the sciences.

In 2022, we launched the Vision for Inclusive Conferences. The Vision seeks to create a positive vision for GSA conferences in which equity, accessibility, and inclusion are foregrounded at each step of planning—just as budget and scientific content are. The document was provided to the #Dros23 organizers in its draft form and will be available to all future Dros and TAGC organizers.

Additionally, we are working on a new offering called the Neighborhood Program, initiated by Alana O'Reilly. This program is an innovative way to develop tight-knit, collaborative groups of colleagues who are intentional in their efforts to improve the understanding of science in the public, specifically within systemically minoritized populations. These "neighborhoods," led by early career scientists, will be united by a common interest in a science-in-society problem. The program will engage scientists from a variety of backgrounds, identities, and career stages, and the resulting neighborhoods will have the potential to address critically urgent research needs of minoritized communities and will enable powerful conversations at the intersection of culture, society and environment, and shared scientific goals. Examples of science-in-society problems include health inequities, mitigating effects of climate change or environmental toxins, understanding developmental impacts of stress or isolation, or leveraging adaptation of animal species to hazardous environments to reduce risk in affected communities.

We are holding a workshop at #Dros23 to help pilot this effort.

FlyBook in GENETICS

Launched in 2015, FlyBook is published and supported by GENETICS. This comprehensive compendium of review articles presenting the current state of knowledge in *Drosophila* research comprises an encyclopedia of approximately 50-60 articles. Publications are ongoing and will be completed by 2025.

Communications

FlyNews: GSA formatted and sent the FlyNews on behalf of the *Drosophila* Board in January 2023.
***Drosophila* Image Awards:** GSA provides design, IT, and administrative support for the *Drosophila* Image Awards and hosts the website. In preparation for the 64th Annual *Drosophila* Research Conference, we updated the website to show last year's winners and new award committee members.
Community Notices: GSA sends occasional email blasts on behalf of the FlyBoard to our distribution list, such as the recent communications on the FlyBoard election, volunteer survey, and community service award.

Finance

In the early 1980s when the FlyBoard approached GSA to manage the conference, there was a small meeting reserve that GSA agreed to hold. In 2017 GSA assumed full responsibility for all financial aspects of the meeting, including registration pricing, and in 2018 FlyBoard was given the full amount of the reserves, which at that time was $164,000. The FlyBoard reserves are maintained in a GSA account, and GSA invests the principal and disburses sums at the direction of the FlyBoard. Full details for that account can be found in the Treasurer's report.

To promote inclusivity and accessibility at our conferences, GSA has historically offered financial aid for early career scientists, parent scientists, and scientists from low- to middle-income countries. We will ask that FlyBoard consider allocating a portion of its reserve funds to support these groups who will plan to attend TAGC.

The GSA Finance Committee of the Board of Directors determines the registration fees for the meeting. They make recommendations for meeting locations to try to maximize attendance at all career stages and keep costs to a minimum. GSA relies on assistance from the meeting organizers to build a strong exhibit and sponsorship program to offset meeting expenses.

***Drosophila* Investments**

GSA has been retained by the FlyBoard since 2018 to maintain and manage the *Drosophila*

Reserves, which includes investment of the principal in a segregated account at Vanguard and disbursement and tracking of FlyBoard grants in the form of outreach awards benefiting the Fly Community. As of February 3, 2023 the balance in the *Drosophila* Reserve was $174K. Awards to recipients in the Fly Community total $17K from grants made in 2021 and 2022.

Victoria Finnerty Fund

GSA maintains the Victoria Finnerty Fund as a restricted account for the Fly Community, from which grants approximating $5K are awarded for undergraduate travel to the *Drosophila* conference, annually. A donation of $6K is provided from the *Drosophila* Conference proceeds, each meeting cycle, to fund these awards, and GSA also accepts constituent donations via the GSA website. In 2020, on GSA's recommendation, a Vanguard investment account was established with $20K of cash from the Fund, for the purpose of generating additional revenues. As of February 3, 2023 the investment account balance was $23K and there was $5K in cash, for a total of $28K.

Larry Sandler Fund

The Larry Sandler Fund is held in a custodial capacity by GSA for the Fly Community and is invested in an account at Vanguard. The account has grown from $28K in 2003 to $97K as of February 3, 2023. In addition to covering expenses for the Larry Sandler Award winner, each cycle, the Fund (along with the *Drosophila* Reserve) has contributed to outreach awards granted by the FlyBoard in 2021 and 2022.

64th Annual *Drosophila* Research Conference (2023)

Organizers

Savraj Grewal, Chair

Angela DePace

Mia Levine

Jennifer Jemc Mierisch

Lucy O'Brien

In 2022 we were able to offer the Drosophila conference in a hybrid format and welcomed 1,020 in person attendees and an additional 542 online. This year the meeting will be held in a hybrid format once again and, as of February 6, we have 1,277 registered to attend in person with an additional 128 participating online.

What to expect in 2023

Conference App - The conference app is an attendee's main resource. There will be no printed book this year (although one is available online for those who wish to print it). Once

you download the App there is no need to connect to the internet except to download updates. You'll be able to send direct messages to other attendees, leave questions for speakers, view abstracts, make a personal schedule, and so much more.

Live streaming - all platform and plenary sessions will be live streamed through the app in Zoom. Presenters who are not able to attend the meeting in person, will be giving their talk in real time with the ability to field questions.

An online audience - Last year was the first time the Drosophila conference was held as a hybrid event with nearly 500 people attending online. This year we are expecting the majority of the people will be attending in person although we still anticipate approximately 150 people will be attending #Dros23 online. Almost 1,300 people are registered to attend in person.

Recordings - All plenary and platform sessions will be recorded and made available through the conference app through April 6.

Posters - All poster authors, whether they are attending in person or online, will be able to upload a pdf of their poster and an oral overview. All in-person authors will display and present their poster during a specific timeframe then take their poster down so the next group can display their posters. With this year's special circumstances, and to allow for a little more room between posters, each poster will be displayed on a single 8' board rather than sharing a board with another poster. Authors have been asked to utilize 3'8" of space (the same as in past years) on the board to naturally create space between boards.

Health and Safety

Our top priority is the safety of our attendees. In-person attendees are required to wear the most protective masks they can access, ideally N95s or KN95s, while attending the conference. If they do not have access to a high-quality mask, complimentary masks will be available at the Registration Desk outside of the ballroom on level 4 in the conference hotel. While oral presenters do not need to be masked when presenting, we do ask for those in the poster sessions to be masked.

All rooms will be set with maximum seating so that attendees can sit at the spacing with which they are comfortable. The large keynote and plenary sessions will be held in Sheraton/Chicago 4-7 and streamed in Chicago 9-10 for those who want to spread out a little more. And of course, in-person attendees can also opt to participate online through the App. There will also be meeting rooms on the 2nd floor of the hotel for those who want a little extra space.

Hand sanitizers will be available in all the meeting rooms and public space.

Once again we are asking all in-person attendees to be fully vaccinated, boosted, and take a rapid antigen test within 12 hours before departing for the meeting. If an attendee tests positive we invite them to attend virtually instead of in-person.

Complete health and safety guidelines can be found here.

GSA LOCI

GSA LOCI (Local Outreach Community Initiatives) is a volunteer-led community service initiative conceived by the GSA Conferences Committee that aims to give back and build a sense of community, especially for early career researchers.

The pilot will be held in conjunction with the 64th Annual *Drosophila* Research Conference in Chicago. GSA is collaborating with one of the nation's largest LGBTQ+ organizations, Howard Brown Health, and their Broadway Youth Center, in their ongoing efforts to provide care to the LGBTQ+ community, their families, and allies.

Volunteers will be packing hygiene kits just prior to the start of the meeting. People can also make a monetary donation through the GSA website and drop off gently used clothing at the conference registration desk. For more information, please visit https://genetics-gsa.org/drosophila-2023/gsa-loci/

What is Hybrid?

As defined by the Professional Convention Management Association (PCMA) hybrid is *a single event that serves both in-person and virtual audiences.*

The professional development section outlines many of the conference components that are being held online and in-person. In addition, all abstract driven sessions, like the platform and plenary sessions, will be live streamed. Workshops are being held in-person and online based on the preference of the workshop organizer(s). In-person workshops will not be streamed or recorded. Posters will be held in the traditional manner for those attending in person. All poster authors have the option of uploading a pdf and audio overview of their poster. Delegates can leave questions for the author in the App and, if the author provided a link to their personal scheduling program, people can set up an appointment to talk to the author.

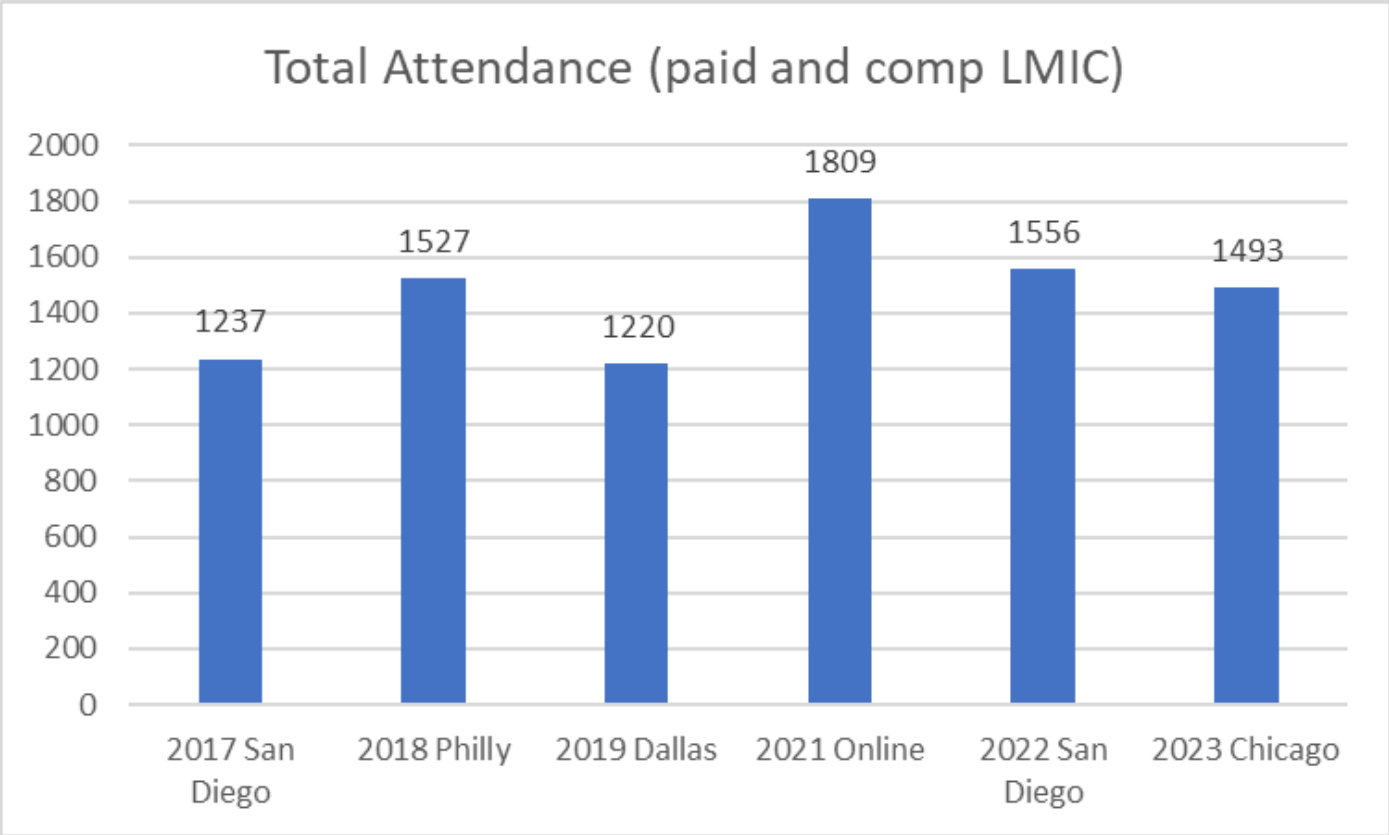
In 2022, 32% of the attendees were online. This year we estimate that only about 10% of the attendees will be participating online. Data from the past two years, for all GSA meetings, will be used to help inform the structure of future meetings.

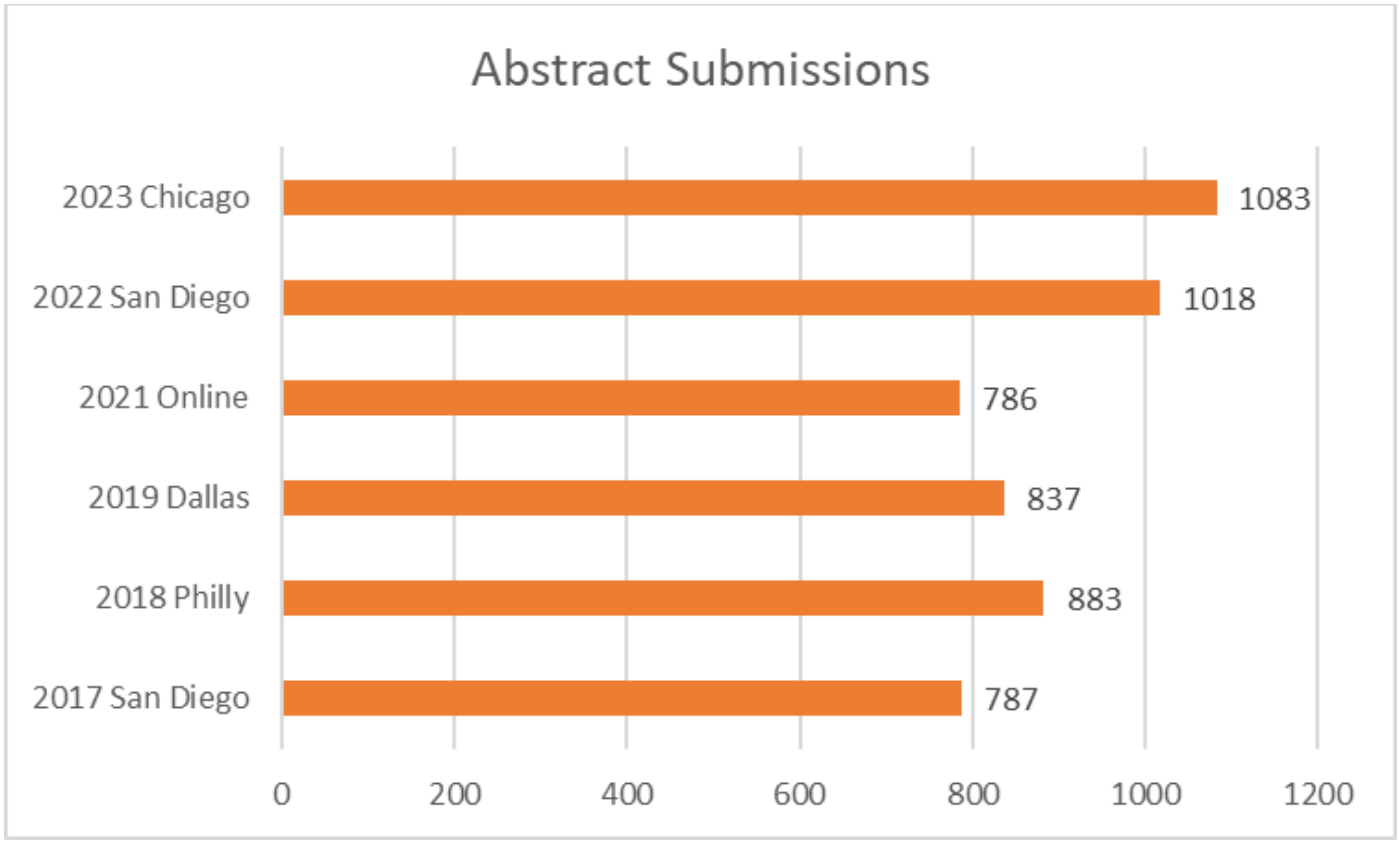
Exhibitors and Sponsors

Please stop by and say hello to the exhibitors. We appreciate their support and their participation helps keep registration prices down, and they really value meeting leaders in

the Fly Community. Burroughs Welcome provided funding for 33 people to attend #Dros23 online. The funding was specifically for people doing *Drosophila* research from low-income and middle-income economies.

