Minutes from the 2024 North American Drosophila Board of Directors Meeting
The Allied Genetics Conference, March 6, 2024
Gaylord National Resort and Convention Center, National Harbor, Maryland

The meeting was run by President Harmit Singh Malik in a hybrid format with some participants joining via Zoom. Detailed reports from the various committees and resource centers were submitted prior to the meeting and can be found at the end of this document. These minutes attempt to capture the discussion that occurred in the meeting itself. The reader is referred to the original reports for a more detailed discussion of each topic.

1. Welcome and Introductions

All participants introduced themselves at the beginning of the meeting. New board members were welcomed, and outgoing members were thanked for their service. Harmit congratulated Hugo Bellen on winning the Gruber Prize, which was followed by a round of applause.

2. Approval of the Minutes from the 2023 Meeting and the Nomenclature Report

Minutes - The minutes from the 2023 North American Drosophila Board meeting were approved by a show of hands. This document and current officers of the Flyboard can be viewed at: https://wiki.flybase.org/wiki/FlyBase:Fly_Board#The_Drosophila_Board_203-24

Nomenclature report – Kevin Cook briefly described the final report from the nomenclature committee, which was charged with identifying and changing the names of Drosophila genes that might be considered offensive. Kevin pointed out that the full list was given to the Fly Board last year. It was also noted that there was not time to go over everything again this year. FlyBase is working through implementing the changes in collaboration with community members. In summary, the committee recommended changing the names of 42 genes. 25 of these genes are known from mutation only and are, therefore, basically extinct. The one outstanding issue deals with changing the name of the Gypsy transposon, which is problematic because the name is used across multiple organisms. He hopes to enlist the help of the GSA in addressing this issue. The same show of hands that approved the minutes was also used to approve the final report of the nomenclature committee.

3. Brief Reports

a) Fly Board elections - Past-president Tin Tin Su (Chair) announced the results of the Fly Board Elections on behalf of the nominations committee (Erika Bach, Michael Welte, Frank Macabenta, and Quan Yuan). As in previous years, voting was between two candidates for each of the six positions up for election and the community survey was used to help identify candidates. Candidates who were not elected on this round are all considered excellent, so their names will be forwarded to the next committee to be considered again for future elections. The results of the 2024 election are as follows:

Vice President: Eric Lai (will serve as President in 2025)
Canada representative: Rodrigo Fernandez-Gonzalez
Great Lakes representative: Laura Musselman
Southeast representative: Don Fox
Heartland: Jocelyn McDonald
Midwest: Daniela Drummond-Barbosa

In total, 406 people voted, but some did not cast ballots in all six elections. Tin Tin noted that the number of votes cast for the last two years have been fewer than in some previous years, which

could be due to GSA adopting a voting system that prevents repeat voting. Even at the higher numbers, however, only a small fraction of the community votes, which led to a discussion of how to increase participation. Ideas included starting the election earlier or holding it at the fly meeting. We should also re-do the survey this year. Tracey DePellegrin said that there will be a smoother interface for the web-based voting next year. Harmit suggested that everyone who votes be entered into a lottery with three winners receiving free registration at the fly meeting. Laurel Raftery felt that we need to better educate the community about why the Fly Board is important. Several members of the Flyboard agreed this was a good idea.

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. She noted that the accounts took a hit in 2023 but have rebounded this year. There is a standing policy that ~5% of the reserve funds are to be used each year to fund travel and outreach awards to encourage trainee participation and DEI efforts in the Drosophila community. Decisions are made by a Trainee Award Committee that in 2024 consisted of Jessica Treisman (Chair), Rachel Smith-Bolton, Blake Riggs, Grace Lee and Shefali. In the previous three years, awards were made to national and international groups seeking to increase participation of underrepresented groups in Drosophila research. Six awards of this type were made in 2023, and there was a brief description of each program. This year, the committee instead honored a request from the organizers of the TAGC to fund certain programs associated with the meeting. $5000 was awarded to support childcare at the TAGC and another $5000 was earmarked for individual travel awards for Historically Black College or University (HCBU) or Low and Middle-Income Countries (LMIC) attendees. The committee also decided to cover the abstract and virtual registration fees for any 2023 outreach awardees who wanted to attend the TAGC. For the outreach awards, Tania Reis asked if we might join forces with the European Fly Board to make a bigger impact on the international awards. Jessica felt that $2,000 was likely sufficient for most applications. Harmit mentioned that all childcare requests for the TAGC were funded and asked about the blog posts from awardees that were suggested at last year's meeting. Jessica said that some had been posted. Finally, Harmit asked if there are any dark clouds ahead for our finances and Jessica said no.

c) Sandler Award: Elizabeth Rideout (Chair) was unable to attend the meeting, so Harmit summarized the results of this year's competition on behalf of the committee (Michelle Bland, Thomas Hurd, Parthive Patel, and Li Zhao). 24 nominations were received of which 22 were complete (CV, nomination letter and thesis abstract). These were ranked by the committee based on the significance, originality and clarity of abstract. The top five candidates were then asked to provide their full thesis for review. The winner of the 2024 award is Dr. Sherzod Tokamov from the University of Chicago, who presented his thesis work in the first Keynote Session of TAGC. The two runners up, Dr. Heya Zhao of University of Massachusetts and Dr. Wei Song of Wuhan University, were also lauded for the excellence of their work. Recommendations for the future include continuing to allow people other than the thesis advisor to make nominations (as happened for the first time this year), starting the process earlier in the year, and having all committee members read literature about how to avoid bias before reviewing. Also, due to the different metrics reviewers often use when assigning numerical scores, it is both more efficient and more accurate to simply have each reviewer rank the candidates. There was discussion that any PI who is sponsoring a candidate for the award should not serve on the committee. A detailed list of procedures and timelines to follow was prepared by Dr. Rideout to help future Chairs of this important committee in subsequent years.

d) Drosophila Image Award - Julie Brill (Chair) announced the winners of this year's awards on behalf of the committee (Tina Tootle, Clemens Cabernard, Jose Pastor-Paréja, Girish

Melkani, and Syed Mubarak Husain). They received 95 submissions (67 images and 28 videos) which is up 25% from last year and 50% from the year before. This increase is likely due to the hard work of the committee to advertise the competition on social media and solicit submissions from compelling images they saw in journals. All committee members made a ranked list of the images/videos they felt were most impactful. This year's Image Award went to Anthony Dornan and the Video Award to Federica Mangione. Julie is grateful to have the community survey when picking new committee members because it is great for diversity and avoids the problem of always inviting the people you know. She also noted that the committee continues to have issues with people submitting in the wrong format, which she will fix by making a submission template for next year. Finally, several people submitted 3-4 images, which proved to be a disadvantage because the committee's votes were often split among the multiple images from the same person. Next year, submissions will be capped at two per person to avoid this issue.

e) Drosophila Community Service Award - Past President Michelle Arbeitman (Chair) announced the recipient of this year's Community Service Award on behalf of the committee (Elizabeth Chen, Amy Kiger, Nadia Singh, Nasser Rusan, and Steven Marygold). This year's award went to the Bloomington Drosophila Stock Center for "*cataloging, maintaining, and distributing Drosophila stocks for the worldwide research community".* The group of awardees includes senior staff members (Drs. Kevin Cook, Annette Parks, Cale Whitworth, and Sam Zheng) as well as the large team that works with the senior staff to ensure the success of BDSC. Michelle encouraged the group to think of people they want to nominate next year. She plans to do more outreach to increase submissions for the award and has asked that the call for nominations be featured prominently on the annual meeting website alongside the calls for the Sandler and Image Awards. There was discussion of whether the nominees who did not receive the award should be notified of their nominations, as this is an honor all by itself. Michelle thought not, because these nominees might be the winners in later years.

f) GSA Conferences - Suzy Brown provided a report on behalf of GSA. Suzy told the group that GSA loves the support it gets from fly community, noting that we made up ~40% of attendees at TAGC. She pointed out that there are banners throughout the conference venue to help the communities meet up and that one of the main advantages of holding a big meeting like TAGC is the ability to do more things like hold workshops on NSF funding for early career researchers. The Fly Meeting will be in San Diego next year and Chicago the year after. Harmit asked if there were any dark clouds on horizon. Suzy said no, but hotels cost a lot of money. We are lucky that Town and Country is treating us like old valued customers. The Chicago meeting is scheduled at an awkward time of year to keep prices affordable. Travel is getting more expensive too. Ruth Johnson asked if there could be a registration category for technicians that was less expensive. Harmit supported this idea by suggesting that a technician who is no more than two years past graduation and who works in an academic lab could still be allowed to register as an undergrad. Suzy said she will take this to GSA board. Harmit noted that registration costs in general are getting higher and wondered if we can keep registration high enough to cover the cost of the meeting, but then offer partial coverage for some people with need. Suzy suggested that some of the budget reserves in Fly Board accounts could be used for such things. Harmit encouraged board members to do fundraising to help cover undergrads, etc. Suzy noted that there is a conferences committee who is the perfect body to deal with these issues.

g) TAGC #Dros24 - Melissa Harrison (Chair) provided a report on behalf of the organizing committee for the Drosophila portion of TAGC (Amanda Larracuente, Daniel McKay, and Blake Riggs). Melissa noted that organizing the Drosophila portion of TAGC is very different than organizing a normal fly meeting. As a community, we were allotted, five two-hour blocks of time. The first was used as plenary session to make the community sessions feel as much like a

normal fly meeting as possible. For the remainder, some of the scientific topics for TAGC had to be massaged to better fit for our community. Also, although the largest group of abstracts came from the fly community, it was challenging to put together a balanced program in the fly-specific sessions because abstracts were first reviewed by the chairs for the cross-organismal sessions and then handed to the communities after they made their selections. There was also an issue with researchers who study insect evolution submitting their abstracts to the PEQG community instead of the fly community. Melissa highlighted the community-building activities that would be available, like a board where you can share a picture of your favorite mutant phenotype or a haiku. Finally, Melissa raised a concern that the people who are chairing sessions should not be speaking in those sessions and that there should be a policy stating this so that it does not become an issue during the planning of future meetings. This proposal was seconded by other members of the group.

h) #TAGC24 - Harmit Malik made a brief report on #TAGC24 as one of its two Co-organizers. He noted that the issue with abstract allocation mentioned by Melissa primarily affected the worm and fly communities because they are the largest. For general sessions, the percentage of talks that were allotted to each community was tied to their overall representation at the meeting (i.e. a fly abstract might be scheduled for a talk over a yeast abstract so as to not penalize the big communities). As for session chairs not giving a talk in their own sessions, Harmit suggested we might also place a moratorium on the chairs choosing the abstracts of their own trainees. However, Melissa thought that trainees shouldn't be penalized. Harmit suggested that incoming president Sally Horne-Badovinac form a committee with Savraj Grewal (2023 Chair), Melissa Harrison (2024 Chair), and Todd Nystul (2025 Chair) to set some guidelines on this topic for future meetings. Tania Reis asked how session chairs are chosen. Harmit noted that the conference chairs have access to the community survey to help them identify candidates and felt that they should not be micromanaged in making these decisions.

i) NEW Mentor-mentee matching program – Graduate student representative Shefali presented her proposal to establish a new program that would allow graduate students and postdocs to identify secondary mentors outside their home institution. The proposal is based on a successful program that is already well established in the worm community. In brief, PIs would volunteer to serve as mentors and the list of PI volunteers would then be shared with interested trainees to allow them to choose a mentor who best fits their interests. Final pairings will be made by a "match committee" composed of former/current members of the Fly Board. Priority will be given to students form underrepresented groups and schools without many fly labs. The initial commitment is for one year but could be extended if the relationship is working well. There was a suggestion that it might be helpful to provide guidelines about the expected number of meetings per year. Harmit said that he has people who attend and present in his group meetings remotely - he thinks that the mentor-mentee pairs could do something similar. Tania Reis felt that identity should be considered when making matches (if that is what the student wants). Tin Tin Su asked about role of thesis PI and concerns they may have about sensitive data being presented in someone else's lab meeting. It was suggested that setting up this program could be a lot of work, and it might be best to start on a small scale. Harmit countered that we know how it works in the worm community, which will make things easier. Shefali was encouraged to develop this idea by recruiting other members of the Flyboard (including Harmit and other trainee representatives, getting more information from the worm mentoring committee, and launching the project in pilot scale this year.