#Dros23 by the numbers (as of February 6)





Future Meetings

March 5–10, 2024
65th Annual *Drosophila* Research Conference
as part of the
The Allied Genetics Conference
National Harbor
Washington, DC Metro Area

March 19-23, 2025
66th Annual *Drosophila* Research Conference
Town and Country Resort
San Diego, CA

2026
Open (Chicago?)

Report of the 2023 Annual Drosophila Research Conference Organizing Committee: Savraj Grewal (Chair), Angela DePace, Mia Levine, Jennifer Mierisch, Lucy O'Brien.

The 2023 Organizing committee was assembled in late Spring 2022. Tin Tin Su and Michelle Arbeitman invited Savraj Grewal in March 2022 to chair the organizing committee for the 2023 meeting. Savraj invited Angela, Mia, Jenny, and Lucy to join the organizing committee to diversify the representation of research area expertise and knowledge, and the committee was confirmed in May 2022. The organizers communicated through monthly zoom meetings and email. This report provides an overview of the process we followed to organize the meeting.

Gratitude to Suzy Brown and the GSA staff

The organizers would like to thank Suzy Brown (GSA) and all the GSA staff for their help in organizing the meeting. Suzy was involved in all stages of planning and was invaluable in helping set up our meetings, providing feedback, ideas, and input, facilitating, and enabling all our ideas about the scientific, professional development and culture-building components of the meeting, and keeping our planning on track. We could not have been successful as an organizing committee without the help of Suzy and the GSA staff.

Overview of Meeting Organization

A Theme for #Dros23: Pay it Forward. In our early organizing committee meetings, we decided to have a theme for the conference. We articulated this idea in a message to the community on the Dros#23 site: *"As we began our work together as a committee, we reflected on what the fly meeting has meant to us over the years. We, each in different ways, are grateful for how the fly meeting enables and fosters a sense of community, sharing of knowledge, and professional growth. In recognition of this, we decided to develop the 2023 meeting around the theme of "Pay It Forward." We recognize all we have received from mentors, peers, trainees, and colleagues and accept responsibility for relaying their gifts of attention, insight, and opportunity to others. We also acknowledge the barriers many face in joining and participating in our community. We accept responsibility for doing our part to make the fly field a welcoming, creative, and caring community for everyone. "*

We used this theme to help guide our choices and decisions as we developed the content for the meeting. We also hoped this theme would invite us all to reimagine how we come together at the Fly Meeting to share our work, connect with friends and colleagues, and develop our community.

Keynote Speaker. The organizing committee agreed to have a single Keynote Speaker for the opening evening. We began by developing a rubric for identifying nominees focusing on a) a

strong body of work of general interest, b) contributions to the fly community, and c) representation of the diverse backgrounds in our community. Based on nominations from individual organizing committee members, we began with a list of 13 potential Keynote speakers (9 female, 4 male). We then ranked our choices for Keynote speakers and used these initial rankings to discuss our top picks over Zoom. We unanimously chose **Yukiko Yamashita** as our Keynote Speaker. An invitation to Yukiko was sent and accepted in **July 2022.**

Plenary Speakers. We chose to have ten plenary speaker talks for the meeting, 5 in the first session on Thursday morning and 5 in the final session on Sunday morning. We decided early in the planning process to have 4 of these speakers be new PIs (which we explain further below), with the remainder being mid-career or senior researchers who had not given a plenary talk in any previous fly meeting. We then invited each organizing committee member to nominate candidate New PI plenary speakers and candidate med/senior career plenary speakers in 6 broad research topics (cell biology, neurobiology, evolution, gene expression, immunity and physiology, and stem cells and regeneration). Using career stage, research area, institution type and geographic locations as our first selection criteria, 65 candidate Plenary Speakers were initially nominated. Each organizing committee member ranked the candidates in each category, and we then discussed the nominees via Zoom. We reached a consensus on ten plenary speakers - eight based in the USA, one in Canada and one in France. Invitations were sent, and attendance of all speakers was confirmed in **July 2022.** The final ten plenary speakers are Amanda Amodeo, Allison Bardin, Edan Foley, Sally Horne-Badovinac, Karla Kaun, Erin Kelleher, Mustafa Mir, Caroline Palavicino-Maggio, Kausik Si, and Lesley Weaver.

New for the 2023 Fly Meeting:

1. Spotlight on New PIs

In keeping with our meeting theme, we invited four early career faculty members to share their work with our community as plenary speakers. As we articulated in a message to the community on the Dros#23 site: "*Our goal is to lift up scientists at multiple career stages because we believe we can all draw inspiration from being part of the long multi-generational project that is scientific discovery. We can look to the current and previous generations for guidance and wisdom, lessons learned, and the way science can change as we grow and become leaders. We can also look to the next generation for their aspirations and new ideas as they experience and respond to the rapidly changing world. We hope that hearing fantastic science from these multiple perspectives will inspire us to engage deeply and imagine widely.*"

2. A community session

An important point of emphasis in recent Fly meetings (and other GSA meetings) has been the inclusion of a DEI session. For the 2023 meeting, we invited Raquell Holmes from Improv

Science and Tania Reis (UC Denver) to lead a session on building and nurturing an inclusive community. Raquell and Tania have shared: "*In any setting, everyone plays a part in creating a welcoming, creative, and caring environment. By showing up and trying something new—together as scientists—we will discover in-the-moment ways to foster belonging and develop new relationships that last well beyond Dros23." We want* to thank GSA for their generous support in enabling Raquell to participate in this session. In addition, funds from a Company of Biologists meeting grant (described below) helped to defray costs.

We have also invited the plenary speakers to share what the theme of Pay it Forward means to them in their talks. If the speakers take up our invitation, they can create different ways of sharing their thoughts: a story, a piece of advice, or a reflection. We feel such "leading by example" will prove helpful to trainees: Studies of science communication and teaching show that sharing something about ourselves increases our connection to our audience and improves how we learn from one another. We hope this invitation creates space for us to share a little more about ourselves as individuals and scientists.

3. A community Vision Board

We will develop a vision board at this year's meeting to illuminate our aspirations for science and ourselves as scientists. This will be a community art project in which all attendees will be invited to make origami flies, write or draw their aspirations for our community, and to read and respond to what others have shared. Everyone will be invited to place their work on a set of boards that will stay in place throughout the meeting. We hope that together we will create a place where we can all pause, reflect, connect, and be inspired to cultivate a community that reflects our shared values.

Platform Session Co-Chairs

In our early organization meetings, we identified 16 topic areas for abstract submissions based both on topics from previous years and data on the number of abstracts submitted in each of these areas in past years. We followed the format of earlier meetings and had two PI co-chairs who were then asked to invite a trainee (senior graduate student or postdoc) to join them as a co-chair for the session. In selecting potential Faculty co-chairs, we focused on ensuring that they collectively contributed to a diverse representation of the Fly community and were chosen from a broad selection of institutes and universities (PUIs and R1) and geographical locations. Members of the organizing committee then nominated co-chairs for each of these 16 sessions. We ranked our nominations and then selected our final choices through Zoom meetings. Invitations were sent to the PI co-chairs in September 2022, and all the PI and trainee co-chair positions were filled by November 2022.

Abstract Categories and Session Topics

We decided on 16 categories for Abstracts and Sessions. These were based on the 18 topics initially developed for the 2022 meeting, with one exception. We eliminated Cell Signaling since it received no request for platform talks in 2022. We also merged DEI and Educational Initiatives into one topic. The sixteen topic areas are: 1) Physiology, metabolism and aging; 2) Models of human disease; 3) Regulation of gene expression; 4) Patterning, morphogenesis and organogenesis; 5) Evolution; 6) Cell biology: Cytoskeleton, organelles and trafficking; 7) Reproduction and gametogenesis; 8) Neural development and physiology; 9) Neural circuits and behavior; 10) Stem cells, regeneration, and tissue injury; 11) Chromatin, epigenetics and genomics; 12) Techniques and technology; 13) Immunity and the microbiome; 14) Cell division and cell growth; 15) Cell Stress and cell death; 16) Initiatives in Education and DEI.

Meeting Attendance

1,574 people from **34 countries** are registered for the meeting, with **nearly 1,300** planning to attend the event in person in Chicago. This in-person attendance will be higher than the 2022 meeting and comparable to attendance at meetings before the pandemic (2019 - 1220 attendees; 2018 - 1527; 2017 - 1237).

Submitted Abstracts

The original abstract deadline for the 2023 meeting, November 17, was extended to November 25 in acknowledgement of the University of California student/postdoc strike, which may have affected submissions from this large university system. Late abstracts (for posters only) were accepted until January 5, 2023. A total of **1074 abstracts** were submitted in **16 different categories**. Totals of abstract submissions in recent in-person meetings were 994 (2022), 832 (2019), 889 (2018), 716 (2017), 692 (2016/TAGC), 977 (2015), 894 (2014), 966 (2013), 1005 (2012). Hence, the 2023 meeting has the highest number of submitted abstracts for the last ten years.

Platform Session organization and selection of Platform Talks

523 of the total number of abstracts were submitted for consideration for platform talks in each of the 16 topic areas (see Table below).

Topic	Total	Oral	Regular Poster	Late Poster
Total	**1074**	**523**	**492**	**59**
Physiology, metabolism and aging	100	54	41	5
Models of human disease	114	49	61	4
Regulation of gene expression	90	47	41	2
Patterning, morphogenesis and organogenesis	94	45	42	7
Evolution	91	45	41	5

Cell biology: Cytoskeleton, organelles and trafficking	73	43	28	2
Reproduction and gametogenesis	82	35	44	3
Neural development and physiology	67	35	31	1
Stem cells, regeneration, and tissue injury	53	28	21	4
Chromatin, epigenetics and genomics	54	25	27	2
Techniques and technology	45	23	18	4
Neural circuits and behavior	62	22	31	9
Immunity and the microbiome	48	22	21	5
Cell division and cell growth	48	22	25	1
Cell Stress and cell death	39	22	16	1
Initiatives in Education and DEI	14	6	4	4

A total of 22 separate platform session slots (6-8 short talks) were scheduled in the draft. One slot was a stand-alone session for the Techniques and Technology topic area on Saturday evening. The remaining 21 slots were seven concurrent sessions (3 topics per session). Six of the topic areas received 43 or more abstracts for platform talk consideration and were allocated two platform session slots (8 + 6 talks). These are 1) Physiology, metabolism, and aging; 2) Models of human disease; 3) Regulation of gene expression; 4) Patterning, morphogenesis, and organogenesis; 5) Evolution; 6) Cell biology: Cytoskeleton, organelles and trafficking. The remaining 15 topic areas received between 6 and 35 abstracts and were allocated one platform session slot (8 talks). The “Initiatives in Education and DEI” topic area received 6 abstracts for consideration for platform talks, so we invited the co-chairs to speak in the session and/or invite their own choice of speaker to present to ensure we had eight talks for this session.

The process for selecting platform talks was similar to previous years. Session chairs were allocated their abstracts to review on November 22. They submitted their final choices (plus two alternates per session) on December 16. These final choices were then sent to the organizers, who then reviewed across all the sessions to ensure that the platform talks collectively had appropriate balance and representation in terms of speaker demographics (gender, ethnicity, career stage, geography) and, in a few cases recommended that session chairs select alternate choices to ensure appropriate balance. The table below shows the demographics (as self-identified by registrants) for both submitted and accepted platform talk abstracts. The final platform talk selections were sent to Suzy on January 6, 2023.

	% of accepted	**% of submitted**
Asian	34	38
Black or African American	6	4
Hispanic or Latino	12	8
Native Hawaiian or Other Pacific Islander	1	1
White	43	43

Middle Eastern	<1	<1
Prefer not to answer	3	5
Male	39	44
Female	58	51
Gender Non-conforming	1.5	2
Prefer not to answer	1.5	3

Poster Sessions

There are currently 898 abstracts scheduled to be presented as posters at the meeting780 will be presented in person, while 118 will be available for online viewing.

Hybrid Format

Of the 1574 registrants, approximately 200 will be attending virtually. In addition, six of the platform talks will be via zoom. Hybrid attendance or presentation was not considered in the selection of platform talks.

Poster Awards

Six poster awards will be given at the meeting (3 for best GSA graduate posters and 3 for best undergraduate posters). The prize values are 1st - $300, 2nd - $200; 3rd- $100. Poster judging will be similar to previous years. The co-chairs for each session will be asked to initially judge the posters in their topic area and pick their choices for top graduate and undergraduate posters. Given the time constraints, these choices will be based on scientific content and poster design rather than poster presentation. These choices will be communicated to the organizers by Saturday, March 4th, and they will select the final prize winners from these choices. Poster presentations will be completed for the final session on Sunday, March 5th.

Workshops

We received 11 applications for workshops. Each member of the organizer committee reviewed and ranked these applications, and the final selections were made by Zoom. Two applications, “Feeding-fasting rhythms mediated health span for the regulation of metabolic and aging disorders” and “Machine learning of contractile dynamics in the Drosophila heart aging model”) appeared to focus on the work of one lab and were thus declined as having too narrow a scope for this international conference. The remaining nine were accepted. One workshop will be delivered online before the meeting, and the Ecdysone workshop will take place in its usual spot on the Wednesday of the meeting. The remaining workshops will be either on Thursday (7.45-9.45) or Friday (7.45-9.45).