4. Resource Center Reports

(j) Bloomington Drosophila Stock Center (BDSC) – Cale Whitworth updated us on the latest news from BDSC. He announced that the BDSC received a perfect score on the renewal of their grant from NHGRI and noted that the reviewers had highlighted the exceptionally strong support from the fly community in their reviews. Shipments have been going down in recent years; however, they seem to have levelled off, which may suggest that we have hit a "new normal". The BSCD recently acquired several new collections, including stocks with split-GAL4 driver combinations from Janelia (they also provided some funding), the Drosophila Genetic Resource Panel stocks from Trudy Mackay, and the Drosophila Synthetic Population Resource stocks from Stuart Macdonald. Cale noted that the BDSC is grateful for the Community Service Award and that the part-time stock keepers were ecstatic. He highlighted the efforts of Kathy Mathews and Kevin Cook in guiding the center's operations for so many years and said that the staff had originally nominated Kevin for the award. Allan Spradling asked whether the Fly Board could give a certificate or some other token to the stock keepers when they leave, retire, etc – something that shows the how much the community appreciates them. Harmit followed up by suggesting that Fly Board provide certificates to the full BDSC staff commemorating the Community Service Award and host a celebratory pizza party for the group. There was general enthusiasm for this idea. Harmit asked about progress with cryopreservation of fly lines. Cale said that Tom Hayes has a protocol that works at small scale and that the BDSC is on grant with him to adapt it for larger scales. This has proven to be difficult, however. The Kyoto Stock Center has a method to freeze primordial germ cells, but this is also technically challenging.

(k) Vienna Drosophila Resource Center (VDRC) – Lisa Meadows presented for the VDRC. Orders for stocks are relatively stable but operating costs keep going up. 70% of revenue comes from user fees and the rest from other resources. One way the VDRC is dealing with funding deficits is that 10% of stocks (ones that are lesser used) are now kept in only a single copy and they are trying to decide on other strategies going forward, one of which could be a subscription model. There was a question about whether researchers ordering from other countries should pay more. Lisa answered that 40% of the orders come from the US and that she does not want to discourage this by asking US researchers to pay more. Harmit asked if the Fly Board could help with grants to fund the center, but Lisa said that Europe does not offer funding for resource centers like the VDRC.

(l) Drosophila Genome Resource Center (DGRC, Bloomington) - Andrew Zelhof reported on behalf of DGRC. He announced that their most recent grant will be funded but they don't yet know the amount they will receive. They now have the new tissue specific cell lines from Amanda Simcox. They have also been rotating some new members onto their advisory board and have instituted a new three-year term limit. Associate Director, Kris Klueg, who has been with the DGRC since its founding, is retiring this year. There was a round of applause for Kris.

(m) DRSC/TRiP at Harvard Medical School - Stephanie Mohr provided an update on the DRSC, which also received a perfect score on their most recent grant application. CRISPR-based cell screening has largely supplanted RNAi. In general, the RNAi screening is being phased out, except for small, customized screens, and CRISPR-based screening is being expanded to cell lines from other insects/arthopods. The grant includes funds for courses in cell screening. Newly released tools for in vivo studies include more CRISPR knock-out and activation lines, more split Gal4 lines, new tissue-specific drivers based on QF and LexA technologies, and a set of LexAop and QUAS shRNA lines for popular genes. A new preprint was just released on bioRxiv introducing Fly Predictome, which is a new resource that uses binary protein-protein interaction prediction based on protein 3D structure from alphafold. They

also published FlyBi, which is another proteomics project that involved all-by-all screening of 10,000 *Drosophila* ORFs to produce a new a high-confidence protein-protein interaction network.

(*n) Flybase -* Susan Russo Gelbart presented on behalf of Flybase. Flybase just received a new 5-year grant, but the budget was cut significantly. User fees are becoming increasingly important for operations. The link on the website to pay your user fees is about to get very bright. Harmit asked how the Fly Board can help. Although the website lists an amount for the fee, they will take whatever you can give. Approximately 500 labs have paid user fees to date. Brian Calvi pointed out that there are ~2000 labs in the new database and asked if we can use peer pressure to help drum up business. Harmit asked if there can be a screen that pops up where the user must click on whether or not they have paid their user fees before gaining access to content. Susan said they used to post a list of labs who had paid but people complained that their name had been left off. Tania Reis pointed out that some people legitimately don't have research funds. Also, the need for an invoice can be problematic at some institutions. Ruth said she was on Flybase now and liked what she saw in the payment section. Brian Calvi suggested (and Daria Siekhaus seconded) putting a gold star next to the names labs that pay their user feels on the list of fly labs.

(o) Gene Disruption project and human cDNA project – Oğuz Kanca and Shinya Yamamoto presented an update to the group. Using the CRISPR mediated T2A-Gal4 approach, they are generating 500-600 loss of function alleles per year, but these insertions can also be used to detect endogenous patterns of expression using UAS-GFP. In addition, GFP-insertion lines for endogenous protein tagging have been created. All lines generated are sent to Bloomington. They recently submitted their renewal application to NIH. A recent focus has been to generate fly strains expressing each of the SARS-Cov2 proteins (during the lockdown). A new exciting direction is a resource to create fly for expressing one of 8000 human cDNAs (5300 have already been created) in D. melanogaster for complementation and other downstream analyses. The human cDNA project is a collaboration with Sue Celniker and the Kyoto Stock Center; Sue sends the plasmids, which are injected at Baylor or Kyoto.

5. Additional Items

(p) Open discussion - Harmit feels that we need to do a better job telling the community what the Fly Board can do for them. He suggested a "meet the presidents" question and answer session. Brian Calvi pointed out that there used to be a meet the Fly Board mixer at the Fly Meeting with drink tickets that members can give away. This was about 10 years ago.

Harmit then asked the board if we can extend the proposed mentoring program to junior faculty who may run the only fly lab at their institution. The mentor could be someone at a nearby institution that can share their expertise. It can be isolating when you are just starting your faculty position and you run the only fly lab. Harmit asked Ruth Johnson if she could write an article on what it is like to start a fly lab by yourself - how you learn to make fly food, etc. Stephanie Mohr talked about the value of regional fly meetings like those held in Boston to help bring isolated people into the fold. Laurel Raftery noted that the entire state of Nevada only has two fly labs and they are far apart, so regional meetings wont work for everyone. Tania Reis said that it can also be hard to be the only fly person at a rich medical center, not just a PUI. Wu-Min Deng talked about a group he started called Fly Bayou initially for people in Louisiana but now with a bigger outreach thanks to Zoom, which allows people to attend from a distance.

Harmit asked if it was possible for the groups building new tools for the community to make five-minute videos that introduce these resources as they are released. There is so much happening that it is hard for people to keep up. He asked if Fly Board can help with this. Can we give out grants to have freelancers or trainees make these videos? Andrew Zelhof talked about ways they advertise their resources. Harmit suggested that the President's address at the 2025 Fly Meeting could highlight what is new at each resource center (*this was done by Michelle Arbeitman at the 2023 meeting*). Julie Brill suggested that the deck of slides that are typically shown in between sessions could include slides that advertise these new resources.

Preparation of the minutes - These minutes were written by Sally Horne-Badovinac, with the help of notes taken during the meeting by Michele Arbeitman and the detailed written reports provided by the committees and resource centers prior to the meeting. Harmit Malik, Michelle Arbeitman, and Eric Lai edited the report to improve its clarity and correct factual errors.

In-person attendees - Harmit Malik, Sally Horne-Badovinac, Eric Lai, Michelle Arbeitman, Tin Tin Su, Jocelyn McDonald, Hakeem Lawal, Shyama Nandakumar, Melissa Harrison, Rachel Smith-Bolton, Julie Brill, Susan Russo Gelbart, Brian Calvi, Don Fox, Laurel Raftery, Cale Whitworth, Kevin Cook, Stephanie Mohr, Andrew Zelhof, Kris Klueg, Lisa Meadows, Jessica Treisman, Ruth Johnson, Oğuz Kanca, Shinya Yamamoto, Wu-Min Deng, Tania Reis, and Shefali.

Zoom attendees - Sofia Araujo, Laura Musselman, Rodrigo Fernandez-Gonzalez, Daria Siekhaus, and Brain Lazzaro.

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.

Report of the 2023-2024 Fly Board Nominations/Elections Committee
Respectfully submitted by Tin Tin Su on Feb 22, 2024

The committee (constituted in September 2023) consisted of: Erika Bach, Michael Welte, Frank Macabenta, Quan Yuan, and Tin Tin Su (Chair). Erika and Michael were on the committee last year and provided continuity and advice about what worked best.

We had 6 positions up for election:

1. President
2. Canada Rep
3. Great Lakes Rep (Upstate New York, Ohio, Western Pennsylvania, Michigan)
4. Southeast Rep (North Carolina, South Carolina, Georgia, Florida, Alabama, Mississippi, Kentucky, Tennessee, Louisiana, Puerto Rico)
5. Heartland Rep (Colorado, Kansas, Nebraska, North Dakota, South Dakota, New Mexico, Texas, Arizona, Oklahoma, Arkansas)
6. Midwest Rep (Minnesota, Wisconsin, Iowa, Illinois, Indiana, Missouri)

We began the process in late September 2023 with a zoom call to go over the timeline, share the Elections Committee report from last year, and to divide up the tasks.

For President: All committee members generated names of potential candidates.

Regional Reps: Each committee member took charge of identifying (and giving an initial ranking of) ~4 potential nominees for one rep position, choosing constituencies with which they had the most familiarity, when possible.

Potential nominees for all positions were identified by the following methods: (1) Each committee member asked the outgoing regional Reps for their respective region for suggestions of potential nominees for their replacement. (2) We mined the list of community members interested in service positions in the community survey conducted in 2022 (obtained from the GSA). (3) We obtained nominations (including self-nominations) from the community following an email solicitation sent to the fly community by the GSA (many thanks to Sana Hussein/GSA). (4) We considered the previous unsuccessful candidates for the President position from last year. (5) Committee members produced names themselves.

Lists of potential nominees were added to a shared Teams spreadsheet for all on the committee to view. We then met by Zoom in October to discuss the nominees for each position and put them in a rank-order. Attention was paid to nominees' career stage; diversity and representation of the Drosophila community at large was also considered. In general, we avoided selecting non-tenured people as candidates for regional reps because of the workload and concern for effects on their tenure cases if potential promotion-referees might have been unhappy with a Board decision. We also avoided nominating relatively junior people to be candidates for the President position. For this position, we also considered that experience/familiarity with NIH/NSF to be important. For Reps, we avoided nominating people who had previously been Rep for the same or any other constituency.

For the President position, the committee considered and ranked five candidates by each committee member assigning the candidates numbers 1 (highest) to 5 (lowest). While the top choice was unanimous, the next two had a tied score as did the last two. Therefore, the

committee had a second round of voting to break the ties and generate a rank order among all candidates.

Each committee member contacted the top two nominees for their assigned Rep position; Tin Tin also contacted the President nominees. Potential nominees were referred to the Fly Board Wiki site for more information, and we also answered their questions about the position. We explained that their travel costs to the TAGC/Board meeting would not be covered but that they could Zoom into the Board meeting if necessary.

For three of six positions, the first two people we contacted agreed to run. For the other positions, one of the top two candidates declined to run citing already heavy administrative duties or being on sabbatical, 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 because GSA has the version of Survey Monkey software that prevents multiple voting per Elections Committee report from 2022. Kaitlyn Sudol and Matt Benusa at GSA kindly set up the ballot, sent out the emails alerting (mid Jan), and then reminding (late Jan and early Feb), the community to vote, and tabulated the results. Brian Calvi/Flybase posted a commentary on the FlyBase home page and a call to vote on X and Mastodon. FlyBase and Tania Reis also sent reminders to vote via Twitter/X. We are incredibly grateful for all their time and effort. The ballot (included at the end of this report) was sent out to the Fly community on January 19, 2024, with voting open for 3 weeks; a reminder was sent after 10 days and again 3 days before polls closed on February 9, 2024. 406 people voted, but the votes received for each position were fewer because not everyone voted for every position.