The selected workshops are:

- (Virtual) CRISPR/Cas and related technologies in Drosophila cells and in vivo workshop
- Ecdysone

- Spotlight on Undergraduate Research
- The Neighborhoods Project: Leveraging cultural community connections to develop novel, collaborative genetics research projects
- Developmental Mechanics
- Non-traditional fly models: Contributions and research opportunities
- Everything You Wanted to Know About Sex
- Evolutionary and Population-omics at the Scale of Model Clade Drosophilidae
- Immunometabolism: Flying 10 Years later

Compensation for organizers, speakers, and special awards

The meeting Organizers (5), the Keynote (1) and Plenary Speakers (10) each received free conference registration. Exhibitors that purchased booths also received free conference registration. Everyone had to cover their lodging and travel costs. The Larry Sandler Award Winner receives complimentary airfare, registration, housing, and GSA lifetime membership. The Victoria Finnerty Memorial Fund travel grants were awarded to undergraduate researchers presenting posters, and these recipients were chosen by a Flyboard sub-committee. The inaugural *Drosophila* Community Service Award will also be presented at the meeting.

One question that was raised by several of the PI session co-chairs was whether the trainee co-chairs would be eligible for any subsidized conference attendance. This is something that the GSA and future organizers may want to consider because it may lower barriers to participation for these trainees.

Fundraising

An application was submitted to the Company of Biologists to support the costs of the DEI session, “Discover and Develop Your Community Session.” The organizers were notified in January 2023 that the application was approved for funding in the amount of 3000 GBP.

Assistance to Future ADRC organizers

Material available to the 2023 organizers will be placed in a Dropbox folder with information that Savraj Grewal received from the organizers of the 2022 meeting for future organizing committees. This information includes lists of past speakers and session chairs and templates for solicitation letters sent to potential session chairs and speakers.

DIS Report (Jim Thompson)

Volume 105 (2022) of Drosophila Information Service was published in early January 2023. We are in the process of redesigning our web site, so for now the most direct access can be obtained at: www.ou.edu/journals/dis/byissue.html. It continues to attract a broad range of research reports, technique articles, and teaching activities, although most contributions in this issue were research papers. But we also include two very nice reflections on the contributions of two past contributors to *Drosophila* genetics. Edith M. Wallace (1881?-1964) produced the incredibly detailed *Drosophila* illustrations of many mutations in Lindsley and Grell (1968, *The Genetic Variations of* Drosophila melanogaster) and numerous other publications. J.P. Gupta (1939-2021) was an influential *Drosophila* researcher for five decades in India.

One important project this year was to catch up on the production of printed copies of recent back issues. With help from Benjamin Houston, an undergraduate in my lab, printed copies of recent issues through volume 105 (2022) are now available from www.lulu.com, with high quality illustrations in color, when provided that way by contributors. In addition, we continue to respond to other requests for assistance in locating information for researchers and graduate students. When it comes up on computer searches, our title is sometimes thought to indicate we are an open public information resource, which can invite surprising inquiries. We respond to all of them and help wherever we can.

First published in 1934, DIS remains an active source for research, teaching, and technique articles relevant to our field. Most submissions occur in response to our traditional "Call for Papers", in which we are assisted by the excellent help of staff at FlyBase, University of Indiana. 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.

Finnerty Undergraduate Travel Award Report to the 2023 Fly Board

Justin DiAngelo, Finnerty Undergraduate Travel Award Committee Chair

Selection committee: Justin DiAngelo (chair), Jennifer Bandura, Daniel Cavanaugh, Jennifer Kennell, Judith Leatherman, Matthew Wawersik.

This year we received 40 applications for the Victoria Finnerty (VF) Undergraduate Travel Award. Following an initial round of evaluation, 14 applications were moved to a second round of consideration and were all recommended for funding. In order to maximize the number of students who received funding, money was awarded on a sliding scale, according to their ranking, with the highest amount being $599 so that the students wouldn't have to pay taxes on their award. In total, we awarded $5999 for Finnerty Undergraduate Travel Awards this year.

The awardees are:

Dunham Clark, University of Michigan, $599
Lia Mahal, Rutgers University, $500
Salome Ambokadze, Vassar College, $500
Dominique Doyle, Kean University, $500
Daniel Ruiz, College of Holy Cross, $500
Helen Zhou, Brown University, $500
Kyra Lockett, Lewis-Clark State College, $500
Abbigayle Gamble, Indiana State University, $400
Lelia Lin, UC Irvine, $400
Max Lu, University of Alabama, $400
Mia Hoover, University of North Carolina, $300
Mia Jones, Kennesaw State University, $300
Jonah Boardman, Brown University, $300
Seohee Ma, University of St. Thomas, $300

BLOOMINGTON DROSOPHILA STOCK CENTER

Stock Holdings as of February 7, 2023

- 82,165 stocks with 85,086 unique genetic components

2022 Use Statistics In calendar year 2022, the 171,299 samples sent in 10,208 shipments represented a decrease of 13,719 (7%) samples and 943 (8%) shipments from 2021.

On average, we saw 2 orders per stock. 53% of stocks were ordered at least once, 10% were ordered 6 or more times, and 3 stocks were ordered >95 times. The most popular stock was Canton-S (#64349), which was ordered 125 times. 74% of stocks available for 2020–2022 received at least one order demonstrating that the majority of the collection is being used by the fly community.

User base

- 3,908 registered user groups, 1,825 of which ordered stocks in 2022
- 8,344 registered users, 2,483 of whom ordered stocks in 2022

Growth 3,179 stocks were accessioned in 2022:

- 1,079 Drosophila Synthetic Population Resource stocks from Stuart Macdonald and colleagues
- 387 CRIMIC stocks from Hugo Bellen, Norbert Perrimon, Genetivision and colleagues
- 278 UAS-human cDNA stocks from Hugo Bellen, Sue Celniker and colleagues
- 124 Exelixis FRT insertion stocks from the Japanese National Institute of Genetics
- 120 Fourth Chromosome Resource Project stocks from Stuart Newfeld, Mike O'Connor and colleagues
- 104 stocks expressing guide RNAs for gene knockout or overexpression from the Transgenic RNAi Project
- 93 lexA driver stocks from Janelia Research Campus
- 68 smORF knockout and UAS stocks from Norbert Perrimon and colleagues
- 59 UAS stocks expressing COVID proteins from Hugo Bellen, Oguz Kanca and colleagues
- 35 stocks with PI signaling gene knockouts from Deepti Trivedi, Padinjat Raghu and colleagues
- 33 stocks expressing tagged transcription factors from the modERN project
- 27 Drosophila Protein Interaction Map stocks from Deepti Trivedi and colleagues
- 20 UAS stocks for autism-related genes from Hugo Bellen and colleagues
- 749 assorted stocks from the community at large

Staff 68 stockkeepers (8 full-time and 60 part-time to make 26 full-time equivalents) and 9 managers/scientists.

Funding We are in year 4 of a 5-year grant from NIH with $453,911 in direct funds contributed by OD, NIGMS and NICHD and $86,674 of supplemental funds from NINDS for maintenance and distribution of split-GAL4 stocks. Fee income covers our remaining expenses and, in recent years, has accounted for ~79% of our regular funding. OD provided two administrative supplements during the 2021–2022 period: $222,187 direct for upgrades to our data management systems and $95,543 direct for improvements to the media kitchen and dishwashing facility. We also receive salary support for participating in consortium projects to improve stock resources (R24OD028242 and R24OD031952), cryopreservation (R24OD034063) and genetic dissection of complex traits (RO1OD034064).

New Stocks We expect to add 8,700–9,900 new stocks in 2023:

- 3,700–4,700 split-GAL4 and stable split-GAL4 combo stocks from the Janelia FlyLight Project Team
- 1,600 DGRP stocks from Trudy Mackay and colleagues
- 1,000 sgRNA and shRNA stocks from the Transgenic RNAi Project
- 700 CRIMIC, KozakGAL4 and GFP protein trap stocks from Hugo Bellen, Norbert Perrimon and colleagues
- 400 UAS-human cDNA stocks from Hugo Bellen, Sue Celniker and colleagues
- 337 Drosophila Synthetic Population Resource stocks from Stuart Macdonald, Tony Long and colleagues
- 150–250 TRiP knock-in stocks (split-GAL4, lex-GAD, QF2, etc.) for cell and tissue-specific expression

- 130–200 RMCE, UAS and KO stocks from the Fourth Chromosome Resource Project
- 50 stocks expressing tagged transcription factors from the modERN Project
- 700 assorted stocks from the community at large

Pruning We conducted no systematic culls during 2022. We lost or discarded 353 assorted stocks.

Scientific Advisory Board

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

Intramural Advisory Board

- Justin Kumar
- Jason Tennessen

Vienna Drosophila Resource Center (VDRC), Vienna, Austria

The VDRC (**www.vdrc.at)** is part of Vienna Biocenter Core Facilities, 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.
User fees are subsidized ~30% by the Austrian Federal Ministry for Science and Research and the City of Vienna.

Key changes during 2022

- 28 new lines acquired in "Other Resources" from the European community.
- Links added to search the fTRG fosmid construct library of 10,000 GFP-tagged clones
- Some stocks maintained in reduced copy number and staff reduced accordingly.

Usage Statistics 2022

- **27,590** stocks delivered to **568** user groups in **1,204** separate orders.
- Average orders/stock = 1.03.
- 47% of stocks were ordered at least 1x.

Resources as of March 2023

Total stocks currently available to the community: **26,904**

- 23,416 RNAi lines (12,934 in GD, 9,679 in KK and 803 in the shRNA collection).
- 21 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.
- 1,920 UAS-sgRNA and 23 Cas9 toolkit lines for CRISPR-mediated genome engineering (Heidelberg, HD-CFD).
- 200 enhancer-GAL4 lines (VTs, Vienna Tiles). Expression patterns annotated in adult brain and embryo. Searchable databases available.
- 895 Tagged FlyFos TransgeneOme (fTRG) lines.
- A small, but growing number of plasmids and stocks made available to the community from Private Stock Collections, including mutant alleles, tagged constructs and reporters.
- 13,848 DNA constructs used for the generation of the GD collection.

Services

VDRC is open to **donations** of highly used stocks for integration into its community stock center collection (complementary to other stock centers).
In addition, we offer:

- Private Stock Keeping Service to maintain and distribute personal fly stock/plasmid collections on a cost recovery basis.
- On-site screening to facilitate large scale RNAi screens.
- Fly food service - primarily for fly groups in the Vienna area.

Future

Working on cryopreservation – using published protocol (Zhan *et al.* NatureComm, 2021)

To become more financially self-sustaining our strategy is to consolidate and replace rarely used or obsolete lines with more current lines.

We are actively trying to acquire new stocks, especially those created by fly researchers in Europe.

We are keen to discuss involvement at an early stage to help develop new resources. As well as stock maintenance and distribution, our team has significant experience in high throughput construct generation, Drosophila injection and transgenic production.

Drosophila Genomics Resource Center (DGRC): Booth #7

Critical Changes to Report:

Personnel:
Andrew C. Zelhof Ph.D. Director
Kris Klueg Ph.D. Associate Director
Arthur Luhur Ph.D. Associate Director
Daniel Mariyappa Ph.D. Associate Director
Johnny Roberts – Research Technician
Laura Multini Ph.D. – Research Technicican

Advisory Board:
Susan Parkhurst Ph.D.
Deborah Andrew Ph.D.
John Abrams Ph.D.
Erika Bach Ph.D.
Stephen Rogers Ph.D

Funding: NIH P40OD010949 - The DGRC is finishing our final year (April 1, 2022 to March 31, 2023) of our five-year cycle. We have resubmitted the renewal application.

Year	Vectors/cDNAs Shipped	Cell Lines Shipped	Products Shipped[1]
2018	2357	250	3039
2019	1894	268	2995
2020	1645	171	2381
2021	1741	239	2459
2022	1666	151	2310

Table 1: Summary of items shipped over the last five years of this grant. Years are represented from Jan.1st – Dec.31st. [1] Products shipped is the total number of items shipped and not limited to cell or cDNA/vector clones.

DGRC continues to run an online survey through Qualtrics

DGRC Publications (2022):

- Mariyappa, D., Rusch, D.B., Han, S., Luhur, A., Overton, D., Miller, D.F.B., Bergman, C.M., Zelhof, A.C. (2022). A novel transposable element-based authentication protocol for Drosophila cell lines. G3 Feb 2022 4;12(2). PMID**:** 34849844**,** PMCID: PMC9210319

New Product/Updates in the past year:

Updates:

a. **RRID's** – All DGRC cell lines and DNA reagents now have a unique RRID identifier. The DGRC requests the Drosophila community to adapt using the unique RRID's to report reagents in publications as per the NIH guidelines.
b. **Transgenic cell service** – We have continued to expand the attP containing cell lines catalog. The research community can continue to avail a fee-based service to generate stable cell lines containing their transgenic construct of choice.

Cell Lines: No new cell lines were added since the last report.

Vector/DNA Reagents added

Reagent(s)	**Originating Lab**	**Description (number)**	**NIH grant/Other funding**
CRISPR vectors	Han Lab	Vectors (8)	R01 NS099125 R21 OD023824 R21 HD088744
Kozak GAL4 vector	Bellen Lab	Vector (1)	R01 GM067858 R24 OD031447 U54 NS093793 GM067761 GM084947 HHMI Huffington Foundation Carnegie Inst. Of Science
Other funding sources/Non-US Labs			
Nanobody LexAop>UAS>QUAS vector	Baena Lopez Lab	Vectors (1)	Non-US Lab
RFP fluorescent vectors	Magali Lab	Vectors (14)	Non-US Lab

2023 Report for the Fly Board

DRSC/TRiP at Harvard Medical School
https://fgr.hms.harvard.edu/

1. Background: The DRSC began in 2004 to support cell RNAi screening and the TRiP in 2008 to support in vivo RNAi studies. Currently, we function as a unified group, the Drosophila Research & Screening Center-Biomedical Technology Research Resource (DRSC-BTRR). **The overall mission of the DRSC-BTRR is to develop and improve technologies for cell-based and *in vivo* functional genomics in *Drosophila* and other species, then broadly disseminate mature technologies through outreach, training, and dissemination.** We accomplish these goals with input from technology partners and from collaborators who test technologies in specific applications. Our wet-bench team works together with a bioinformatics team that supports reagent design, data analysis, and more, and develops and maintains a suite of online resources available to the community at large for reagent identification, ortholog mapping, data mining, and other applications. Although our primary focus is on technologies for *Drosophila* research, our CRISPR cell screen technology development includes application other arthropod cell lines, and many of our bioinformatics resources are relevant to studies in other species. The group is led by Norbert Perrimon (PI) along with Stephanie Mohr, Jonathan Zirin, and Claire Yanhui Hu. We are located in an ~2200 sq ft. lab space that includes molecular bench areas, a fly-pushing area, and a tissue culture room, and available equipment includes automated liquid handling robotics, automated confocal imaging, and a luminometer/fluorimeter.

2. Funding: The DRSC and TRiP are supported together as the NIH NIGMS P41-funded DRSC-BTRR. In January 2023, we applied for 'renewal' in the form of RM1 funding of our groups as the DRSC-Biomedical Technology Development and Dissemination center (DRSC-BTDD). The DRSC-BTDD would similarly focus on cell-based and *in vivo* technologies, with greater emphasis on technology improvement, training, and dissemination. **We are very grateful for the support of the Drosophila Board for our application for RM1 BTDD funding.** In addition to P41 funding, we also have past and current R24 funding from the NIH Office of Research Infrastructure Projects (ORIP) to development of cell line resources (with A. Simcox) and fly stock resources (with H. Bellen); and we were recently awarded R21 funding from NIH NIAID to support application of CRISPR technologies to cell lines from the Lyme tick *Ixodes scapularis* (with J. Pedra, Univ of MD).

3. Key metrics of success:

- Our recent DRSC-BTRR collaborators include investigators from 15 US states (CA, IA, IL, IN, MA, MD, MI, MO, NV, OR, PA, RI, TN, TX, UT) and several other countries
- We deposited plasmids and sgRNA libraries at Addgene, which distributed 151 of our plasmids in 2022 alone (36 for NanoTagging, 20 for proximity labeling, 95 for CRISPR)
- We deposited new fly stocks for CRISPR technologies, NanoTagging, and proximity labeling at the BDSC, which shipped >70,000 TRiP-associated fly stocks in 2022 alone
- We deposited GFP-tagged cells, knockout cells, and CRISPR 'screen-ready' (attP, Cas9+) *Drosophila* and mosquito cells at the DGRC, and since fall 2019, the DGRC has shipped 146 cell lines to other labs, including 30 distributions of 'screen-ready' cells
- Our online resources were widely used, including >180,000 total pageviews of our online tools in 2022 alone and >300 publications in the period 8/2019-01/2023 that mention use of one or more online tool

4. What's new in cell and in vivo technologies: Below, we outline what's new since our 2022 update in the areas of cell technologies, *in vivo* technologies, bioinformatics, and outreach.

a. Cell CRISPR screens:

- We developed a pooled CRISPR activation (CRISPRa) cell screening platform for *Drosophila* S2R+ cells and did a genome-wide screen (Xia et al. 2022 bioRxiv)
- We participated along with the DGRC in a project led by Amanda Simcox (The Ohio State University) that resulted in generation by the Simcox lab of tissue-specific *Drosophila* cell lines (Coleman-Gosser, Raghuvanshi, Stitzinger et al. 2023 bioRxiv)
- We developed a 'version 2' of our pooled CRISPR knockout screen platform that results in improved data quality and will be presented pre-publication at the ADRC 2023

- We performed a set of genome-wide pooled CRISPR cell screens in cells from the *Anopheles* mosquito in collaboration with R. Smith (Iowa State)
- Results from genome-wide *Drosophila* CRISPR or RNAi cell screens were newly published together with collaborators C. Chow (University of Utah; Dalton et al. 2022), M. Dong (Children's Hospital Boston; Hu et al. 2022), and T. Walther (Harvard School of Public Health; Song et al. 2022)

b. In vivo technologies:

- We generated over 400 new fly stocks as part fly stock resource targeting ~300 fly orthologs of human genes identified as SARS-CoV-2-interactors
- We generated over 800 sgRNA and shRNA lines for the TRiP RNAi, TRiP-CRISPR-KO, and TRiP-CRISPR-OE collections, and deposited 500 fly stocks to BDSC
- We generated a set of >50 LexA and QF tissue-specific driver lines using CRISPR/Cas9-mediated knock-in that will be deposited soon to BDSC
- We generated both activation domain and DNA binding domain split-Gal4 lines for 10 gene pairs to produce new highly tissue-specific driver lines
- We published a detailed protocol as a follow-up to our previous report in eLife of establishment of an epitope tag-nanobody system (NanoTags) for *Drosophila,* and generated 10 new endogenous NanoTag knock-in lines that will be deposited soon to BDSC (Kim et al. 2022)
- We published a detailed protocol that outlines steps to design, generate, and express prime editing components in transgenic flies (Bosch et al. 2022)

c. Bioinformatics resources:

- We launched and published a new online resource, Paralog Explorer, to support search and analysis of potential paralogs within *Drosophila* or other common models (Hu et al. 2022)
- We published a new online resource, FlyPhone, to support prediction of signaling between cell types based on single cell RNAseq data (Liu et al. 2022)
- We updated our DIOPT ortholog prediction tool (v8.5 and beta v9 both available), with a new user interface, new species, and new algorithms added
- We provided custom large outputs based on DIOPT that were then integrated into FlyBase, the Alliance for Genome Resources, Echinobase, and other sites

5. Outreach:

- At the ADRC 2023, we will present talks and posters, including a talk on our 'version 2' pooled CRISPR cell screen technology in the technology session
- On Feb. 24, 2023, we hosted an ADRC 2023 online workshop with a focus on CRISPR technology in *Drosophila* that included talks from our group and other labs
- On Feb. 17, 2023, we hosted a technology workshop for the Drosophila Research and Training Center of Nigeria that included talks from the DRSC-BTRR and Perrimon lab, and R. Cagan (Glasgow)
- On June 16, 2022, we presented a talk that included discussion of our new DRscDB online resource of single-cell RNAseq data at the Boston Area Drosophila meeting at Boston College
- We presented additional technology-focused talks, posters, seminars, etc. at regional and national conferences focused on *Drosophila* research, CRISPR technology, and other topics
- In addition to protocol publications noted above, we also published a technology-focused review article (Zirin et al. 2022 on CRISPR technologies in *Drosophila*)
- We summarized the basic considerations and capabilities of insect cell CRISPR screens in a news post at our website, "So you want to do a CRISPR pooled screen in insect cells? Here's How"
- We summarized reports related to TRiP RNAi fly stock troubleshooting and considerations in a news post at our website, "Important new considerations for TRiP stock users"
- Interested in visiting for technology training or cell screening, becoming a collaborator, getting troubleshooting advice, etc.? Inquiries welcome. Contact: stephanie_mohr@hms.harvard.edu

6. Technology dissemination (summary table):

	Insect cell CRISPR technologies	***Drosophila in vivo* CRISPR technologies**	***Drosophila in vivo* NanoTag technologies**	***Drosophila in vivo* proximity labeling technologies**

Research publication(s)	✓	✓	✓	✓
Step-by-step protocol(s)	✓	✓	✓	
Technology review(s)	✓	✓	✓	✓
Associated online resource(s)	✓	✓	✓	
Materials provided to other labs	✓	✓	✓	✓
Materials provided to repository(ies)	✓	✓	✓	✓
Informal consultations	✓	✓	✓	✓
Talks, posters, workshops, etc.	✓	✓	✓	✓

7. New Preprints:

N Coleman-Gosser, S Raghuvanshi, S Stitzinger, Y Hu, W Chen, A Luhur, D Mariyappa, M Josifov, A Zelhof, SE Mohr, N Perrimon, A Simcox. **Continuous muscle, glial, epithelial, neuronal, and hemocyte cell lines for Drosophila research.** bioRxiv 2023.01.18.524445; doi: https://doi.org/10.1101/2023.01.18.524445

B Xia, R Viswanatha, Y Hu, SE Mohr, N Perrimon. **Pooled genome-wide CRISPR activation screening for rapamycin resistance genes in Drosophila cells.** bioRxiv 2022.12.09.519790; doi: https://doi.org/10.1101/2022.12.09.519790

8. New Publications:

Kim AR, Xu J, Cheloha R, Mohr SE, Zirin J, Ploegh HL, Perrimon N. **NanoTag Nanobody Tools for Drosophila In Vitro and In Vivo Studies.** Curr Protoc. 2022 Dec;2(12):e628. doi: 10.1002/cpz1.628. PMID: 36571722; PMCID: PMC9811555.

Hu Y, Ewen-Campen B, Comjean A, Rodiger J, Mohr SE, Perrimon N. **Paralog Explorer: A resource for mining information about paralogs in common research organisms.** Comput Struct Biotechnol J. 2022 Nov 24;20:6570-6577. doi:10.1016/j.csbj.2022.11.041. PMID: 36467589; PMCID: PMC9712503.

Xu Y, Viswanatha R, Sitsel O, Roderer D, Zhao H, Ashwood C, Voelcker C, Tian S, Raunser S, Perrimon N, Dong M. **CRISPR screens in Drosophila cells identify Vsg as a Tc toxin receptor.** Nature. 2022 Oct;610(7931):349-355. doi:10.1038/s41586-022-05250-7. PMID: 36171290; PMCID: PMC9631961.

Dalton HM, Viswanatha R, Brathwaite R Jr, Zuno JS, Berman AR, Rushforth R, Mohr SE, Perrimon N, Chow CY. **A genome-wide CRISPR screen identifies DPM1 as a modifier of DPAGT1 deficiency and ER stress.** PLoS Genet. 2022 Sep 27;18(9):e1010430. doi: 10.1371/journal.pgen.1010430. PMID: 36166480; PMCID: PMC9543880.

Song J, Mizrak A, Lee CW, Cicconet M, Lai ZW, Tang WC, Lu CH, Mohr SE, Farese RV Jr, Walther TC. **Identification of two pathways mediating protein targeting from ER to lipid droplets.** Nat Cell Biol. 2022 Sep;24(9):1364-1377. doi: 10.1038/s41556-022-00974-0. PMID: 36050470; PMCID: PMC9481466.

Zirin J, Bosch J, Viswanatha R, Mohr SE, Perrimon N. **State-of-the-art CRISPR for in vivo and cell-based studies in Drosophila.** Trends Genet. 2022 May;38(5):437-453. doi: 10.1016/j.tig.2021.11.006. PMID: 34933779; PMCID: PMC9007876.

Liu Y, Li JSS, Rodiger J, Comjean A, Attrill H, Antonazzo G, Brown NH, Hu Y, Perrimon N. **FlyPhoneDB: an integrated web-based resource for cell-cell communication prediction in Drosophila.** Genetics. 2022 Mar 3;220(3):iyab235. doi: 10.1093/genetics/iyab235. PMID: 35100387; PMCID: PMC9176295.

Bosch JA, Perrimon N. **Prime Editing for Precise Genome Engineering in Drosophila.** Methods Mol Biol. 2022;2540:113-134. doi:10.1007/978-1-0716-2541-5_5. PMID: 35980575.

FlyBase Report to the Drosophila Board
13-February-2023

For the past thirty years, FlyBase has provided a centralized resource for Drosophila genetic and genomic data to enable researchers to further their research. Drosophila is one of the premier model organisms and provides cost-effective help in elucidating the etiology of human genetic diseases. FlyBase has three main goals.

1. To continue curation of literature and reagents relevant to Drosophila research, so that researchers can continue to rely on FlyBase to find the latest innovations in the field. We will prioritize curation of data sets relevant to gene expression, cellular functions, signaling pathways, and human diseases, and display the information in an intuitive, integrated, readily searchable format.
2. To improve FlyBase's utility to the human genetics and population genetics communities, by curating and integrating relevant data sets, and developing tools that enable better access to this wealth of data. As a member of The Alliance for Genomic Research (AGR), FlyBase will work closely with other Model Organism Databases (MODs) to integrate data sets and develop tools to enable cross-species analyses. This effort will have a major impact on the fly community, accelerating the development of models of human diseases.
3. To facilitate more integrative analyses and approaches, FlyBase will continue to expand its utility as a platform for integrating and displaying large-scale studies, transcriptomics and proteomics data sets. In addition, FlyBase will improve access and display of tools available within the community, and incorporate the most useful data sets and tools for visualizing complex data sets to enable more researchers to take a more global approach to their genetic research.

April 1, 2023 begins year 6 of our current grant cycle with NHGRI. We submitted a 5-year renewal proposal in January 2023 in which our projected budget will be 50% of what it was in 2016. Additional funds FlyBase receives are an NHGRI supplement for the Alliance; an NSF grant; and funding from a BBSRC, Wellcome Trust and ritish Medical Research Council grant which altogether bring FlyBase's funding closer to 60-65% of 2016. Finally, we continue to collect some fees from the community to cover the budget deficit. As of 01-February-2023 (nearly 6 years since fees were implemented), ~555 labs have contributed ~$665,000. We plan to continue the user-fee collection to supplement FlyBase funding.

We are grateful for the strong support from our community and appreciate the support of the FlyBoard in reminding the community of this *extremely necessary* user fee collection.

FlyBase is a mature project with an experienced staff of long-term employees and many continuous activities. In this report, we include minimal descriptions of on-going activities and highlights of new or modified activities, as well as web site usage statistics.

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

Many literature curation and high throughput curation activities will continue unchanged. Some highlights are:

- Automated triaging pipeline: We will use the SVM system to flag disease-related papers and integrate this into our triage pipeline.
- An emphasis has been placed on genome feature curation and physical interaction curation, with goals of bringing genome feature curation completely up to date, and keeping pace with new physical interaction curation while also addressing the backlog.
- Human disease model curation: curation effort continues for human disease models, including creation of free-text summaries and capture of the genes, both fly and human, used in these investigations. There has been an increase in characterization of disease-implicated variants using Drosophila models; while these are highlighted in the human disease model summaries, the growing number has led us to plan for a more integrated view. This information will be presented in tabulated formats in the human disease model reports and in gene reports. Variants introduced into fly genes as analogous mutations (as transgenes or at the endogenous locus) are mapped to the genome. The next step is development of the Web presentation of these data.
- We continue allele-based curation of disease models based on the Disease Ontology (DO); this curation is compatible with the approach used by the Alliance. A key aspect of FlyBase DO curation is the capture of genetic interactions that ameliorate or exacerbate a disease-related phenotype.
- We will use available orthology data and expand our representation of orthology calls especially as they relate to the other MODs and human genes.
- Gene Group curation: We continue to update our links between fly Gene Groups at FlyBase and human Gene Groups at the HGNC. This facilitates comparison between equivalent protein complexes and other functional classes.
- We will curate select datasets deemed to be of highest general interest to the FlyBase user community.
- We will coordinate with the DGRC and DRSC to create FlyBase reports for new cell lines added to the DGRC, many of which come from the DRSC.
- Signaling Pathways: We have continued to expand our Pathway page resource, using GO annotation as a basis to compile experimental evidence-weighted lists of genes that encode either core pathway components or pathway regulators. All FlyBase-curated pathway data can now be viewed in a dedicated 'Pathways' section of Gene Reports and can be searched via a new 'Pathways' tab on the QuickSearch tool. As part of the second phase of development, we have added graphical network representations to pathway pages. We will continue to add new pathways and update the 16 signaling pathway reports available in FlyBase and produce downloadable thumbnail pathway images as a simplified text-book style guide and downloadable resource, to complement the computational network diagrams and table of genes already available.
- With combined funding from VFB (Virtual Fly Brain) and FlyBase, we will continue adding new anatomy terms and enhancing the existing terms by an ongoing review process, with a focus on new neuroanatomy terms and definitions.
- We will continue to review and improve the phenotypic class ontology and, focusing on terms for behavioral, learning and memory phenotypes in collaboration with VFB.
- Development of Chado modules for gene groups and human disease models will be maintained and updated as necessary. Work on new modules of the FlyBase Chado central database will continue.
- We are actively working with the Fly Cell Atlas and single Cell Atlas to annotate all Drosophila cell types and curate scRNAseq data sets.
- Continue to establish pipeline to fetch scRNAseq datasets from the EBI's Single Cell Expression Atlas, annotate them, and load the metadata into FlyBase as dataset reports.
- Continue curation of GAL4 drivers.