Results are on the next page. Tin Tin notified the committee and past Presidents of the results and notified each candidate of the outcome on Feb. 14, 2023. She also notified Sally Horne-Badovinac (Board President elect) and Harmit Malik (Board President) who then extended an invitation to the winners to attend the 2024 Board meeting.

For every position, the person who did not win the election was also considered outstanding by the committee. The committee will pass along their names to the next committee chairs to be considered for future election slates.

Results (winner in **bold**):
President Elect
Wu Min Deng
Eric Lai

Canada Rep
Edan Foley
Rodrigo Fernandez-Gonzalez

Great Lakes Rep
Deepika Vasudevan
Laura Musselman

Southeast Rep
Jun-yuan Ji

Don Fox

Heartland Rep
Rob Unckless
Jocelyn MacDonald

Midwest Rep
Vikki Weake
Daniela Drummond-Barbosa

Turnout compared to historical numbers

Year	votes received	voting administered by	voting period	# reminders	notes
2024	406 (331-372 for different positions)	GSA SurveyMonkey	Jan 19-Feb 9 (3 weeks)	2	
2023	366 (302-338 for different positions)	GSA SurveyMonkey	Jan 9- (2 weeks + *'a few extra days'*)	1	
2022	733-1179 for different positions	FlyBase SurveyMonkey	*first week of Dec*'-Jan 22 (~8 weeks)	1	
2021	712	Redcap survey app, Huntsman Cancer Institute's department of Research Informatics, University of Utah	Dec 2-Jan 15 (6 weeks)	1	rank choice voting with 3 or 4 candidates/position
2020	328-367 for different positions	information not in report	Nov 7-Dec 6 (4 weeks)	none stated	
2019	702	FlyBase SurveyMonkey	Oct 26-Dec 11 (6.5 weel	none stated	ballot emailed twice because the first one was missing Presidential candidates
2018	518	information not in report	Oct 20-Nov 25 (5 weeks	1	
2017	652	information not in report	Nov 14-Dec 2 (2.5 week	1	
2016	1795 (449 if votes from one region were subtracted)	SurveyMonkey (FlyBase?)	Oct 9-Dec 11 (9 weeks)	1	a candidate forwarded the link locally, resulting in a large number of votes from one region, including from non-fly voters
2015	355-557 for different positions	FlyBase SurveyMonkey	Oct 14-Dec 6 (8 weeks)	1	

Historical numbers from 2015-2022 in the table shown are from past reports of the election committees, all but one of which are available on Drosophila Board Wikipedia page (the 2022 report is not on the Wiki page, but Tin Tin has a copy from being on the Board). The numbers from 2023 were provided by Matt Benusa of GSA. The number of people who voted this year (406) is similar to that of last year (366). Voting in these two years was administered by GSA using SurveyMonkey, with a feature added to prevent repeat voting by the same voter. Voters in these two years are fewer than in 7 of the previous 8 years. It could be that in years with 700+ votes, multiple voting happened and that 300-400 is the typical number of voters each year. Even 700 is only a fraction of the fly community. Fly Board should investigate why many fly community members are not voting, with the goal of increasing voter participation.

The ballot with candidate bios follows.

President Elect candidate 1

Wu-Min Deng

Professor, Tulane University

Wu-Min Deng earned his PhD in 1998 from the University of Edinburgh in the UK, specializing in the study of oogenesis and follicle cell patterning in *Drosophila* under the guidance of Mary Bownes. His fascination with fruit flies began even earlier during his MSc studies at the Shanghai Institute of Cell Biology, Chinese Academy of Sciences.

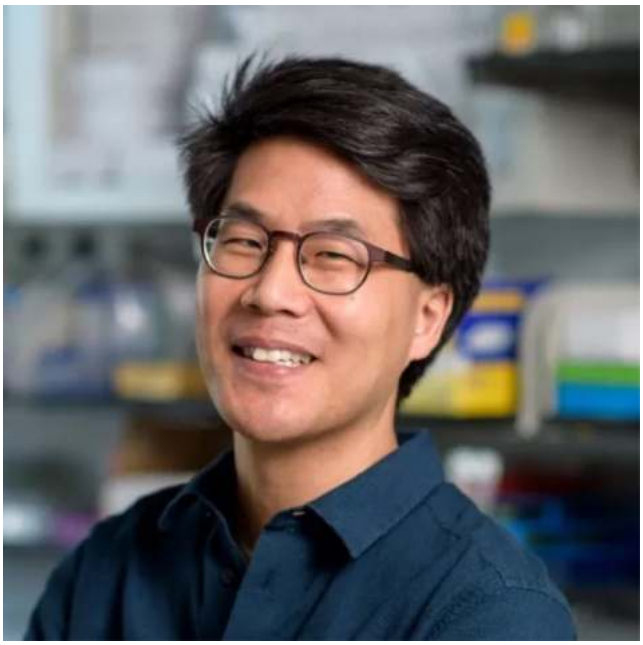
Following the completion of his postdoctoral training with Hannele Ruohola-Baker at the University of Washington in Seattle, where he focused on Notch signaling and germline-soma interaction in the ovary, Wu-Min Deng established his independent lab at Florida State University in 2003. There, his group delved into various *Drosophila* tissue models, exploring cell polarity, polyploidy, as well as cell competition. They also developed models to investigate tumor initiation in *Drosophila*. Subsequently, in 2019, his lab relocated to Tulane University School of Medicine in New Orleans.

Presently, Wu-Min holds the position of a Gerald & Flora Jo Mansfield Piltz Endowed Professor in Cancer Research and is a member of the Louisiana Cancer Research Center. His research focuses on various aspects of tumorigenesis and tumor-host interactions, utilizing the fly tumor models cultivated in his lab. Noteworthy contributions from his group include introducing novel concepts like tissue "tumor hotspots," "compensatory cellular hypertrophy," and identifying new components and mechanisms in Notch and Hippo signaling. He has successfully secured substantial funding from NCI, NIGMS, and NSF. In addition to his achievements in funding, he has been honored with several awards, including the Developing Scholar Award, Honors Thesis Mentoring Award, and the Faculty Research Award (Basic Science) at both FSU and Tulane, respectively.

Wu-Min actively engages with the fly community, demonstrating his commitment through the organization of workshops at Annual *Drosophila* Research Conferences. Furthermore, he co-organized the Polyploidy Across the Tree of Life and the Jiujiang fly meetings, and played a key role in initiating and organizing community fly meetings in Florida ('Fly Masters') and Louisiana ('Fly Bayou'). The impact of these efforts is evident, as the 'Fly Bayou' community has expanded to include labs from multiple cities in Louisiana, as well as from Arkansas, Arizona, Nevada, Oklahoma, and Florida. In addition, Wu-Min edited a book titled "*Drosophila* Model in Cancer" and serves as a standing member of the NIH Dev-2 Study Section. He passionately advocates for research using the *Drosophila* model system and is actively involved in training young biologists. Currently, he holds the position of the Southeast Representative on the *Drosophila* Board.

President Elect candidate 2

Eric Lai
Member, Sloan Kettering Institute



I started my career in *Drosophila* exactly 30 years ago. I trained in molecular genetics during my PhD with Jim Posakony at UC San Diego and my postdoc with Gerry Rubin at UC Berkeley. During this time, I studied classical topics in developmental biology, including Notch signaling and transcriptional regulation in neural development. These projects also led to new regulatory paradigms, including general insights into miRNA mechanisms, before miRNAs had been identified as a class. My personal experiences convinced me that anyone, from the titans to fellow grad students, could harness the power of *Drosophila* to unveil fundamental principles. I found the democratic nature of this model organism invigorating.

Since starting my lab at Sloan Kettering Institute in 2005, I have been fortunate to work alongside stellar trainees at all levels, whose efforts led us into myriad scientific questions, disciplines and models. These include the biogenesis pathways of small regulatory RNAs, the biology of miRNAs in development and behavior, alternative mRNA processing strategies that diversify the transcriptome, the language of RNA modifications, a structurally novel family of DNA binding domains, and insidious selfish meiotic drive elements that meddle with gametogenesis. While many group members use mammalian systems, all of these projects were founded in *Drosophila*, which continues to be our discovery playground.

Our research has always been aided by the fly community's legendary commitment to resource sharing, and reciprocally, our lab has fulfilled hundreds of reagent requests over the years. Equally critical has been our reliance on public resources and knowledge bases (FlyBase, Bloomington Stock Center/VDRC, DGRC, Gene Disruption Project, Interactive Fly, etc.). While in the Rubin lab, I had a front-row seat to the catalytic power of community resources with sequencing of the *D. melanogaster* genome by the BDGP, for which primary data was submitted to GenBank weekly. As a new PI, I was one of the lead investigators within the modENCODE consortium, which collectively generated >1000 genomewide datasets as a community resource. A decade after the conclusion of modENCODE, I am proud that our contributions of small RNA data and substantially revised gene models remain in broad and continual usage.

An important component of this position is to advocate for funding to maintain our *Drosophila* databases and community projects. I have substantial experience on both sides of the NIH granting system, serving as ad hoc and standing study section member, and having been funded by five different Institutes, and renewed at several. I will draw on this experience for this endeavor. In addition, I believe the vitality of our field depends not only on *Drosophila* researchers supporting each other, but also by increasing awareness of model organisms amongst young and diverse students. I am interested to explore how *Drosophila* researchers might engage curious minds and increase public outreach. This can only pay dividends down the line not only for our field, but also may help stem the corrosive effects that denial of science has caused during the pandemic.

I have met hundreds of fly folks across all stages of their journey in science, and consider myself an eternal student with broad interests in *Drosophila* research and techniques. I continue to be astounded by what this remarkable animal model can teach us. I would be privileged to represent and advocate for our community.

Canada Rep candidate 1

Rodrigo Fernandez-Gonzalez
Professor, University of Toronto

I am Professor in the Institute of Biomedical Engineering at the University of Toronto, cross-appointed to the Department of Cell and Systems Biology. My research program investigates the mechanical and biochemical signals that coordinate cell behaviors during embryonic development and tissue repair, using quantitative microscopy, image analysis, computer modelling, and genetic, biophysical and pharmacological manipulations in the *Drosophila* embryo.

My interest in image analysis began as an undergraduate studying Computer Engineering at the Universidad Autonoma de Madrid, in Spain. Looking for interesting images I moved to the Bay Area, where I conducted my Ph.D. in Bioengineering at UC Berkeley and UCSF, working on computational microscopy methods to image the mouse mammary gland. It was during my Ph.D. that I fell in love with microscopy and epithelial morphogenesis, and decided that the fly embryo was the ideal system to investigate the questions that I was interested in. I then moved to New York, to conduct postdoctoral work with Jen Zallen, at the Sloan-Kettering Institute, where I found how mechanical signals regulate the dynamics of the cytoskeleton and contribute to the coordination of cellular behaviors during *Drosophila* axis elongation. We have continued this line of work in my lab, focusing on the collective cell movements that drive the rapid and scarless embryonic wound healing response. Most recently, we expanded our work to investigate the mechanisms of collective cell migration during embryonic heart development (with some surprises in the form of myosin waves!), and the importance and mechanisms of cell volume regulation in epithelial morphogenesis.

Since starting my lab in 2012, I have regularly attended the Annual *Drosophila* Research Conference (ADRC). I have co-organized the Developmental Mechanics workshop at the ADRC over the last ten years, trying to highlight the diversity of our community and to create a friendly environment that facilitates the exchange of ideas. I also contribute to my local *Drosophila* community as a co-organizer of the biweekly Toronto Fly Group meeting. In 2019, I co-chaired the Organizing Committee of the Canadian *Drosophila* Research Conference. In that role, I had the opportunity to familiarize myself with many of the Canadian fly labs that work in areas different from mine. I continue to be amazed by the breadth and strength of the Canadian *Drosophila* community.

The *Drosophila* community has been extremely welcoming and supportive. I find this particularly remarkable in my case, as my training is very different from most of my colleagues. And yet, that difference has always been celebrated. I am now looking forward to giving back to the community as the Canadian representative to the Fly Board.

Canada Rep candidate 2

Edan Foley
Professor, University of Alberta

My fly journey started in the lab of Dr. Frank Sprenger at the University of Cologne, where I completed a PhD in cell cycle regulation. In Cologne, I worked with an engaged research community that ignited my passion for flies as a discovery vehicle. From there, I was fortunate to join the lab of Dr. Patrick O'Farrell at UCSF as a postdoctoral fellow, where I made my first steps towards using flies to understand innate immune signaling. Throughout my time in UCSF, I encountered a research environment that transcended disciplinary barriers in favor of discovery-driven research. From there, I moved to the University of Alberta in Canada where my group explores links between immune signals and intestinal homeostasis in flies.

For me, the fly gut community encapsulates all that is good about *Drosophila* research. I am struck by how this field makes such imaginative use of a relatively simple epithelium to ask foundational questions about cell or developmental biology. As is so often the case with fly researchers, groups working with the gut happily share reagents, support each other's progress, and advocate for the inherent value of discovery. At the outbreak of the COVID pandemic, I had the opportunity to co-host a virtual seminar series that brought this group together to present new or recent discoveries. I drew inspiration from the many scientists willing to share their work and was grateful for the opportunity to support emerging talent.

Outside of my own group, I am primarily interested in EDI initiatives that break all barriers to participation in science, and in providing professional development and mentorship to trainees and established investigators. The Fly Board has a tradition of fostering talent, and I feel a focus on equity and professional support will benefit all of us.

Greatlakes Rep candidate 1

Laura Palanker Musselman
Associate Professor, Binghamton University

I have been a *Drosophila* researcher for over 20 years and an educator for ten years. As fate would have it, I started my training as a PhD student focusing on the developing embryonic neuromuscular junction with Kendal Broadie and Emma Rushton at the University of Utah. When the Broadie lab moved, I joined Carl Thummel's lab, where I studied the role of nuclear receptors in larval development and during metamorphosis. Under the mentorship of Carl and others in the lab, I became interested in metabolism and physiology. So, as a postdoc, I worked with Tom Baranski and Ross Cagan to develop and explore models of human disease, especially diet-induced obesity. These days, my lab and I focus on the biochemistry and pathophysiology that arises from overnutrition, mostly in adult flies.

I'm an Associate Professor of Biological Sciences and Biochemistry at Binghamton University, part of the State University of New York. As faculty, I have collaborated with researchers around the world and have contributed to interdisciplinary research, outreach, and teaching efforts across my institution and in the local community. Working in a basic science department at an R1 institution has enabled me to mentor those from different backgrounds and to serve on committees for hiring, budgeting, curriculum, and peer review of manuscripts and grants.

Although I don't have much formal experience serving the *Drosophila* community, I'm eager to do so. You can often find me chatting at a *Drosophila* conference poster or sharing protocols or unpublished data by email. Some may recognize me from my YouTube video, "*Drosophila* hemolymph collection procedure," or the platform session I co-chaired at the ADRC in 2023. The people and resources of the fly community have helped me and all of us grow, and now is a good time in my career to give back. As a *Drosophila* Board member, I would prioritize quickly getting up to speed on the current plans and seeing where I can fit in and best serve the community, given my skill sets, which include being frank, ethical, and attentive to detail and deadlines.

If asked to identify a platform on which to run for election, it would be "champion the underserved." The folks I envision as needing our support the most are historically excluded people who may not feel comfortable in the spaces we occupy. As a neurodivergent tenured faculty member, I recognize the challenges in "being yourself" without masking identities like autism and ADHD. Although I'm a cis white heterosexual, I consider myself a progressive ally. I lived in inner-city St. Louis and was raised by a single mom, so I'm familiar with some of the challenges of being a minority, but don't have the extra labor of being a minority. The burden of equity should fall on tenured, privileged people like me, and I'm prepared to work harder to serve the underprivileged in this position.

As a grad student, I was welcomed into this community and I'm still here. It's an honor to be nominated and regardless of the outcome, I'll continue to promote and encourage fellow "fly people" whenever and however I can.

Greatlakes Rep candidate 2

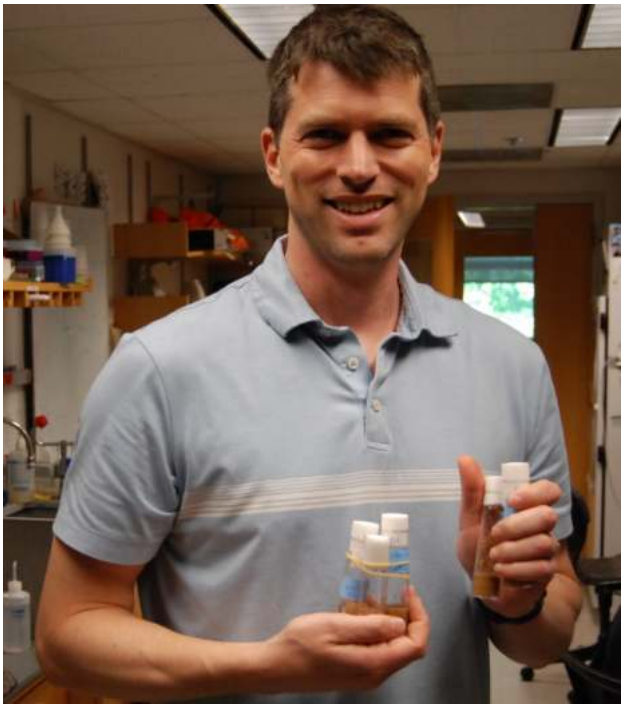
Deepika Vasudevan
Assistant Professor, University of Pittsburgh

I began working with *Drosophila* as a postdoctoral fellow, having first fallen in love with this model as a rotation student. And though I've technically been working with flies for nearly ten years now, any research using the *Drosophila* model still elicits the same awe in me as it did when I was a neophyte. I am now an Assistant Professor at the University of Pittsburgh, having started my lab at a time when the COVID19 pandemic was not quite over in June 2021. Predictably, this presented unconventional challenges and yet I have only fond memories of my early months as a new PI because of the support from the research community- colleagues in my department offered bench space, some shipped me reagents from across the country, and most memorably, fly biologists overseas somehow navigated the complex shipping landscape to send me stocks. My priority as a Fly Board representative will be to sustain and boost such comradeship, which I believe is an essential ingredient in the success of early career scientist such as myself.

The overarching goal of my research program is to gain fundamental understanding of why stress response factors are required for homeostatic functioning of some tissues, and how their mechanism of action changes during stress. My recent work has focused on selective mRNA translation downstream of stress response activation using a powerful combination of genetics and molecular biology. The two primary tissues my lab studies are the fat body and the retina. As I transitioned into my independent position, I looked to expand my lab's tool kit. Again, the research community came to my aid, and I was able to establish live imaging and electrophysiology in my lab. All these efforts were also in no small part due to the innovators in the Fly community making the ever-expanding fly tool kit accessible to everyone.

In addition to my research efforts, I invest considerable resources in mentoring trainees from diverse backgrounds at all levels from high school to post-graduate. My trainees have a strong track record of research accomplishment as exemplified by co-authorships, and retention in science as indicated by their current pursuit of scientific research careers. I have also observed that regular attendance at the annual Fly Meeting to be a crucial ingredient for retaining talented trainees in science, making a strong case for increasing access to the meeting. As someone who has often benefitted from the culture of cooperative research and collaborative science, my goal as a member and representative of the Fly community is to ensure that the support I received is extended to all its young and future members. I hope to accomplish this by fostering open exchange of ideas and tools, inter-institutional mentoring programs, integrating research efforts across geographies, and most importantly ensuring inclusion of anyone who is united with us in the pursuit of knowledge.

Southeast Rep candidate 1
Don Fox
Professor, Duke University



I am a Professor of Pharmacology & Cancer Biology at Duke University. The goal of my research program is to study the biology of genomic extremes, namely whole genome doubling (polyploidy) and rarely used codons. While our work is founded in flies, we've collaborated with HIV clinicians, cardiologists, oncologists, plant biologists, and many more.

My love of *Drosophila* as a model system began in 2001 in Mark Peifer's lab at UNC Chapel Hill, where I revealed a new role for the Abelson kinase in apical cell constriction during gastrulation. As a postdoc with Allan Spradling at the Carnegie Institute, I discovered polyploid cell division in the developing hindgut, and (with Vicki Losick) discovered examples of quiescent adult tissues that lack stem cells yet regenerate upon injury. Our lab has also built new research tools including DEMISE, a genetic system that enables study of genes required to repair a cell ablation injury.

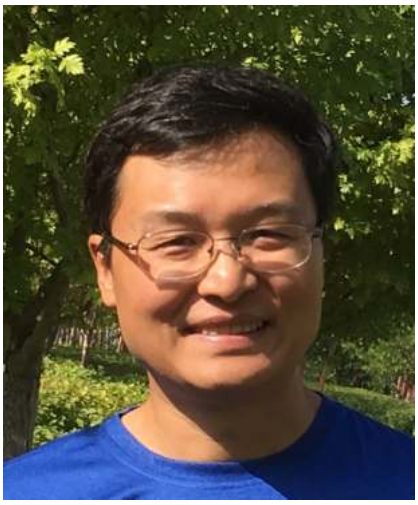
Since 2011, our lab has focused on how polyploid cells re-wire genome maintenance mechanisms, how polyploidy productively regenerates injured tissues, and how specific tissues (the testis and brain) can uniquely express a proteome derived from rarely used codons. We've been supported by grants from 8 separate funding agencies-including the Pew Foundation, NIH, and even NASA! At Duke, I have received multiple forms of recognition for my student and postdoc mentoring.

My efforts in diversity and inclusion encompass multiple career stages. At the postdoctoral level, I established and led Duke Next Generation Leaders, a program aimed at assisting postdoctoral fellows from historically underrepresented backgrounds with the faculty search process. At the graduate level, as director of graduate studies of a large Genetics and Genomics umbrella program, I have been active in outreach efforts to advise and recruit prospective PhD students from underrepresented backgrounds about pursuing a biomedical PhD. I'm very passionate about mentoring new scientists and recruiting individuals from all walks of life into the next generation of researchers.

My lab has an annual presence at the *Drosophila* meeting, and I attended my first fly meeting in 2001. I have served previously on the GSA's DeLill Nasser and *Drosophila* image award committees. More locally, with colleagues at Duke I helped to establish the Triangle Fly meeting, an annual gathering of fly researchers in North Carolina, South Carolina, and Virginia. I'd be honored to represent the southeast region on the *Drosophila* board. My goals would include advocating for funding support for model organism research, to communicate needs for better research tools, and to enhance connectivity and collaboration in our southeast region and beyond.

Southeast Rep candidate 2

Jun-Yuan Ji
Professor, Tulane University



I am a professor in the Department of Biochemistry and Molecular Biology at the Tulane University School of Medicine in New Orleans. In my lab, we explore the role of the Mediator complex and Wnt signaling in the transcriptional regulation of lipid metabolism in *Drosophila*.

I grew up in a rural oasis in Xinjiang, located in the northwest of China. I received a B.Sc. in Cell Biology from Lanzhou University in 1994, focusing on the ultrastructure of the obturator in *Allium Cepa L*. for my thesis. Driven by my interest in developmental biology, I pursued an M.Sc. in Developmental Biology under the mentorship of Dr. Fang-Zhen Sun at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, in 1997.

Under the tutelage of Dr. Gerold Schubiger at the University of Washington (1997-2003), my graduate training focused on analyzing the role of CDK1-Cyclin B in regulating the early embryonic cycles in *Drosophila*. As a postdoctoral fellow in Dr. Nicholas Dyson's lab at the Massachusetts General Hospital Cancer Center (2004-2009), I studied the regulation of the key cell-cycle regulator E2F1 in *Drosophila*, leading to the discovery of CDK8-Cyclin C as a negative regulator of E2F1-dependent transcription.

During my tenure at Texas A&M University College of Medicine (2009-2021), my research expanded to explore CDK8 and other Mediator subunits using *Drosophila* as a model. We identified two new downstream targets of CDK8: SREBP (regulating lipid metabolism) and EcR (regulating developmental timing). In addition, we delved into the role of Wnt signaling in regulating lipid homeostasis in larval adipocytes, revealing that Wnt signaling promotes lipid mobilization through signal-induced transcriptional repression.