- Experimental tool report development continues.

FlyBase web site production and development will continue as planned with 6 releases to flybase.org each year. There are extensive ongoing activities to maintain the website include internal and external group coordination, pipeline management and maintenance, and system administration tasks including:

- Participation in development, web development, and ontology committee video conferences
- Chair of web development committee
- System administration of personal development machines
- Administration of on-premise server cluster in IU Biology Building (system updates, hardware failures, backups, and configuration changes)
- Administration of cloud resources (system updates, backups, and configuration changes)
- Internet security monitoring and response
- Project wide support for JIRA (ticketing system), Fisheye (subversion browser), FlyBase GitHub repository, and subversion server (version control)
- Produced 6 releases of FlyBase from Sep 2020 to Aug 2021
- Managed archives of designated FlyBase releases
- Collecting web access fee vouchers
- Maintained FTYP pipeline
- Maintained FlyBase Wiki
- Maintained BDSC to FlyBase pipeline to ensure that critical stock information is in sync between the two groups
- Mediate communication between FlyBase and the Fly Board and help with the Fly Board elections
- Participated in Alliance of Genome Resources conference calls
- Lead preliminary efforts for a new centralized BLAST service at the Alliance of Genome Resources and FlyBase.

FlyBase improves the utility of the resource for the core community of Drosophila research and to attract additional users through a variety of outreach activities including:

- Community outreach via commentaries and the FlyBase Newsletter
- The FlyBase Community Advisory Group (FCAG) who respond to surveys, make suggestions, etc.
- Video tutorials round at the 'FlyBase TV' YouTube channel: https://www.youtube.com/c/FlyBaseTV.
- Twitter**:** We promote FlyBase using Twitter: @ FlyBaseDotrOrg https://twitter.com/flybasedotorg?lang=en
- FlyBase Help Desk: We maintain a project-wide help desk to provide support to users with data/web interface questions or suggestions.
- A "New to Flies" icon is on the home page and includes links to various Drosophila resources, and an international list of laboratories. This arose from discussions at the 2023 Annual Drosophila Conference. The graduate student representative of the Fly Board shared survey results from graduate students exploring online resource use**,** prompting valuable suggestions that are being implemented**.**

Future development goals:

For the next year, the FlyBase website team will focus on providing support for development required for new FlyBase projects that are being initiated at the other sites. In addition, we plan to continue improving and optimizing the production web site and release pipelines as time

permits. An immediate target is to complete implementation of a stacked ribbon tool integrated with the FlyBase hit list machinery. Near term projects include the new BLAST service (with the Alliance) and the DIOPT 9 upgrade.

- Implement stacked ribbon tool integrated with the FlyBase hit list machinery
- Upgrade orthology tools to DIOPT 9
- Implement Gene Toolkit section in gene reports
- Complete the FlyBase aspect of the Alliance BLAST service and integrate it into our website
- Merge new bulk data files into the FlyBase web and FTP sites
- Coordinate with DRSC to connect FlyBase gene lists to their enrichment tool
- Handle split GAL4 combination FlyBase objects in website presentations
- Synchronize Batch Download with current FB data types and report fields
- Implement scRNA-seq expression histograms on gene reports
- Overhaul GO annotation table in gene reports
- Optimize usability in FlyBase based on user feedback and observations
- Provide support for new FlyBase curator projects
- Continue to expand our use of cloud-based services where it makes technical and financial sense
- Evaluate open-source tools for automating cloud deployment and management
- Enhancement of public programmatic endpoints (APIs) to improve data access for external collaborations (*e.g.,* Alliance) and advanced users
- Continue to coordinate with Alliance development teams
- Continue security improvements for cloud and on-premise compute resources

Flybase website future development goals planned include:

- Basic Chemical reports based on ChEBI
- Move BLAST to a centralized system at the Alliance of Genome Resources
- Implement required changes required after the genotype curation overhaul
- Further tweaks and customizations to JBrowse tracks
- Stacked ribbons for summarizing gene expression and function
- Improvements to integration and display of DGRC data on FlyBase
- Optimize usability in FlyBase based on user feedback and observations
- Provide support for new FlyBase curator projects
- Continue to expand our use of cloud-based services where it makes technical and financial sense
- Evaluate open-source tools for automating cloud deployment and management
- Enhancement of public programmatic endpoints (APIs) to improve data access for external collaborations (*e.g.,* AGR) and advanced users
- Continue to coordinate with AGR development teams
- Continue security improvements for cloud and on-premise compute resources

FlyBase will continue to obtain community input through FlyBase Community Advisory Group, feedback at the US and European Drosophila Research Conferences, input through the FlyBase help desk and from the FlyBase Scientific Advisory Board.

FlyBase will attend conferences either virtually or in person of other research communities (such as other model organism communities and the human genetics community) to advertise FlyBase and to get feedback on how to make FlyBase data more accessible to these communities. We will also continue the production of a series of training videos on the best

methods for using, browsing and searching FlyBase.

FlyBase will have a 3 day project meeting in the fall of 2023. One day will be devoted to a meeting with FlyBase SAB members/experts in specific fields. The remainder will be discussions amongst staff and PIs. This meeting will guide priorities for FlyBase for the remainder of the funded grant period including FlyBase's role in The Alliance effort. We will continue to contribute to Alliance working groups within our remit and areas of expertise.

Alliance of Genome Resources FlyBase is a member of the Alliance of Genome Resources which was organized to provide an integrated web portal of several model organism resources to integrate their data and develop tools to enable easily accessible cross-species analyses between *D. melanogaster*, *C. elegans*, *S. cerevisiae*, *D. rerio*, *M. musculus* and *R. norvegicus.*

FlyBase staff currently are members to several working groups within the Alliance: 'Disease and Phenotypes', 'Literature Acquistion', 'Interactions', 'Pathways', 'Alleles', 'Variants', "Orthology", 'User Outreach', 'Gene Summaries', "Searches", helping to specify commonalities in the content/format of data exchange, as well as the display and searching of integrated data in the Alliance website. Developers are involved in producing and integrating data for the Alliance website members of the Architecture working group, and setting up website management. Two FlyBase members have served as Alliance Data Quartermasters (responsible for overall dataset integration / liaison between working groups and developers), one person is the Alliance Twitter Master, and one person administers the Jira software and organizes the all-developer weekly Technical Calls discussions. Significant contributions have been made to supporting the Alliance cloud infrastructure and maintaining developer tools utilized throughout the entire project. FlyBase has also continued to contribute to the development of search tools, created software for supporting gene annotations, worked to harmonize allele, variant, and genetic interaction data across MODs, and helped to develop the "LinkML" unified cross-organization model of Alliance data. We continue to contribute to working groups within our remit and areas of expertise.

2022 FlyBase Web Usage

The following are web statistics from the FlyBase website as captured by Google Analytics. Unless otherwise stated, all usage statistics in this document cover the period of Jan-Dec for the years 2017-2021 and Jan-Sep for 2022. In summary, the usage statistics for Jan-Sep 2022, when compared to the same period in the previous year, indicate that our overall pageviews have decreased slightly (1.3%), our sessions have increased slightly (~1%), and the number of users has increased (8.8%). Last year in this report we noted significant increases in these statistics (25-50%); these were attributed to web bots, mostly from China. These bots are still operating, so our numbers for traffic from China are likely greatly inflated when compared to the traffic from other countries.

Pageviews

Figure 1 shows FlyBase pageviews for the previously mentioned time periods. A pageview is defined as a hit to an HTML page, script output or other content that does not include non-document files (CSS, images, JavaScript, etc.). The average number of pageviews per month for 2022 thus far is 731k, with a high of 881k and a low of 643k. The periodic dips in this plot all correlate with expected seasonal patterns that we typically experience. Compared to Jan-Sep of 2021, pageviews are down 1.3%.

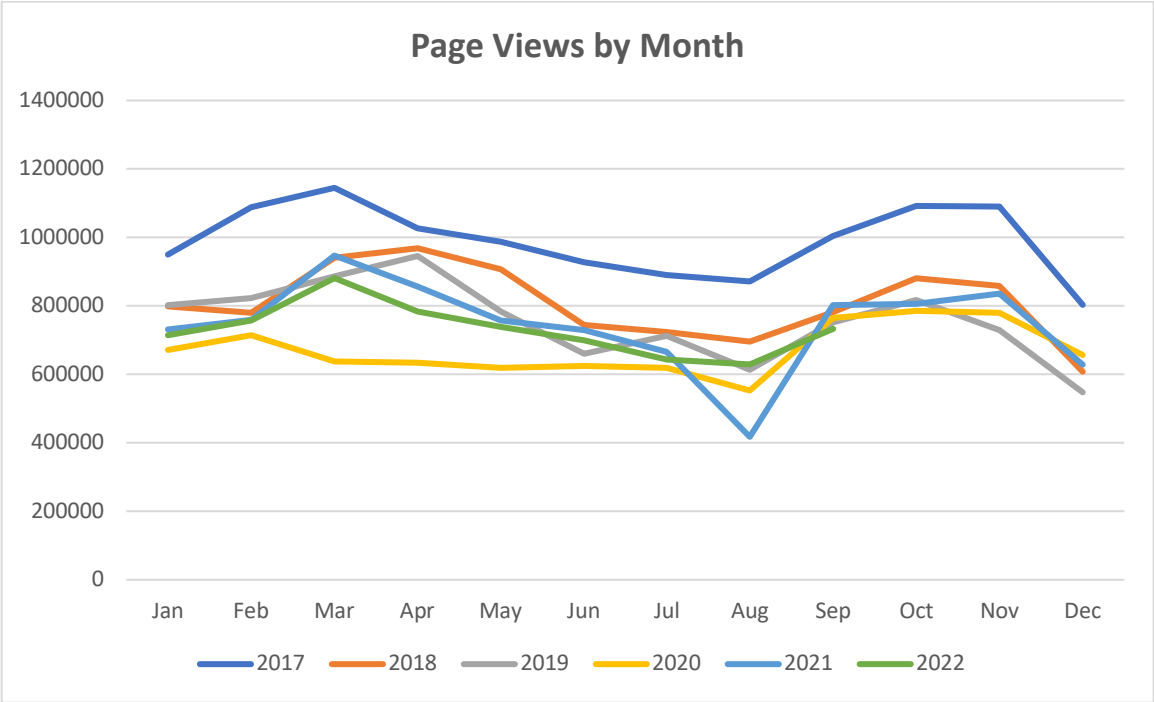


Figure 1 – FlyBase Pageviews for Jan 2017 – Sep 2022

Sessions

Figure 2 shows FlyBase sessions (visits) for the same period as pageviews. A session is defined as a period of activity by a unique web user. If no activity is recorded for 30 minutes, any subsequent activity is counted as a new session. The average number of sessions for 2022 thus far is 169k, with a high of 196k and a low of 147k. Compared to Jan-Sep of 2021, sessions are virtually the same (up <1%).

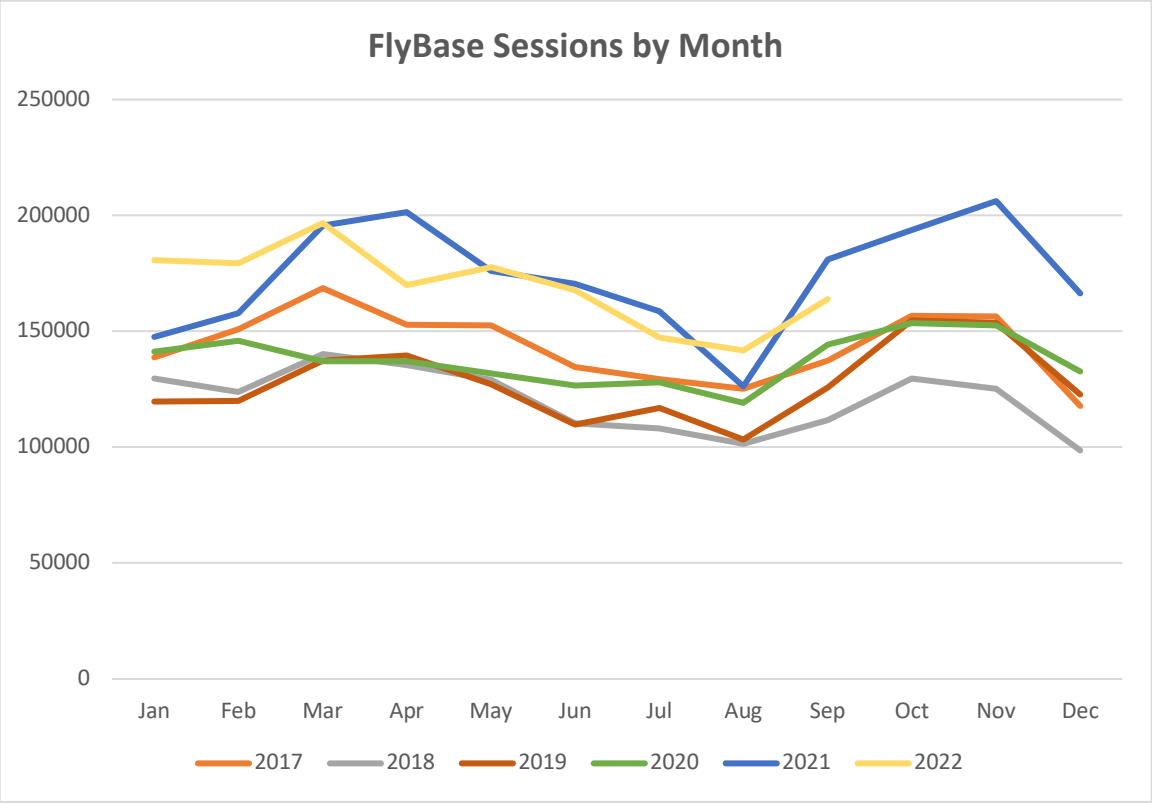


Figure 2 – FlyBase sessions for Jan 2017 – Sep 2022

Users

Figure 3 shows FlyBase users for the same period. A user is defined as a unique session ID that Google analytics generates. This value does not account for a single user using multiple computers and/or browsers in some cases (*e.g.* not logged into a Google account). The average number of users for 2022 thus far is 69k/month, with a high of 85k and a low of 51k. Compared to Jan-Sep of 2021, the number of FlyBase Users is virtually the same (up <1%). Note that the number of users steeply increased at the beginning of 2021, doubling our total user statistic between December 2020 and April 2021. This is when the web bot traffic came online.

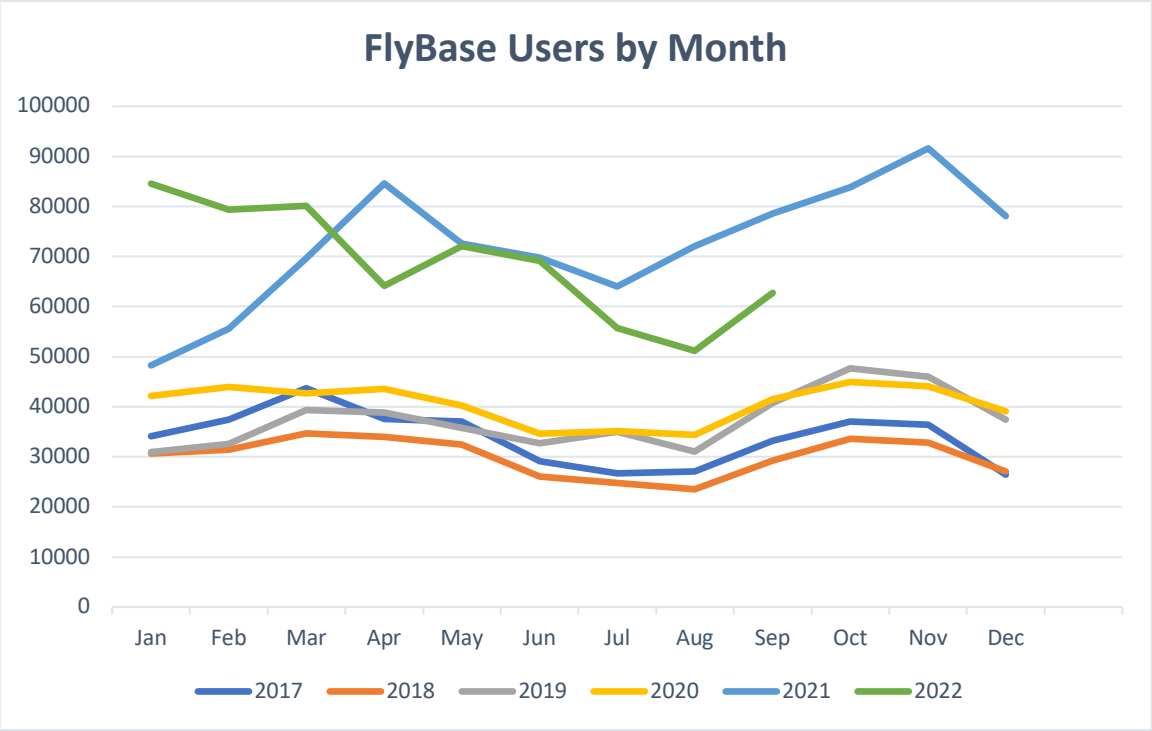
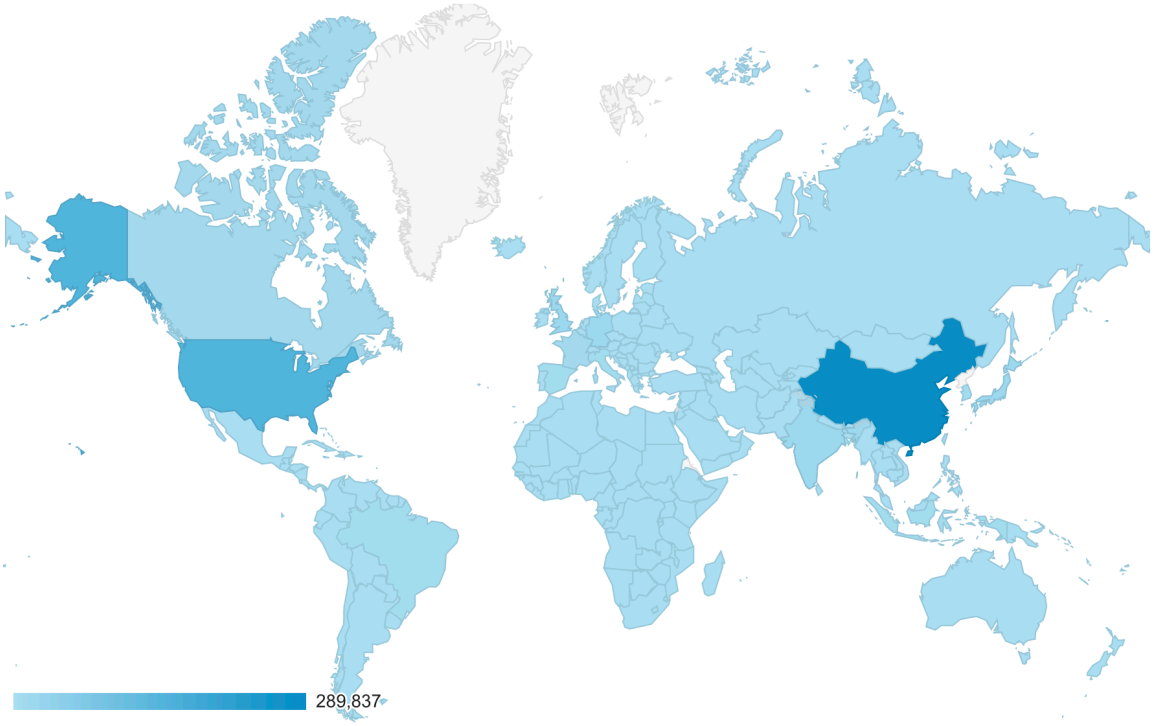


Figure 3 – FlyBase users for Jan 2017-Sep 2022

Geographical Distribution

The majority of user traffic to FlyBase now comes from the U.S. and from China, with the number of ostensible Chinese users being about twice those from the U.S. This represents a dramatic increase over the last several years – by a factor of 12 between 2020 and 2021, specifically. These are the bots mentioned above, to which we must attribute more than 90% of Chinese user traffic. Disregarding bots, user traffic from China would be comparable to that from the U.K.



	683,558 % of Total: 100.00% (683,558)	683,558 % of Total: 100.00% (683,558)
1. China	**289,837**	42.00%
2. United States	**143,222**	20.75%
3. United Kingdom	**24,233**	3.51%
4. India	**23,271**	3.37%
5. Japan	**22,744**	3.30%
6. Germany	**21,596**	3.13%
7. France	**10,866**	1.57%
8. Canada	**10,399**	1.51%
9. South Korea	**8,680**	1.26%
10. Indonesia	**8,588**	1.24%

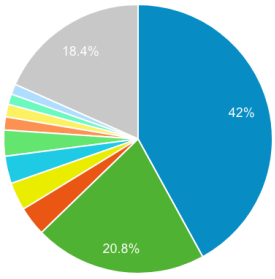


Figure 4 – FlyBase Users by Country (Jan-Sep 2022)

Data Class Usage

Table 1 and Figure 5 below show the proportions of page views of FlyBase data class reports for the one-year period Oct 15, 2021 – Oct 15, 2022. Gene report views account for more than half of our data class pageviews, with Reference reports coming in second again this year. The next five classes (Allele, Insertion, Stock, Construct, and Clone) are the same as last year, but there has been some movement among them (Alleles moved up, Constructs moved down, *etc*).

Page Views, Oct 15, 2021 to Oct 15, 2022	
Gene	2,841,347
Reference	711,710
Allele	318,765
Insertion	313,505
Stock	204,466
Construct	185,006
Clone	115,444
Gene Group	85,944
Aberration	57,332
Tool	52,515
Transcript	47,730
Polypeptide	45,099
Balancer	28,883
Human Disease Model	22,783
Physical Interaction	21,899
Sequence Feature	19,027
Dataset	10,059
Image	5,333
Molecular Construct	5,221
Natural Transposon	5,123
Strain	4,118
Cell Line	2,707
Molecular Segment	819
Chemical	618

Table 1 – page views by FlyBase Data Class.

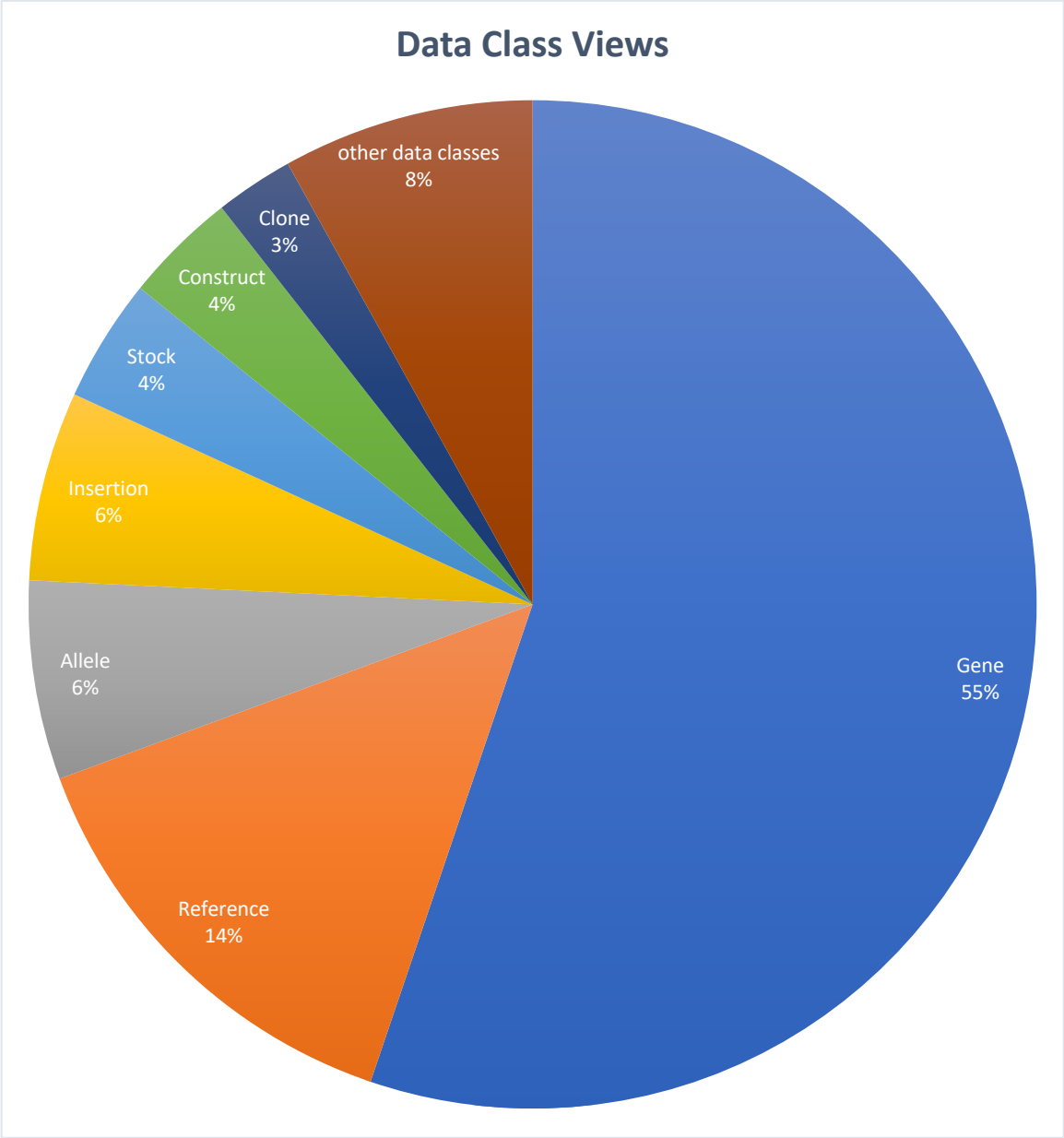


Figure 5 – Pie chart of page views by FlyBase Data Class. Percentage values are based on total data class page views (calls to pages with URLs ending in **/reports/***).

Tool Usage

Table 2 and Figure 6 show that our top 4 tools are again Simple Search, BLAST, Jump to Gene, and Sequence Downloader. The data below is again for the period Oct 15, 2021 – Oct 15, 2022. Note that JBrowse usage is undercounted by Google Analytics due to technical issues related to how it is implemented, and is not shown here. We had intended to move to GA4 to help address this issue, but were not able to do so this year. GA3 will not be supported beyond July of 2023, so this migration will happen before our 2023 fall meeting.

Tool Name	URL	Page Views
Simple Search	/search/	709,094
BLAST	/blast/	608,807
Jump to Gene†	/cgi-bin/uniquery*	273,545
Sequence Downloader	/download/sequence/	155,090
GBrowse2	/cgi-bin/gbrowse2	111,503
Homologs (in QuickSearch)	/cgi-bin/orthosearch*	26,994
ID Validator	/convert/id	16,857
Batch Download	/batchdownload	14,544
Gene Groups (in QuickSearch)	/search/FBgg	7,472
Vocabularies	/vocabularies	6,712
Interactions Browser	/cgi-bin/get_interactions*	5,785
RNA-Seq tools	/rnaseq/*	5,668
Human Disease (in QuickSearch)	/search/disease	4,817
References (in QuickSearch)	/search/references	4,612
Fast-Track Your Paper	/submission/	4,016
Chromosome Maps	/maps/chromosomes	3,917
GAL4 etc (in QuickSearch)	/search/GAL4	3,144
Coordinates Converter	/convert/coordinates	3,100
CytoSearch	/cytosearch	2,163
QueryBuilder	/cgi-bin/qb.pl	1,973
Feature Mapper	/featuremapper	1,821

Gene Disruption Project (Kanca, Bellen, Levis, Perrimon, and Zirin)

Update of the GDP

The Gene Disruption Project (GDP) aims to enable the research community to conduct in depth functional studies of all the fly genes that are evolutionarily conserved by generating highly versatile genetic tools. We have generated thousands of mutant alleles for Drosophila genes mainly through transposable element based methods. However, in the past 7 years, the GDP has switched to targeted insertion of artificial exons for generating gene trap and protein trap insertions. We have currently generated 3200 gene trap alleles and 700 GFP protein trap alleles through targeted insertion of artificial exons with the methods described below.