In March 2021, our lab relocated to Tulane University. A recent unexpected discovery revealed the involvement of the Mediator complex in maintaining telomere length by regulating telomeric retrotransposon transcription through E2F1-Dp and Scalloped/dTEAD. This discovery highlights the tight coupling of telomeric retrotransposon transcription and the host cell-cycle machinery, ensuring genomic stability during cell division in *Drosophila*. Regarding Wnt signaling, our current focus includes analyzing the mechanisms regulating adipocyte heterogeneity and the stability of α-catenin.

I have actively participated in service activities, serving as a reviewer for organizations such as AHA (2013-2019) and DOD (2023). I have also contributed as an ad hoc reviewer for multiple NIH study sections, several local funding agencies, and various scientific journals. Beyond these activities, I co-chaired a session at the 59th Annual *Drosophila* Research Conference. Moreover, I served on the graduate admission committees at both Texas A&M and Tulane, participating to the selection and interview processes at each institution.

My scientific journey has been shaped by the extraordinary contributions of numerous ingenious and generous drosophilists. I am deeply grateful for the support I have received from colleagues in the *Drosophila* research community. Serving as a regional representative on the Fly Board for the Southeast states would be a great honor for me. In this role, my aim is to advocate for the immense value of *Drosophila* research, not only within the *Drosophila* community but also to wider audiences, including graduate, undergraduate, and high school students. It is also my goal to ensure the effective representation of my colleague's voices and concerns in the *Drosophila* community of the Southeastern states.

Heartland Rep candidate 1

Jocelyn MacDonald
Associate Professor, Kansas State University

Although I was a biochemistry major as an undergraduate, I became fascinated with genetics, cell biology, and developmental biology by my senior year. This led me to pursue a PhD in cell and developmental biology at the University of Illinois, Urbana-Champaign, in the lab of Chris Doe. From the start, I very much enjoyed working with *Drosophila*, using the power of fruit fly genetics to understand how cells are specified in the developing nervous system. I then went to the lab of Denise Montell for my post-doctoral training, staying with *Drosophila*, but now studying how and why cells move in collectives during development. This has ended up being a “fruitful” line of research, as I am still studying this intriguing problem in my own lab, now at Kansas State University. I feel strongly that *Drosophila* is a highly relevant model organism both for understanding the basic mechanisms of biology from the molecular to the organismal levels, but also for elucidating the conserved underpinnings of human health and disease. Through research, I am committed to training people from all backgrounds. I have trained over 25 undergraduate students and six graduate students in my lab, many of whom are women, first-generation students, and/or who identify as members of historically excluded groups. I am active in the *Drosophila* research community. I routinely review manuscripts for major journals, review grant applications for major research foundations including the NSF, and I serve on several journal editorial boards. My goal is to continue advocating for *Drosophila* research at the regional, national, and international levels, as well as to ensure that our community is inclusive and diverse.

Heartland Rep candidate 2

Rob Unckless

Associate Professor, University of Kansas

I grew up thinking that I would be a musician. In fact, I began college as a music major, then switched

to education and was poised to be a history teacher. I took a distribution requirement one summer called the *History of Evolution* with Will Provine and it got me hooked on biology and evolution. I quickly switched gears, completed a master's degree in science education and taught high school science for seven years. While I was teaching, I realized how much I enjoyed the discovery involved in research and completed a second master's degree, this time in biology with a focus on freshwater ecology. I began my PhD at the University of Rochester with no idea I would eventually work with *Drosophila*. But, through a rotation experience, I became enthralled with the biology of flies, leading me to a dissertation co-advised by John Jaenike and Allen Orr. My path to flies went through evolutionary ecology, studying host/symbiont and host/pathogen interactions. I still love collecting wild flies and discovering the myriad pathogens and parasites they harbor. I moved to Cornell University of my PhD and was co-advised by Brian Lazzaro and Andy Clark. My work at Cornell was still inspired by evolutionary questions but became more molecular and more genomic. We focused on the selective pressures shaping the evolution of immune genes. As I became more involved in *Drosophila* research, I also became more enamored with the camaraderie of the community. I started a faculty position at the University of Kansas in 2016 and was promoted to Associate Professor in 2021. My lab focuses on three systems that developed from my PhD and postdoctoral work that address fundamental questions about genomic conflict from multiple perspectives: host/virus coevolution in *Drosophila innubila*, the evolution of innate immunity in *Drosophila melanogaster*, and the genetics and evolution of meiotic drive in *Drosophila affinis.* The projects involving non-*melanogaster* species have taught me patience since tools are so much further behind, but also reinforce my fascination with the incredible diversity of interesting biology in the genus. At KU I teach undergraduate genetics each fall, and I am the director of the KU Center for Genomics. I've co-organized *Drosophila* Research Conference workshops and chaired platform sessions. I have eight undergraduates, six graduate students and two postdocs in the lab and mentoring is an important part of my day. In all of these efforts, we (the lab and I) prioritize creating a diverse, equitable and inclusive atmosphere.

Midwest Rep candidate 1

Daniela Drummond-Barbosa

Professor, University of Wisconsin - Madison, Morgridge Institute for Research

Daniela Drummond-Barbosa is a Professor in the Department of Genetics at the University of Wisconsin-Madison and an Investigator at the Morgridge Institute for Research. Her research focuses on identifying the physiological mechanisms that link the behavior of stem cell lineages to diet, stress, exercise, and other systemic inputs using *Drosophila melanogaster* as a model organism. Daniela was born in Los Angeles, California, and grew up in Belo Horizonte, Brazil, where she received a BS degree in Biochemistry and Immunology from the Universidade Federal de Minas Gerais. She earned her PhD in Genetics at Yale University, working on the interaction between the bovine papillomavirus E5 protein and the platelet-derived growth factor receptor under the mentorship of Dr. Daniel DiMaio. During her postdoctoral training with Dr. Allan Spradling in the Department of Embryology at the Carnegie Institution, Daniela initiated a new research area investigating how tissue-resident stem cells are regulated by diet using the adult *Drosophila* ovary as a model system. In 2002, Daniela joined the Department of Cell and Developmental Biology at the Vanderbilt University Medical Center as an Assistant Professor. In 2009, she relocated her laboratory to Hopkins, where she became a tenured Professor. In 2022, she moved her laboratory a final time to Madison. Daniela co-organized the 55th Annual *Drosophila* Research Conference in San Diego (2014), co-chaired several fly meeting sessions, and served on the Larry Sandler Award Selection committee in 2015 and, as Chair, in 2016. She also served as a regular member of the Development and Differentiation in Cancer Peer Review Committee of the American Cancer Society (2012-2017) and of the National Institutes of Health Cellular Mechanisms in Aging and Development Study Section (2016-2020), and she is currently an Associate Editor for *Genetics*.

Midwest Rep candidate 2

Vikki Weake
Associate Professor, Purdue University

I am an Associate Professor in the Department of Biochemistry at Purdue University in West

Lafayette, Indiana where my lab study the mechanisms associated with aging and neurodegenerative disease. I started as a plant biochemist at Massey University in New Zealand before becoming fascinated by the transcriptional mechanisms involved in dosage compensation in *Drosophila* in my PhD studies with Max Scott. I then moved to the US in 2005 for a postdoc with Jerry Workman at the Stowers Institute. Together with Susan Abmayr, we identified tissue-specific roles for the SAGA chromatin modifying complex, and showed that SAGA had specific roles in controlling photoreceptor axon targeting during development. After joining the Biochemistry Department at Purdue in 2012, I became interested in how and why transcription changes in the aging eye, and this has been the major focus of my lab over the past 10 years.

I have been so grateful over the years to the generosity and organization of the *Drosophila* community, and I realize how fortunate we are to have resources like FlyBase, the *Drosophila* Genomics Resource Center, and the Bloomington *Drosophila* Stock Center. I was so excited at the most recent Fly meeting to see such a large number of junior researchers who were so passionate about their work, and I was proud to introduce my own students to this welcoming and amazing community. I would be honored to serve as regional representative for the Midwest and support the ongoing mission of the Fly Board overseeing our community resources and advocating for *Drosophila* research.

Treasurer's Report 2024 (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
4/30/23	Fly Board Awards			(10,360)			155,113

6/30/23	custodial fee 2023-24				(2,327)		152,786
12/31/23	dividends and capital gains		7,364				160,150
12/31/23	market value adjustment					18,035	178,185
1/1/24	awards to TAGC Dros attendees			(8,800)			169,385
as of 2/7/24	market value adjustment					1,493	170,878

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
2023	10,531	1,500	1,282	118	7,632	97,701
2024 as of 2/7	864	1,200			(336)	97,365

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

No travel expenses for 2020 or 2021 due to virtual meetings

	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
2023	150	3,145	(1,037)	6,000	5,999	37,804
2024 as of 2/7		529		6,000	5,999	38,334

Investment account established October 2020
2023 Awards: 13, 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 Rachel Smith-Bolton (for a third year), Blake Riggs (for a second year), Grace Lee, and Shefali Shefali (trainee representative). At their meeting, the committee decided on what type of awards to make. In the previous three years, we had made outreach awards to national and international groups seeking to get students from under-represented groups involved in *Drosophila* research. This year, we had a request from the TAGC organizing committee for money to support attendance at the conference. The committee decided to use the 2024 awards money for this purpose. We donated $5000 to support child care at the TAGC, preferably onsite care, but otherwise individual caregiver awards. We also gave $5000 for individual travel awards for Historically Black College or University (HCBU) or Low and Middle-Income Countries (LMIC) attendees, whichever category had more deserving applicants. In addition, we voted to cover the abstract and virtual registration fees for any of our 2023 outreach awardees who were interested in attending the conference.

The 2023 outreach awardees were selected in April by the previous committee (Brian Lazzaro, Rachel Smith-Bolton, Blake Riggs and Ana-Maria Raicu) from 22 applications received (up from 7 in 2022 and 16 in 2021, probably because we delayed the timing of the announcement so that we could advertise it at the fly meeting). Following the Trainee Awards Policy, we planned to use approximately 5% of the value of the Reserve Fund ($8,790) and $1210 from the Sandler Fund. However, after the 5 winners had been chosen it came to the committee's attention that one application had been eliminated because of a misunderstanding. With the permission of the Fly Board President, we were able to include this application and fund 6 rather than 5 awards this year.

The 2023 awardees were asked to provide a progress report:

eCLOSE was given an award to support 8 undergraduates in their 10-week summer Bridge to Research program. Participants identified a major disease impacting a community important to them, and carried out a chemical genetic screen to identify nutrients that altered the phenotypes in fly models of the disease. They used the results to design further independent research projects. Two of the students have already taken research positions in fly labs and plan to use their projects for their honors theses.

The *Drosophila* Stock Center at the University of Mysore, India, was given an award to support a hands-on training program in December 2023 to introduce teachers of undergraduate students to lab techniques to use in their classes. These techniques included mutant morphology, polytene chromosome inversions, behavioral exercises, polygenic traits and reporter constructs to study gene expression.

Engage Nepal with Science received an award for "Games of Flies and Genes," a plan to enable educators and students from 5 schools in Nepal to visit the Research Institute for Bioscience and Biotechnology. Participants were expected to look at flies under the microscope, play a game based on the laws of heredity, and make their own fly models with modeling clay. The educators will then incorporate these methods into their own teaching programs.

Osamu Shimmi is using Fly Board funding for an initiative to improve *Drosophila* research and education in Estonia. He is developing study materials in the Estonian language for middle and high school students, and writes articles for a popular science magazine to introduce *Drosophila* to biology teachers in middle and high school. On September 29, 2023, he hosted school children in the lab as part of the activities for Science Day at the University of Tartu, Estonia, to promote *Drosophila* research through outreach.

Small but Mighty received an award for a workshop held in December 2023 to educate secondary school students in Akure, Nigeria, about the possibilities of *Drosophila* research. 40 students participated in a program that included lectures on *Drosophila* genetics and husbandry as well as practical sessions including behavioral experiments. The students were given flies to take back to their schools to start fly clubs.

Enhancing Biology Education was funded to conduct a 3-day workshop including talks, practical sessions and micro-teaching in November 2023 to train teachers-in-training in Nigeria to use *Drosophila* as a teaching tool in high school biology. There were 20 in-person participants (60% female) and additional applicants joined virtually.