The first methodology we developed to generate protein trap and gene trap alelles was based on repurposing MiMIC alleles that we had generated. MiMICs constitute the most versatile tools for gene annotation (Venken *et al.*, 2011). A MiMIC in a coding intron of a gene can be converted into a GFP protein trap (GFP-PT) by RMCE, facilitating detection of the gene product, allowing affinity purification of protein complexes that include the targeted protein and conditional knock-down of the targeted protein in any tissue in a reversible manner (Nagarkar-Jaiswal *et al.*, 2015) (Bateman, Lee and Wu, 2006). Alternatively, MiMICs can be converted into T2A-GAL4 gene traps that generate a strong loss of function allele that expresses GAL4 in the spatial-temporal pattern of the targeted gene (Diao *et al.*, 2015; Lee *et al.*, 2018). The GAL4 can then be used to detect the expression domain of the targeted gene using UAS-GFP and allows rescue of the GAL4-disrupted gene with UAS-cDNAs. Using UAS-cDNA of human orthologs of the gene allows us to assess whether potential human variants are pathogenic and permit to conduct a systematic structure-function analysis of proteins. Given that the MiMICs are transposable elements and their insertion in the genome is nearly random we decided to switch to CRISPR/Cas9 to insert MiMIC-like elements (CRIMIC) to tag conserved genes at precise locations (Lee *et al.*, 2018).

We reported (Lee *et al.*, 2018) the generation of a library of ~1000 *Drosophila* stocks containing *T2A-GAL4* artificial exons in coding introns of genes. ~400 of these genes were targeted by CRIMIC and ~600 were generated by converting MiMICs in coding introns of the genes into T2A-GAL4 gene trap alleles through RMCE. We showed that these strains allow numerous applications based on testing of a sample of this extensive collection. First, ~90-95% of insertions in essential genes cause a severe loss-of-function phenotype, demonstrating that the insertion of the *T2A-GAL4* cassette is an effective way to mutagenize genes. Second, 70% of lethal insertions tested were rescued with a single UAS-cDNA construct, even when many transcript isoforms are annotated in FlyBase. This permits rapid testing of variants and hence structure-function analyses. Third, loss-of-function phenotypes associated with CRIMIC *T2A-GAL4* insertions that are flanked by FRTs can be reverted by excision with *UAS-flippase.* This has many advantages: mutagenic cassette can be excised to generate a control genetic background to test whether observed phenotypes are specific to the loss of function caused by the *T2A-GAL4* gene trap, akin to use of precise excision of a P element as a genetic control of alleles generated by P element insertions. It also shows that the CRIMIC library does not contain other lethal or visible mutations introduced by CRISPR/Cas9 while generating the allele. Importantly, excision of the mutagenic construct also allows assessment of the need for the gene product in any given tissue, as the *flippase* can be expressed tissue specifically using another binary expression system. Fourth, *GAL4* driven *UAS-GFP/RFP* reports tissue and cell-type of gene expression with high sensitivity. This has allowed us to report the expression pattern for hundreds of previously unreported genes. In summary, these stocks comprise a very powerful resource and integrate many elegant features that allow assessment of gene function, protein structure, and many other features that are dependent on the *GAL4* system. Given its

great versatility and usefulness, we decided to continue to expand the development of this library using a modified approach (see below).

The Drop-in technology

The main issue with our original protocol for generating CRIMIC T2A-GAL4 lines (Lee et al. 2018) was not conceptual but technical. There were two hurdles: cost and efficiency. dsDNA homology donors for insertion of large cassettes in Drosophila typically require stretches of at least 500–1000 nt of homology on either side of the SIC (Beumer *et al.*, 2013; Bier *et al.*, 2018; Diao *et al.*, 2015; Lee *et al.*, 2018; Rong and Golic, 2000; Zhang, Koolhaas and Schnorrer, 2014). The large size of the homology regions affects cloning efficiency of the donor constructs using Golden Gate cloning (Lee *et al.*, 2018). We typically achieve an overall success rate of ~50%: ~80% cloning success rate; ~80% transformation rate and ~80% rate of proper integration as assessed by PCR (0.8 X 0.8 X 0.8 = ~50%).

We therefore dedicated a lot of time to developing an alternative strategy that makes use of commercial gene synthesis methodology to integrate full length CRIMIC cassettes of ~ 5 kb flanked by short homology arms. We first established that linearizing homology donor vectors *in vivo* increases the CRISPR mediated homologous recombination rate even with short (100 nts on each side) homology arms. However, even when the homology arms are shortened, synthesis of a full length 5 kb CRIMIC cassette is cost prohibitive (>$1,000) especially for a thousand genes.

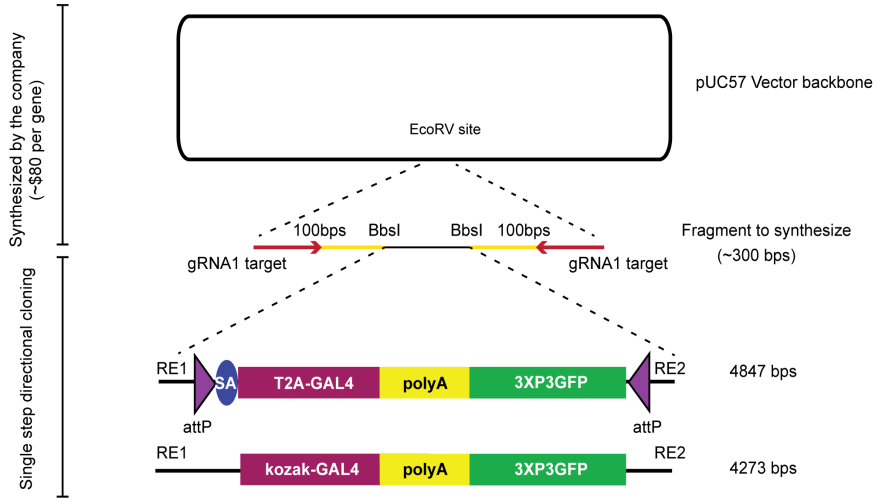


Figure 1. Single step cloning of CRIMIC donor constructs using Drop-in. An intermediate containing gene specific homology arms and a restriction cassette is commercially synthesized. A single step cloning of SIC in this intermediate is sufficient to prepare a homology donor construct. FRT sites are omitted for simplicity

To reduce the cost, we synthesize a gene-specific small plasmid carrying a gRNA1 target-100nt left homology arm-Restriction cassette-100nt right homology arm-gRNA1 target in a pUC57 backbone (cost of synthesis is $80). The SIC containing the *attP-FRT-T2A-GAL4-polyA-3XP3-EGFP-FRT-attP*, which is shared for all target genes, is then subcloned directionally into this plasmid in a single straightforward cloning step, replacing the restriction cassette with the SIC (**Figure 1**). We refer to these constructs as the Drop-in int100-CRIMIC constructs (Kanca *et al.*, 2019b). The construct is injected together with two gRNAs: gRNA1 to excise the double stranded donor from the donor vector and a gene specific gRNA to cut the target site in the genome (**Figure 2**).

We injected vectors containing the full length CRIMIC cassette in more than 20 genes and obtained an 75% success rate as verified by PCR. Hence, 100 nt homology arms are sufficient to integrate large SICs into target sites in flies because simultaneous excising the homology donor as a dsDNA fragment *in vivo* and cutting the chromosomal target region by Cas9 strongly promotes precise homologous recombination. Note that for Drop-in constructs,

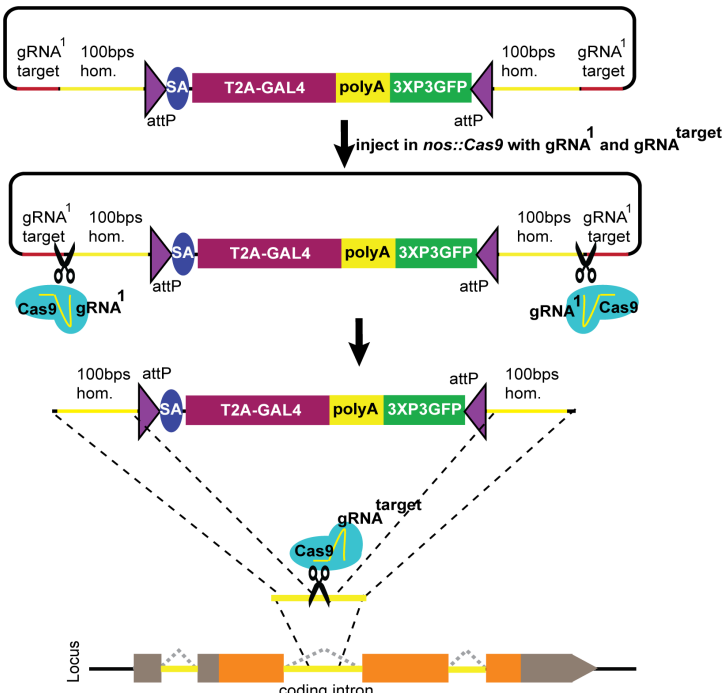


Figure 2. In vivo linearizing the homology donor permits use of short homology arms for integration of large constructs. Linearizing the homology donor construct with gRNA1, a gRNA that does not target the genome, boosts homologous recombination using 100 bps homology. FRT sites are omitted for simplicity.

the presence of short homology arms allows the donor vectors to be synthesized cheaply and introducing larger SICs is done by a single straightforward cloning step, providing a good balance between ease of construct generation and efficient *in vivo* use. Hence, we improved the overall efficiency compared to the CRISPR method described in (Lee *et al.*, 2018) by 1) shortening the homology arms to 100 nt, which allows synthesis followed by a simple cloning step, thus eliminating cloning failure and reducing the cost from ~$300 to ~$100 per construct; and 2) integration of target gRNA1 sites on either side of the SIC to linearize the donor with Cas9 in the germ cells and boost integration efficiency and precision. This reduces the total cost per gene by about 40%, from an estimated $1,500 per gene to an estimated $800-900 (Kanca *et al.*, 2019b).

Recently, we have upgraded the drop-in strategy by employing custom plasmids in the commercial synthesis step. We first tested a custom vector backbone that contain the gRNA1 cut sites flanking the region where the donors are synthesized and U6-gRNA1 in the backbone. This modification decreases the number of plasmids that need to be co-injected and allows increasing the homology arms length to 200 bps without increasing the synthesis cost (**Figure 3**). We injected about 400 constructs with ~65% success rate. We further optimized the custom vector backbone design to allow synthesis of the gene specific gRNA within the donor DNA backbone, which eliminates the need for gene specific gRNA cloning and allows injection of a single vector to achieve CRIMIC integration (**Figure 4**). Using this design boosted the transgenesis

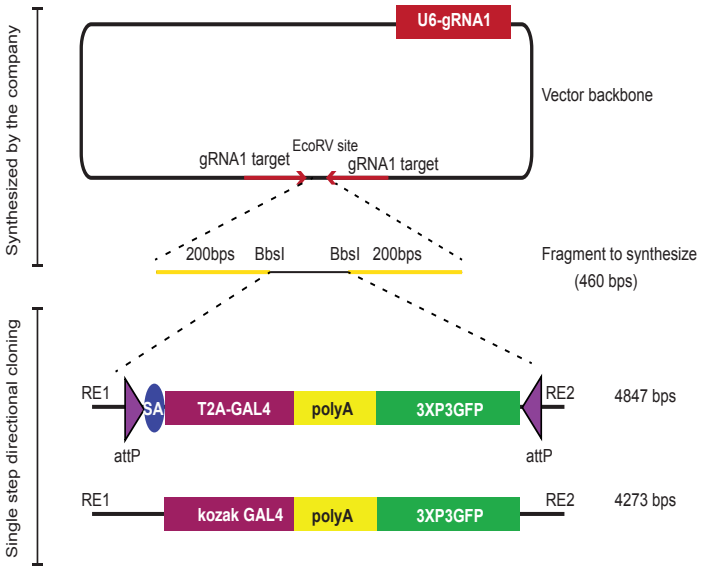


Figure 3. Synthesis of Drop-in intermediates on custom vectors int200 strategy. Custom vector backbones allow synthesis of longer homology arms and decrease the number of constructs to inject.

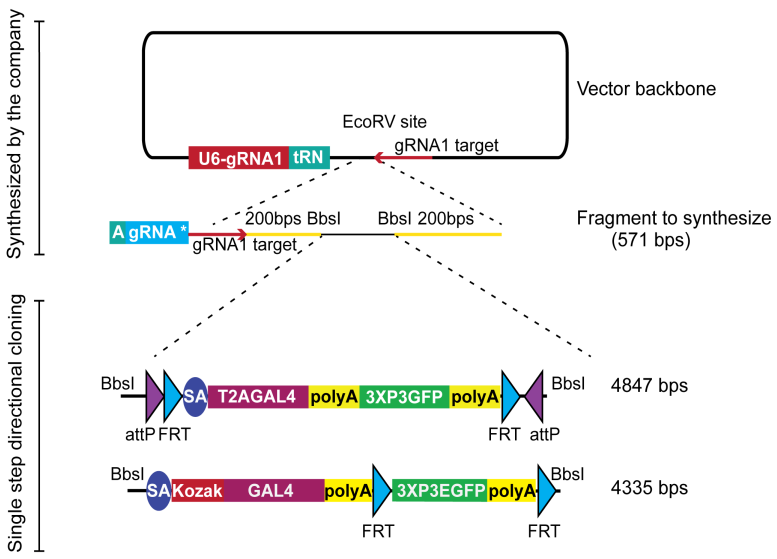


Figure 4. Synthesis of Drop-in intermediates on custom vectors *gRNA_int200 strategy*. Using a partial tRNA sequence that is complemented by synthesized fragment allows integrating gene specific sgRNA in the homology donor construct, decreasing the workload and increasing efficacy.

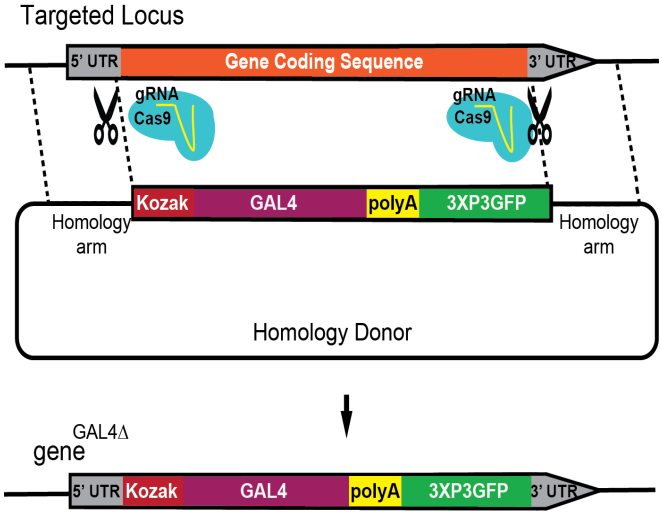


Figure 5. Kozak-GAL4 replacement of CDS of genes. Genes without a suitable intron can be targeted, using kozak-GAL4 replacement to generate a knock-out allele that expresses GAL4 in the targeted gene's expression domain

efficacy to ~80% while decreasing the labor to generate targeting constructs (Kanca et al., 2022).