2024 Larry Sandler Award Report

Committee members[1]

Michelle Bland – associate professor – immunity
Li Zhao – associate professor – evolution
Parthive Patel – Sir Henry Dale Fellow – stem cells
Thomas Hurd – assistant professor – germline biology
Elizabeth Rideout – associate professor – neuroscience/metabolism/sex differences

Process details

Early process.
The entire process started in May 2023 with an email sent to the prospective chair. After accepting this role, the chair identified and invited 4 additional committee members representing diverse topics in *Drosophila* biology and different geographic areas in the first week of June 2023[1].

A poll was sent out to committee members to secure the committee meeting dates at the start of August 2023. The meeting was set and calendar invites were sent before mid-August. Committee members were also asked to provide feedback on process documents for (1) nomination package evaluation and (2) thesis evaluation[2]. Scoring rubrics and score guidance were included in this document as well to collect feedback before the end of August.

The evaluation rubric was adjusted with diversity, equity, and inclusion in mind based on recommendations from past committees. For this reason, we allowed a broader range of individuals to nominate outstanding PhD students this year. We also made attempts at adjusting our evaluation methods to integrate equity, diversity, and inclusion at all stages of the process. For example, to mitigate unconscious bias in evaluating thesis abstracts, they were scored without nominee names, institution names, or journal names in the first of a two-step evaluation process (see details in Appendix 2).

The second evaluation step was to score CV and nomination letters. Knowing that biases and cultural differences exist in reference letters, the committee also carefully worded the evaluation criteria and score guidance for this component of the nomination package. After collecting feedback from committee members on the detailed process and scoring document, a short statement was drafted to advertise the Sandler Award on the GSA website[3]. The Sandler award was also advertised as widely as possible on social media and at conferences.

Nominee details.
The committee received 24 nomination packages (CV, nomination letter, thesis abstract) of which 22 were complete. There was no information to determine nominator demographics, but the geographic locations of nominators were as follows: 10/22 US/Canada, 4/22 India, 3/22 Europe, 2/22 Middle East, 3/22 Asia. Eleven out of twenty-two (11/22) nominees were identified

[1] Emails to invite committee members are provided in Appendix 1.
[2] Detailed process document, evaluation criteria, and scoring guidance are provided in Appendix 2.
[3] GSA website statement provided in Appendix 3.

by their nominator as female. Four out of twenty-two (4/22) nominees were identified as female, white; 7/22 were identified as female, South Asian/East Asian/Southeast Asian; 4/22 were identified as male, South Asian/East Asian/Southeast Asian; 2/22 were identified as male (no demographic); 2/22 were identified as male, white; 2/22 were identified as male, Hispanic/Latino/of Spanish origin, and 1/22 was identified as male, Portuguese. Overall, this indicates we had good representation from multiple geographic regions. However, given the large number of fly labs worldwide we encourage the GSA and the next Sandler chair develop more personalized outreach efforts to contact lab heads to encourage nominations, in addition to the social media and mailing list approaches that have been traditionally used.

Meeting 1 (identify finalists).

Each committee member evaluated all 22 nominees according to the pre-determined scoring rubric and returned their scores to the chair prior to the meeting (see Appendix 2). The chair compiled the scores and set out a meeting agenda[4].

Before discussions on nomination packages, the committee discussed which elements of our process went well, and which needed to be revised for future processes (see comments and suggestion section). An initial analysis of the scores returned to the chair showed inadequate separation between the nominees with some differences noted between individuals in their preferred scoring range (some individuals scored higher overall, some had lower overall scores). Turning the scores into ranked lists for each committee member and then combining this information provided a much easier way to identify the top-scoring nomination packages (see comments and suggestions section).

The committee first identified the top 10 nomination packages, and then focused on identifying the top 5 dissertations from this list. The committee noted potential biases in multiple parts of our evaluation process that are discussed in the comments and suggestions so that the process can be further adjusted in the future. Each committee member declared their level of expertise related to a thesis, and conflicts (where applicable) were declared. Committee members in conflict with the nominator/nominee did not score or contribute to the discussions around the application packages of those individuals.

Identifying the top 10 individuals was reasonably straightforward, the bulk of the discussion focused around identifying the 5 individuals that would be selected to have their full dissertation read by the committee. In particular, while two individuals were relatively straightforward to place in the top 5, there was a lot of discussion around the other three individuals given the very high quality of application packages and nominees. Based on our deliberations, we invited five individuals to submit their full thesis for committee consideration.

Inviting full thesis submissions.

The chair wrote letters to all finalists and to all individuals that were not selected to have their full dissertation considered[5]. The email invitation to submit the thesis was sent to both the student and their supervisor to ensure a rapid response and thesis upload.

Meeting 2 (identify winner and runners-up).

[4] Please see sample agenda in Appendix 4.

[5] Please see sample emails in Appendix 5.

After reading and evaluating all the dissertations according to the scoring rubric, committee members sent their scores to the chair. After compiling the scores, the chair made a meeting agenda[6] and the committee met to select a winner. The committee first reflected on the process for evaluating and scoring the full dissertations. Overall, the committee was happy with the process and the scoring system used, see comments and suggestions section for potential areas of improvement. After brief discussions about the merit of each candidate from all committee members, the committee chose the top three dissertations, and unanimously identified the winner from this group.

2024 Larry Sandler award winner and runners-up.

2024 Larry Sandler award winner:
Dr. Sherzod Tokamov (nominator Dr. Rick Fehon, University of Chicago)

2024 Larry Sandler runners-up:
Dr. Heya Zhao (nominator Dr. Alexey Veraksa, University of Massachusetts, Boston)
Dr. Wenhao Xu (nominator Dr. Wei Song, Wuhan University)

Winning abstract.
The Hippo pathway is an evolutionarily conserved regulator of tissue growth. At the core of the pathway, a kinase cascade represses the activity of a transcriptional effector, an oncoprotein called Yorkie. Inactivation of the Hippo pathway results in the translocation of Yorkie into the nucleus, where it promotes a pro-growth genetic program. Multiple upstream inputs are known to synergistically activate the kinase cascade from the apical cortex of polarized epithelial cells. However, how these components are organized and the mechanisms by which they are regulated remains poorly understood. My thesis work explores how Hippo signaling is controlled, focusing on the regulation and organization of a key upstream Hippo pathway organizer, a multivalent scaffold protein called Kibra. Unlike other Hippo pathway regulators, which localize mainly at the junctional cortex of epithelial cells, Kibra's subcellular localization is distinctly partitioned into junctional and medial domains of the apical cortex. Previous work has shown that medial localization potentiates Kibra-mediated Hippo pathway activation, but the mechanisms that control Kibra activity and subcellular organization remain unknown. In this dissertation, I present evidence that proteolytic degradation, actomyosin cytoskeleton, and apical polarity network converge to control Kibra-mediated Hippo signaling. I first demonstrate that ubiquitin-mediated degradation is a major mechanism that regulates Kibra abundance (Chapter 2). Specifically, upon assembly of the Hippo complex, Kibra is ubiquitinated via the SCFSlimb E3 ubiquitin ligase machinery and is subsequently degraded. A point mutation that prevents Kibra degradation results in dramatic upregulation of Kibra levels, which causes a significant decrease in organ size. Next, I show that ubiquitin-mediated Kibra turnover is modulated by actomyosin-generated cortical tension (Chapter 3). Mechanistically, increased tension results in tighter cortical association of the Ser/Thr kinase Par- 1, and Par-1 promotes Kibra degradation. Finally, I identify the mechanism by which Kirba is partitioned into junctional and medial pools at the apical cortex (Chapter 4 and Appendix A). I show that the apical polarity

[6] Please see sample agenda in Appendix 6.

network, in part via aPKC, tethers Kibra at the junctional cortex to silence Kibra-mediated Hippo signaling, whereas medial actomyosin flows untether Kibra from the junctional cortex and promote its medial accumulation, thereby increasing Kibra-mediated Hippo signaling. Together, these findings provide crucial insights into the regulation of the Hippo pathway and reveal functional relationships between upstream Hippo signaling, actomyosin dynamics, and apical polarity network in tissue growth control. More broadly, this work provides a paradigm for understanding how mechanical forces and epithelial cell architecture organize and regulate intracellular signaling events.

Winner notification.
The winner, runners-up, and the remaining finalists were notified via email[7].

*Full nomination list 2024 (finalists in bold; * indicates winner).*

Nominee	Nominator
Heya Zhao	Alexey Veraksa
Leonard D'Souza	Anurag Sharma
Anna Hakes	Elizabeth Gavis
Kevin Ho	Guy Tanentzapf
Eliano Dos Santos	Helene Cocheme
Jae-Hyuk Lee	Seongsoo Lee
Tae Hoon Ryu	Kweon Yu
Gustavo Agular	Markus Affolter
Marcus Kilwein	Michael Welte
Ayesha Banu	Mohammad Farhan
Aparajita Aparajita	Nagaraj Prasad
Jana Fuhrman	Natalie Dye
Krittika Sudhakar	Pankaj Yadav
Sherzod Tokamov*	Rick Fehon
Gordana Scepanovic	Rodrigo Fernandez-Gonzalez
Pavitra Prakash	Sheeba Vasu
Michael Aimino	Timothy Mosca
Juan Pablo Jauregui-Lozano	Vikki Weake
Wenhao Xu	Wei Song
Scarlet Park	William Ja
Safa Selim	Mohammad Farhan
Meghan Ferguson	Edan Foley

Overall process guidance and important dates.

[7] Please see sample emails in Appendix 7.

This was the overall process guidance we followed for the 2024 Larry Sandler Award. See comments and suggestions section for notes on potential changes for next year. Text highlighted in yellow corresponds to process elements for which we suggest improvements.

Larry Sandler Award Guidelines:

1. Call for Nominations: GSA/Suzy Brown puts out a call for nominations in early Fall for a November 1 deadline.
2. Eligibility: Any student completing a Ph.D. in an area of *Drosophila* research between July of year X-1 and mid-November year X is eligible and may be nominated by his/her thesis advisor. A student may only apply once.
3. Documents required: Nominations must include curriculum vitae, a thesis abstract of one or two pages, and a letter of nomination from the thesis advisor rolled into a single pdf file and emailed to the Chair.
4. Selection of Chair of the Committee: The Chair of the previous year's committee asks one member of the committee to serve as the next Chair.
5. Selection of the Committee: The Chair selects members of the committee who have demonstrated expertise in a particular area of *Drosophila* research. It is recommended that the committee have 4 or 5 members including the Chair, spanning career stages from assistant to full professor ranks. It is suggested that the areas of expertise represent neuroscience, stem cells, evolution, immunity and growth control/patterning. Other areas of expertise are also acceptable and a committee member may be an expert in several areas. While no particular rank (assistant, associate, full professor is required), the committee member should have experience in training graduate students. It is also suggested that the committee include white female members, and members of color.
6. Recommended reading for the committee: To be aware of gender-bias, the Chair should suggest to the committee that Amy Besjovec's Presidential Report on Gender-bias be read as well as Carnes et al Journal of Women's Health Volume 14, Number 8, 2005 "NIH Director's Pioneer Awards: Could the Selection Process Be Biased against Women?". These documents should be emailed to the committee members and also provided in the dropbox where the Chair uploads the application.
7. Reviewing the applications: Soon after the November 1 deadline, the Chair should upload the applications to a dropbox (or similar type of shared folder). It is suggested that the Chair create a document containing the name and gender of the applicant and the name(s) and gender(s) of the nominators and that this file is shared with the committee at the outset.
8. Selection of 3-5 top candidates whose dissertations will be read by the committee. Soon after the Nov 1 deadline, the Chair should set a date for each committee member to email their top 5 candidates to the Chair. A suggested date for this deadline is December 15.
9. Review of the dissertations: The Chair will contact the mentors of the top 3-5 candidates and obtain a pdf file of the dissertation. The dissertations will be distributed amongst the committee members for review over the winter holidays.
10. Selecting a date for a conference call to decide the winner and 2 runners-up. In mid-December, the Chair will use a doodle (or similar) poll to pick a date when the committee

members can participate in a conference call to select the finalists. This should occur in early or mid-January as a decision should be made no later than mid-January.