Note that 50% of the genes have no suitable introns to integrate a CRIMIC cassette (Kanca et al., 2022). Hence, we recently adapted the Drop-in method to replace the coding region of genes that do not contain suitable introns with Kozak-GAL4-polyA-3XP3-EGFP (**Figure 5**). We select a gRNA target in the 5' UTR and one in the 3'UTR of the GOI. We then replace the entire coding region of the gene with a cassette that contains a Kozak consensus sequence followed by the GAL4 ORF. We have shown that this cassette can be efficiently used to rescue the fly mutation induced by the removal of the ORF by driving a UAS-human cDNA for several of the genes tested including *Tom70* (a mitochondrial importer; (Dutta *et al.*, 2020); and *wdr37* (a cytoplasmic WD40 repeat protein; (Kanca *et al.*, 2019a). We have generated 355 KozakGAL4 alleles with ~85% transgenesis efficacy. We are also using the homology donor intermediate vectors to replace the coding region of the genes with sfGFP tagged versions of the coding region to generate GFP-PT alleles.

We have currently generated

7,434 MIMIC
608 MIMIC GFP-PT
620 MiMIC T2A-GAL4
2208 CRIMICs
355 Kozak GAL4
80 CRIMIC_GFP-PT

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Human cDNA project (Shinya Yamamoto, Sue Celniker, Toshiyuki Takano-Shimizu, Hugo Bellen)

We are generating a library of UAS-human cDNA constructs and transgenic lines for the fly community supported buy NIH/ORIP (**R24 OD022005**). These tools can be used in conjunction with the T2A-GAL4 or Kozak-GAL4 lines (see GDP report) to 'humanize' a fly gene and to assess functional conservation of orthologous genes. In addition, one can introduce a variant found in an individual (e.g. a missesense allele identified as being a potential pathogenic variant in a rare disease patient) to assess its functional consequences *in vivo* in flies based on rescue and overexpression experiments. To date, we have subcloned 7,262 full length human cDNAs into the pGW-HA.attB plasmid (some clones generated during the initial phase of the project are in pUASg-HA.attB). 5,317 clones are currently available from DGRC and the remaining will become available in the near future. In addition, constructs corresponding to 4,549 human genes have been made into transgenic flies and are available from BDSC and/or Kyoto Stock Center. I

In principle, we inject our constructs into the VK37 docking site on the 2nd chromosome if the best ortholog candidate gene in fly is on the X, 3rd or 4th. If the best fly ortholog candidate gene is on the 2nd chromosome, we inject them into the VK33 docking site on the 3rd. Note that some transgenes generated in the pilot phase of this project were injected into the ZH-86Fb docking site on the 3rd chromosome (n=417). 2,431 lines corresponding to 2,228 human genes are available from BDSC (some genes have >1 transgenes). 3,311 lines corresponding to 3,050 human genes are available from Kyoto Stock Center. Note that transgenic lines corresponding to some human genes are available from both stock centers (n=729, as duplicates).

Through a supplement on the parental R24 grant, we also generated UAS transgenes that allow expression of the 29 protein coding genes of the SARS-CoV-2 virus and human proteins these viral porotein interact with (untagged or C'-3xHA tagged, BDSC #94220-95281). A paper describing these reagents has been submitted to *Cell Reports*.

- BDGP: https://www.fruitfly.org/humanfly/
  …Human cDNAs subcloned in the Celniker laboratory
- DGRC: https://dgrc.bio.indiana.edu/clones/Catalog#
  …Human cDNAs available from DGRC. Click the 'Human ORF' link from the navigation panel on the left to download an excel file.
- FlyPush: https://flypush.research.bcm.edu/humanfly/
  …Human cDNAs subcloned and injected in the Bellen and Yamamoto laboratory. Also, contains information of human cDNAs obtained from the Celniker laboratory which have been injected in the Bellen and Yamamoto labs.
- BDSC: https://bdsc.indiana.edu/stocks/uas/uas_hsap.html
  …Human cDNAs available from BDSC. Of the 2,957 lines listed here, 2,431 lines were generated through this project.
- Kyoto Stock Center: https://kyotofly.kit.jp/stocks/documents/Humanized_fly_lines.html
  …Human cDNAs available from KIT. All 3,311 lines listed here were generated through this project. 729 lines are duplicates of lines that are available from BDSC.

Berkeley Drosophila Genome Project (Susan Celniker, Ken Wan, Erwin Frise)

A. Introduction

The BDGP was established in 1992 to sequence the *Drosophila melanogaster* genome. We've continued to expand activities with the goals of improving the functional annotation of the genome and expanding community resources. Although our productivity this year has been affected by the SARS-CoV-2 pandemic we've pursued three major projects. We continue to characterize the transcriptome, specifically ultra-conserved smORFs as a collaboration with the Perrimon Lab. In addition, we are part of the modERN consortium (PI Bob Waterston) to map transcription factor binding sites (White Lab, Allada Lab) and transcription factor knock-downs using RNAi following by RNA-seq. We are also generating a human ORF Drosophila expression collection in collaboration with the Bellen lab. In addition to these major projects, we continue to use the cDNAs to generate resources for proteomics studies and as templates for probes to determine spatiotemporal gene expression patterns in the embryo.

B. Reference Genome sequence

After completion of the Release 6 genome sequence, our efforts to improve the genome are centered on incorporating the PacBio long-read whole genome shotgun assembly (MHAP) into Release 6 with the goal of producing an integrated consensus assembly that will become Release 7 with improvements to the heterochromatin and the Y chromosome. There is currently no budget for these studies and they have not progressed since reported in 2019. There is an effort to cross the centromeres a "fly T2T" by the group that did the "human T2T"

C. Reference Microbiome Genome sequence

As part of an LBNL funded program we sequenced the microbiome of the reference genome strain, y;cn, br, sp. These are complete genomes sequenced using the PacBio platform and include conjugative plasmids and virions. They were automatically annotated using the RAST and GenBank annotation pipelines. We cataloged protein-coding genes, RNA genes including rRNA operons, tRNAs, pseudogenes and prophages and published the genomes in Genome Announcements. It would be valuable to consider having them at FlyBase. We suggested this in 2020 but there has been no movement as of yet.

D. cDNA Clone Resources

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

Table 1. Summary of Human Expression Clones.

Collection	Vector	Promoter	C-term Tag	System	Started in 2022 -still in process	Finished this past year (3/2022-3/2023)	Total Finished
hGUHO	pGW-HA.attB	UAS	3xHA	Gal4-UAS	53	1,476	7,619

D. Embryonic Gene Expression

We continue to collect embryonic spatiotemporal gene expression data from high throughput *in situ* hybridizations using the Gold Collection clones as templates for RNA probes. Annotations assigned by stage to each gene are now included in the FlyBase gene reports. In addition to the wild type gene patterns, we are collecting expression patterns for selected CRM-driven reporter constructs from the Rubin/Janelia collection and additional constructs generated as part of our collaboration with the Berkeley Drosophila Transcription Network Project. We incorporate the CRM experiments into the public database (http://insitu.fruitfly.org) with links to the FlyBase sequence feature reports for these constructs. Our homepage includes a separate browse tab for the CRM experiments to improve accessibility. Our improved gene reports include graphical summaries of the stage specific organ system annotations and a graphical representation of the associated modENCODE RNA-seq data. The updated version also allows searches by all known gene name synonyms and human ortholog names. We continue to add new search and discovery tools based on computational image and annotation analysis. We published an advanced method for modeling spatially local gene interactions and networks with our dataset. An interactive viewer based on the annotated patterns of 708 site-specific transcription factor genes, using self-organizing maps to show relationships among transcription factor expression patterns in the context of organ system development, can be accessed at http://insitu.fruitfly.org/som. We are active participants in the development of image analysis within the open-source image analysis platform FIJI (fiji.sc). We are starting to use our recently finished open-source microscope automation software for automated slide loading and imaging with commodity hardware. We have updated our manual imaging tools away from proprietary products to use a prosumer Nikon D5100 camera with open-source Micro-Manager software. The newer camera and open-source software allow us to take high quality images while using well-maintained software that runs on modern operating systems. To date we have completed and annotated experiments for 8558 genes and 336 CRMs documented with over 182,991 images. We have begun projects to image new sets of genes, including Kinases (468 hybridized and currently being imaged) , conserved smORFs (298 and 70 left to be imaged), and lncRNAs (41 imaged)

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

The modERN (model organism Encyclopedia of Regulatory Networks) 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. To date the Celniker lab has produced 401 transgenic GFP tagged-TF fly lines. All but the most recent are deposited at the Bloomington Stock Center. The White Lab intends to perform ChiP-Seq for a total of 597 lines having already completed 502 datasets for 486 lines. The data is being processed through the ENCODE pipeline and is being distributed through the ENCODE DCC. In addition, we produced TF knock down RNAi followed by RNA-seq experiments for a number of TFs [54 sequenced (~324 RNA samples)]. The validated RNA-seq files have been submitted to the ENCODE DCC and are in their process to be made available to the community. Our manuscript describing the putative targets of these TFs is now out in Genetics, 2023 Fisher et al., "A modERN Resource: Identification of Drosophila Transcription Factor candidate target genes using RNAi."

F. Small ORF (Celniker, PI and Perrimon co-PI)

A RO1, "Systematic, Genome-Scale Functional Characterization Of Conserved smORFs" was funded in 2017 to functionally characterize genes that may or may not be coding proteins that have small open reading

frames (<100 aa) and are conserved from flies to humans. Of the two manuscripts submitted last year, one is now out Bosch *et al.,* 2022 "Two neuronal peptides encoded from a single transcript regulate mitochondrial complex III in Drosophila." In eLife and the other is under revision at Molecular Cell

G. Other Resources

In an effort to improve the quality of our web-based user support, we continue to make 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.

H. Technology

cDNA and expression clone sequencing continue to rely heavily on the ABI3730xl capillary sequencer. Characterization of the small ORFeome project has primarily been on the Illumina HiSeq and NovaSeq platforms. We note that sequencing technology continues to evolve rapidly, and access to the latest instruments is essential to our mission. LBNL's BioSciences Division owns a MiSeq, which is located in our lab, providing us with an R&D platform. We also have four Oxford Nanopore MinIONs and software running in the lab. We've used it extensively to sequence microbes from the *Drosophila* gut microbiome and the IARPA FELIX. We have access to the latest Illumina machines through the UCB QB3 sequencing core.

I. Funding

The BDGP is funded almost exclusively by NIH grants (NIGMS). An R01 (SEC) funding the spatiotemporal gene expression studies was renewed in 2019 and expires this year. The mechanism to fund such resource grants has changed and we need to figure out what type of grant we should write. A RO1, "Systematic, Genome-Scale Functional Characterization Of Conserved smORFs" (Celniker, PI and Perrimon co-PI) was obtained to functionally characterize genes that may or may not be coding proteins that have small open reading frames (<100 aa) and are conserved from flies to humans. Manuscripts for this work are in preparation and a NCE was awarded to end this year. We are also funded under a subcontract from Baylor College of Medicine (Bellen, PI, Celniker, co-PI) to construct human ORF clones for expression in flies.

Report of the Ad Hoc Committee on Offensive Gene Names

In 2022, the FlyBoard established an ad hoc committee to evaluate the potential offensiveness of Drosophila gene names. The committee (Scott Hawley, Michelle Arbeitman, Mariana Wolfner, Atanu Duttaroy, John Tomkiel, nonvoting member Steven Marygold and chair Kevin Cook) produced a draft report for the 2023 FlyBoard meeting accompanied by a list of potential gene name changes. Comments were solicited from FlyBoard members, which resulted in this final report.

The committee found few gene names that raised concerns. Most potentially offensive gene names relate to or can be construed to relate to human ethnicity or disability. The issue is difficult, because words are not necessarily offensive in all contexts, and words may not be offensive when applied to flies in the same way they are offensive when applied to people. Nevertheless, the committee agreed that corrections are needed.

The committee recognized that different situations require different actions, and, as described below, it suggested a process for FlyBase to use in renaming genes. It felt that the preservation of historical information is important, so it urges FlyBase to deal with offensiveness in straightforward ways and not to hide objectionable history.

Change the gene name and symbol to reflect molecular function

A straightforward way to deal with a potentially offensive gene name is to change it to emphasize its molecular function. If a gene has an unambiguous human ortholog, it should be renamed to reflect this homology, e.g. *dunce* (*dnc*) would be changed to *Phosphodiesterase 4* (*Pde4*).

The symbols of prominent alleles can be changed to retain relationships to the original designations, e.g. dnc^{1} would be changed to $Pde4^{dnc\text{-}1}$.

Change the gene name, but retain an obvious relationship to the current name

If a fly gene has no clear human counterpart, or the fly gene name is reflected in the human gene name in a way that altering the name would be too disruptive, a "related" name should be used, e.g. *Krüppel* would be changed to *Kr transcription factor*. By deemphasizing original names and removing them from the name fields of gene entries, FlyBase and the Drosophila community will not appear to sanction them.

Replace the gene name with the gene symbol

If a gene has not been identified at the sequence level, the existing symbol should be used as the new name to avoid the appearance of sanctioning the original name, e.g. *midget* would be changed to *mgt*. For most genes in this category, mutation-bearing stocks no longer exist and the mutations were too poorly mapped to match them to annotated genes; consequently, the loci are interesting only from a historical perspective.

In these first three categories, the name changes would be explained in the *Etymology* section of FlyBase gene reports and the original gene names would be retained in the *Synonyms* section to facilitate searches.

Do not change the gene name, but comment on the potential offensiveness

If there is no consensus about potential offensiveness, the existing gene name could be retained (e.g. *Deformed*), but the controversy acknowledged within the gene entry.

The *gypsy* issue

Wei *et al.* (https://osf.io/fma57) have argued for the offensiveness of the *gypsy* transposon name. Because *gypsy* and *gypsy*-like transposons are widespread across species, the committee will refer the issue to a body with broad representation (likely the Genetics Society of America) with the recommendation that the name *mdg4* be considered. The committee recommends that FlyBase comment on the controversy in the relevant entries.

Individual choice

The committee emphasizes that individuals should feel free to use alternative gene names in conversations, talks and publications if they object to any names in FlyBase—as long as the identities of the genes are made clear.

Collective action

FlyBase has always been open to changing gene names when all relevant researchers agree. The committee felt that such grassroots initiatives should be welcomed.

Future status of the ad hoc committee

The ad hoc committee will be available for consultation as the *gypsy* issue is forwarded to a committee representing the broader genetics community, but will be dissolved thereafter. The standing FlyBoard nomenclature committee will advise FlyBase on future issues.