11. In the event that a student defended a significant period of time before the deadline, for example, 12-15 months, and/or if the student remained in the mentor lab for a short postdoc, and had publications post-defense, the Chair may contact the mentor for clarification of what parts of the paper(s) were produced during graduate training.
12. The Chair emails Suzy Brown and FlyBoard President the names of the Winner and Runners up.
13. Notification:
    a. The Chair emails the Winner and her/his mentor(s) that s/he has won the Sandler Award, including the details of when the lecture will take place.
    b. The Chair emails the Runners-up and their mentors.
    c. The Chair emails the mentors of the applicants who were not selected as finalists. This courtesy is much appreciated by all involved.
    d. Suggested formats for the email content are below.
14. The Chair writes a report on the Sandler committee, the applicants, genders of applicants and nominators, the finalists and sends this to the FlyBoard President. A suggested format is below.
15. The Chair makes every attempt to attend the Fly Meeting and arrive in time to present the Sandler Award on the first evening. If the Chair cannot attend the meeting, they ask one of the committee members to present the award. If this is not possible, the FlyBoard President presents the Award.
16. The Chair will be invited to present the report at the FlyBoard meeting, which usually occurs on the afternoon of the first day of the Fly Meeting, typically from 3-6 pm with the Sandler report occurring at ~3:30 pm.
17. Suzy Brown has helped with making PPT slides for the presentation. It is suggested that the first slide have the names of the Runners-up and the committee members. The second slide should contain a photo of the winner with her/his name (provided by Suzy).

Comments and suggestions

Process.

- We suggest that future committees continue to allow nominations from thesis supervisors, department heads, and supervisory committee members.
- We propose that an earlier deadline (before Nov. 1) is set to give committee more time to complete nomination package and thesis evaluations.
- We propose that anonymized abstracts continue to be used to mitigate some aspects of unconscious bias.
- To minimize differences in nomination letters, CV style, and abstract format we propose that the nomination package is standardized to include defined sections that match the evaluation criteria.

- To ensure everyone is aware of the evaluation criteria and scoring rubrics/guidance we propose that these documents are available to all applicants before they submit their nominations.
- 2024 Sandler committee members were familiar with formatting and stylistic guidelines and norms across many geographic locations. This enhanced our ability to evaluate the applications from non-US countries.

Scoring.
Our evaluation process, as outlined in Appendix 2, worked well overall. We identified a few areas for improvement:

1) Focus on completed research works (e.g. primary research papers including preprints) and other scholarly contributions (e.g. review articles) to drive the CV score. Contributions to community was not used much by our committee during the evaluation because we noticed significant differences between geographic regions in this category. In future, the contributions to community section will be useful as a non-scoreable component for choosing between individuals who are otherwise equivalent in the other two sections.
2) Nomination letters were very different depending on the geographic region in which the research took place. We did not rely on this component to make any decisions as it was very difficult to compare between candidates due to these geographic differences. Letters were only useful to provide context for a couple of nominees with specific circumstances (e.g. longer PhD time).
3) Focus on the idea of the science, not where it is published, to score the anonymized abstract. This was challenging for all of us, but there was general agreement that it was one way to mitigate the powerful biases that come from knowing journal names, institution names, and mentor names as proxies for excellence. Concerns over whether nominee abstract quality correlates with scientific excellence were mitigated by also scoring the CV.
4) Committee members should rank the applicants rather than provide scores as this was more informative of an approach overall.
5) Have a conference call to narrow down the nominees to invite for thesis submission, this was the stage at which we had the hardest decisions to make. Committee members found categories such as importance of scientific question, impact to the fly community, and completeness of story useful thesis attributes when deciding on our top nominees. It was valuable to have insights from other committee members on dissertations at this stage, especially for dissertations where the nominee abstract/letter/CV format was different from the widely-used US style. This will be important in ensuring that we recognize the best *Drosophila* science regardless where the research is conducted.

Appendix 1 – Emails to invite Sandler Award committee members

Dear Dr. X,

My name is X; I am an associate professor at X. I am this year's chair of the Larry Sandler Award selection committee, an annual award given to the top *Drosophila* thesis of the year. I am writing to invite you to serve on the committee that selects the person who will receive this award. I think your scientific expertise and your commitment to mentoring and education would be a valuable addition to the committee.

I also like the idea of having people on the committee who are earlier in their career to provide a fresh perspective on award adjudication. However, I am aware this might not be the best time for you, so if you'd rather serve at another time let me know and I will pass your name on to next year's chair.

The Larry Sandler award was established in 1988 by the colleagues, friends, and students of Dr. Larry Sandler after his untimely death in 1987. The award serves to recognize an outstanding recent PhD graduate. The recipient of this prestigious award will present a plenary lecture at the upcoming in-person TAGC meeting to be held in Washington in March 2024. The deadline for the nomination is November 1, 2023. The nomination material is fairly quick to review (thesis abstract, nomination letter [1000 words], nominee's CV) and there are typically no more than 20-30 nominees.

In terms of process, the committee will first score the abstract. The committee will then score the CV and nomination letter, and these two individual scores will be combined to narrow down the top nominees (~3-5 theses). The committee will read and evaluate these top 3-5 theses using a scoring system that accounts for each committee members' confidence and/or involvement in that field. We will then decide on the top nominee and runners-up.

Most of the process will take place over email, with two meetings to (1) narrow down the top theses to read and (2) to select the top nominee. A suggested timeline is as follows:

(1) Nov. 1, 2023	Nomination letter submission by nominator.
(2) Nov. 10, 2023	Committee member abstract scores due
(3) Nov. 25, 2023	Committee member CV and nomination letter scores due
(4) Nov. 26, 2023	Committee members choose top 3-5 nominees, requests for theses sent
(5) Dec. 1, 2023	Committee members receive theses
(6) Dec. 15-20, 2023	Committee members meet to choose top nominee and runners-up
(7) Dec. 31, 2023	Chair will send names of top nominee and runners-up to GSA

Please let me know if you are willing to serve on the committee. If you would like more information, please do not hesitate to get in touch.

With best wishes,
X

Appendix 2 - Process details

Evaluating initial nomination packages

Nomination package

1. Nominee's CV
2. Thesis abstract (anonymized)
3. Nomination letter (1000 words)

After all nominations are received, the committee will begin the process of evaluating the application package to select 3-5 finalists. This will occur in two stages: (i) scoring the abstracts and (ii) scoring the letter and CV.

(i) Each committee member will score all abstracts based on the same evaluation criteria.

Applicants will be evaluated on abstract attributes including:

- Important scientific problem
- Approach to tackling the scientific problem
- Progress made in tackling the scientific problem
- Anticipated impact to community

Score Guidance (points in brackets)

Outstanding (5): discovering new phenomena or starting new fields
Excellent (4): broad reach and impact across fields
Very Good (3): leading their field
Good (2): advanced knowledge within a field
Adequate (1): scientifically sound knowledge

(ii) Each committee member will score all CVs and nomination letters according to the same evaluation criteria.

a. Applicants will be evaluated on CV attributes including:

- Completed research works (e.g., research publications and preprints)
- Other forms of scholarly contributions (e.g., editorials, commentary, reviews)
- Contributions to the scientific community and/or outreach activities

Score Guidance (points in brackets)

Outstanding (4): very significant contributions
Excellent (3): significant contributions
Good (2): good contributions

Adequate (1): some contribution

b. Applicants will be evaluated on nomination letter attributes including:

- Applicant role in developing and testing hypotheses
- Applicant role for the applicant in doing or organizing the work
- Applicant contribution to lab environment
- Applicant scientific growth

Score guidance (points in brackets)

Outstanding (4): describes a leading role for the applicant
Excellent (3): describes a main role for the applicant
Very Good (2): describes a strong role for the applicant
Adequate (1): describes some role for the applicant

For (i) and (ii) committee members will also be asked to rate their confidence in the subject area as poor (little to no knowledge of the field or techniques), reasonable (knowledge of some aspects of the field or techniques), or expert (direct knowledge and/or experience of the field or techniques). This will help us in committee discussions to choose the top candidates for full thesis consideration. Committee members will also declare any conflicts of interest; where conflicts are identified the committee member will not score the nomination package or participate in the committee discussions regarding the individual with whom they are in conflict.

The committee will rank the top nomination packages based on the combined outcome from stages (i) and (ii). For any applications with a large score discordance between stages i & ii, the committee will discuss the nominee carefully to resolve the nature of the score discrepancy and to mitigate unconscious bias in the evaluation of documents such as CVs and nomination letters.

Full thesis evaluation

The committee will read and evaluate these top 3-5 theses using a scoring system that accounts for each committee members' confidence and/or involvement in that field. We will then decide on the top nominee and runners-up.

Full theses will be read and adjudicated according to the following attributes:

- Important scientific problem (literature review, references)
- Approach to tackling the scientific problem (methods)
- Progress made in tackling the scientific problem (data)
- Anticipated impact to community (discussion, open science)

Score Guidance (points in brackets)

Outstanding (90-100): discovering new phenomena or starting new fields
Excellent (80-89): broad reach and impact across fields
Very Good (70-79): leading their field
Good (60-69): advanced knowledge within a field
Adequate (0-60): scientifically sound knowledge

The committee will rank top applicants based on the consideration of their thesis scores, nomination letters, and CV. The top nominee will receive the award, and the committee will also choose two runners-up. This information will be passed to GSA to advertise the Sandler awardee.

Appendix 3 – GSA website announcement

Larry Sandler Award

The Larry Sandler Memorial Lecture is presented by an outstanding recent PhD graduate on the opening night of the annual *Drosophila* conference. The award was established in 1988 by the colleagues, friends, and students of Dr. Larry Sandler after his untimely death in 1987. The award serves to honor Dr. Sandler for his many contributions to *Drosophila* genetics and his exceptional dedication to the training of *Drosophila* biologists.

Eligibility

Any student completing a PhD in an area of *Drosophila* research between July 2022 and December 2023 is eligible. Students may be nominated by their thesis advisor, department chair, or a supervisory committee member. Nomination deadline is Nov. 1, 2023.

Nominate Here

Application materials and evaluation

1. Nomination letter
   Applicants will be evaluated on nomination letter attributes including applicant role in developing and testing hypotheses, applicant role in doing or organizing the work, applicant contribution to lab environment, applicant scientific growth.

2. Thesis abstract (1-2 pages; must omit journal names and institution names)
   Applicants will be evaluated on abstract attributes including identifying an important scientific problem, the approach to tackling the scientific problem, and the anticipated impact to the community.

3. Nominee's CV
   Applicants will be evaluated on CV attributes including completed research works (e.g., research publications and preprints), other forms of scholarly contributions (e.g., editorials, commentary, reviews), contributions to the scientific community and/or outreach activities.

Appendix 4 – Agenda for Meeting 1.

Larry Sander Committee (2023), Meeting 1

Date:
Meeting link:

Agenda

1. Introductions (10 min).
2. Reflection on process so far (20 min).
3. Current rankings (15 min).
4. Identify top 10 (45 mins).
5. Break (20 mins).
6. Identify top 3-5 (60 min).
7. Closing remarks and timelines (10 min).

Appendix 5 - Emails to finalists and individuals who weren't selected as finalists

Finalist email (to both student and supervisor)

Dear Dr. X,

As you may know, your graduate advisor, Dr. X, nominated you for the prestigious Larry Sandler Award. On behalf of the Larry Sandler award committee, I am excited to let you know that we selected you as one of the finalists!

I am therefore requesting an electronic copy of your thesis for full review by the committee. Please send it to me before November 30 2023 as a pdf file via email (address@email.com) or upload to the shared folder (link below) so that the committee has the maximum time to review your thesis.

Congratulations!

X

Non-finalist email (to both student and supervisor)

Dear Dr. X,

Thank you for nominating your student for the 2024 Larry Sandler Memorial Award. We had an extremely strong pool of # applications this year, and it was very challenging for the committee to select the candidates who will move on to the next stage in the process.

I am sorry to let you know that your student was not selected to have their full thesis considered. On behalf of the Larry Sandler award committee, thank you for taking the time to support Dr. X's excellent graduate work. Their research addresses a fundamental question in biology, and represents the very best of our community.

Sincerely,

X

Appendix 6 – Agenda for Meeting 2.

Larry Sander Committee (2023), Meeting 2

Date:
Link:

Agenda

1. Welcome back (5 min).
2. Reflection on full thesis evaluation (10 min).
3. Current scores (5 min).
4. Roundtable impressions - each committee member has ~5 mins to share their thoughts on the current scores/ranks (30 mins).
5. Identify top 3 (20 mins).
6. Break (20 min).
7. Identify top candidate and two runners-up (70 min).
8. Closing remarks and timelines (10 min).

Appendix 7 - Email to winner, runners-up, and other finalists

Email to winner.

Dear Dr. Tokamov,

On behalf of the 2024 Sandler Award Committee, I am delighted to inform you that you have been selected as the recipient of the 2024 Larry Sandler Memorial Award!

As you may know, this award is given to the individual that submits the "best" Ph.D. thesis in *Drosophila* research from the previous year. In this round we had 22 nominations, making the standard of competition very high. The committee (composed of Drs. Parthive Patel, Li Zhao, Michelle Bland, Thomas Hurd, and myself) unanimously chose your body of work on the mechanisms of Kibra-mediated Hippo signaling as the most deserving of the award this year – we think your work will have a long-term impact on the fields of Hippo signaling and cell growth. Your advisor Dr. Rick Fehon also provided a very strong letter in support of your scientific growth and achievements during your PhD. Many congratulations on producing such an elegantly-executed and beautifully-written thesis; you perfectly used the large genetic toolkit available to *Drosophila* researchers to answer your scientific question.

As the recipient of this award, you will have the honor of presenting your thesis work in the Larry Sandler Memorial Lecture at TAGC2024 in Washington, DC. You will give your plenary lecture in front of the large model organism communities at the meeting. In addition to sharing your work with *Drosophila*, we hope that your talk will help to inspire other students just starting or in the midst of their PhDs. Ms. Suzy Brown (cc'ed here) of the GSA will be in touch to make (and pay for) your travel arrangements to TAGC2024.

Again, please accept our warmest congratulations. You join a long list of outstanding *Drosophila* scientists who have gone on to have successful careers.

Please don't hesitate to let me know if you have any questions as you prepare for your talk in Washington, DC. I look forward to meeting you in person at TAGC2024!

Best wishes,

XX (committee chair) on behalf of

Committee members

Email to runners-up.
Dear Dr. X,

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

Although you are not the winner for this year's award, I want to congratulate you on the beautiful body of work contained in your thesis. This year we received 22 nominations, it goes without saying that this year's competition was very intense, and it was difficult to choose only five dissertations from this group. We truly enjoyed reading about your scientific growth and achievements, and have no doubt that you will continue to engage in cutting-edge research in your future. Based on their letter, you supervisor absolutely agrees with this assessment – their letter was extremely strong and supportive.

At your earliest convenience, please send me a headshot that I can use to highlight your work during the Larry Sandler Award presentation at TAGC2024 – perhaps I'll even see you there in person to congratulate you such beautiful work!

On behalf of the 2024 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 wishes,

XX (committee chair) on behalf of

Committee members

Image Award Report (Julie Brill)

This year, Amy Kiger and Dan Bergstralh rotated off the Image Award committee and two new members were added – Girish Melkani (University of Alabama, Birmingham) and Syed, Mubarak Husain (University of New Mexico), maintaining the total committee membership at six (including Julie Brill, Tina Tootle, Clemens Cabernard and José Pastor-Pareja).Tina and Clemens will rotate off this year and two new members will be added. Regular committee members generally serve 2-year terms (with some serving 3-year terms), allowing for steady turnover. The Chair position is a 5-year term, and I am in my second year.

Results of the 2022 competition

For the current competition, we maintained our Twitter presence and Facebook postings, with members of the committee and the Drosophila community sharing my tweets and posts.

This year: 95 total submissions = 67 images and 28 videos.
Last year: 76 eligible submissions = 48 images and 28 videos.

This is a 25% increase from last year, which was a 50% increase from the year before.

Points for discussion

- Historically, new DIA committee members are chosen by the Chair in consultation with other committee members. Last year I raised the question of whether we needed a mechanism to ensure more diversity on the committee, for example by encouraging newer faculty or other underrepresented groups to volunteer. Michelle Arbeitman had arranged a Fly Community Volunteer Interest Survey in 2022, and she sent me the list of all those who volunteered.

- I examined the websites of the 36 PIs on Michelle's list who indicated an interest in the Drosophila Image Award committee. From this group, I decided to invite Girish Melkani because of the terrific images and videos as well as the excellent publications posted on his website. Although he is not someone who was known by anyone on the committee, he has been a great addition. I also invited Syed, Mubarak Husain (FlyGuy) at the suggestion of Clemens Cabernard, who felt Syed's neurobiology and imaging expertise would be helpful to the committee since Clemens is rotating off this year.

- As with last year's competition, quite a few of the authors did not follow the Rules or read the FAQ on the DIA website and sent incomplete submissions that lacked important information, for example a title, or the name(s) of the person or people who should be credited with taking the image or video. Although I intended to have Drew Elias (who maintains the website) post downloadable Powerpoint templates (which I suspect would encourage those submitting files to include all the relevant information), I forgot to do this in a timely manner. However, this is in the plans for next year.

- This year, we had several people who submitted up to four similar images that either they or someone in their lab had taken. This seemed overall to dilute interest in any one image, and none of the people who submitted four images or videos (and only one of the people who submitted three images) won an award. I am thinking of capping the number of submitted images and videos at two per person to increase the chances that they will win an award.

The 2024 DIA winners

Image award: **Anthony Dornan** (J. Dow lab), University of Glasgow

Compromised junctional integrity phenocopies age-dependent renal dysfunction in Drosophila Snakeskin mutants.
Dornan AJ, Halberg KV, Beuter LK, Davies SA, Dow JAT.J Cell Sci. 2023 Oct 1;136(19):jcs261118. doi: 10.1242/jcs.261118. Epub 2023 Oct 5.PMID: 37694602

Video award: **Federica Mangione** (N. Tapon lab), The Francis Crick Institute

Co-option of epidermal cells enables touch sensing.
Mangione F, Titlow J, Maclachlan C, Gho M, Davis I, Collinson L, Tapon N.Nat Cell Biol. 2023 Apr;25(4):540-549. doi: 10.1038/s41556-023-01110-2. Epub 2023 Mar 23.PMID: 36959505

Drosophila Community Service Award Report for TAGC/ADRC 2024

The committee:
Michelle Arbeitman (chair)
Elizabeth Chen
Amy Kiger
Steven Marygold
Nasser Rusan
Nadia Singh

The award committee was formed in the Fall of 2023 by Michelle Arbeitman, in consultation with Fly Board President Harmit Malik. The Chair thought it was best to remove Dr. Kevin Cook from the committee this year, as there were several nominations for the BDSC from last year that were to be considered. The committee wrote an announcement and call for nominations that was sent out by GSA late 2023 and posted on the TAGC website. The announcement was also posted on Twitter and Bluesky by FlyBase, and by colleagues on the committee.

The committee has received a great set of nomination letters for our colleagues over the last two years. 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 second year of the Service Award, we decided to give a group of colleagues the award for:

Cataloging, maintaining, and distributing Drosophila stocks for the worldwide research community.

The group of awardees include colleagues from the **Bloomington Drosophila Stock Center at Indiana University.** We recognize the contributions of senior staff members Drs. Kevin Cook, Annette Parks, Cale Whitworth, and Sam Zheng. The committee also recognizes the efforts of the team of colleagues working with the senior staff that are integral to the success of BDSC.

The awardees will be contacted and told that the award will be presented by Dr. Steven Marygold after the Thursday morning Plenary Session.

After TAGC/ADRC 2024 Michelle Arbeitman 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. We appreciate the support of GSA.

The policy for the award states that committee members serve for two-years minimally. The committee for next year will be comprised of members that are already serving. During the committee's discussion, it was suggested that next year the committee members do more outreach to obtain a broad set of nominees.

List of Awardees

2023: For gathering and organizing the information that drives Drosophila research
Dr James Thompson for Drosophila Information Services
Dr Thomas Brody for Interactive Fly
FlyBase Curatorial Team

2024: For cataloging, maintaining, and distributing Drosophila stocks for the worldwide research community
Bloomington Drosophila Stock Center at Indiana University
Senior Staff Members: Kevin Cook, Annette Parks, Cale Whitworth, and Sam Zheng; all staff members and stock-keepers past and present for their contributions and substantial efforts.

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.

TAGC/65th Annual *Drosophila* Research Conference (2024)

Organizers:
Chair, Melissa Harrison, University of Wisconsin School of Medicine and Public Health
Amanda Larracuente, University of Rochester
Dan McKay, UNC School of Medicine
Blake Riggs, San Francisco State University

In 2022 and 2023 we were able to offer the Drosophila conference in a hybrid format. GSA experienced a significant drop in on-line attendance as we moved through meetings in 2022 and into 2023. For the Drosophila conference in 2022, 34% were online attendees. That dropped to 8% in 2023. For TAGC24, the decision was made to stream the keynote sessions only. The other abstract driven sessions will be recorded and available online through the app for 30 days after the conference.

What to expect for 2024 and TAGC

As you may remember, TAGC was first held in 2016 and the concept for the meeting, driven by survey responses over the preceding years, was to provide an environment where there was more interaction between model organism communities. So if someone was studying, cell death for example, they could get together with colleagues studying this in other organisms and collaborate. Attendees deemed the 2016 experiment to be a success and it was scheduled to happen again in 2020. While we were not able to meet in person in 2020, the meeting format

was taken online and research that had been submitted was still able to be shared across communities. The GSA Board reached out to the participating and additional communities, and there was strong interest to have the meeting again in 2024.

The 65th Annual Drosophila Research Conference is a major part of TAGC. This will give you an idea of how many of your colleagues are at the meeting.

TAGC24 Attendance/Submissions

	TAGC Overall (virtual)	Drosophila Specific (virtual)
Abstracts	1,952	834
Registrants	2,837 (199)	1,178 (67)

Dros Conference Abstract Submissions/Registration 2018-2024

	2024 (virtual)	2023 (virtual)	2022 (virtual)	2021 (virtual)	2019	2018
Abstracts	834	1,023	1,018	786	837	883
Registrants	1,178 (67)	1,620 (195)	1,611 (591)	(1,850)	1,166	1,238

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.

Oral Presentations - all keynote sessions will be live streamed through the app in Zoom. All abstract driven oral presentations will also be recorded and available in the App through April 6 to all registrants. Presenters who are not able to attend the meeting in person will be providing a recorded talk.

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. All in-person posters will be available for viewing throughout the conference.

Childcare

Thanks in part to the generous support of FlyBoard, we have been able to offer $13,975.00 of child and dependent care support to 21 households representing 24 individuals—with $6,890.00 going to 13 Drosophilists. All applicants were awarded support. We are also pleased to offer on-site childcare covering the full meeting through ACCENT on Children's Arrangements, LLC. More information on childcare and family resources is available on the website.

Ambassadors

GSA's Equity and Inclusion Committee is piloting a new program at TAGC 2024 and Fungal24. In the program, so-called Inclusion Ambassadors are attendees who have volunteered to participate in this effort to model inclusion and provide information to others at the conference; they will attend a short training prior to the conference. Inclusion Ambassadors will direct others to conference events focused on equity and inclusion and tell them how GSA is working toward an equitable future. In the event someone needs to report a Code of Conduct violation, they will facilitate contacting GSA staff. Inclusion Ambassadors will be identified by the rainbow ribbon on their conference badges.

Pending successful pilots, we plan to have Inclusion Ambassadors at all GSA Conferences moving forward.

Health and Safety

Our top priority is the safety of our attendees. Attendees are anticipated to be fully vaccinated against COVID-19 and have been asked, as a precaution, to take a rapid antigen test within 24 hours before departing for the meeting. A limited supply of N95s or KN95s masks will be available at the registration desk. Full health and safety information can be found here.

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

Exhibitors and Sponsors

Please stop by and say hello to the exhibitors, many of whom come to the *Drosophila* meeting every year. We appreciate their support and their participation helps keep registration prices down, and they really value meeting leaders in the Fly Community.

Future Meetings

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

Organizers:
Todd Nystul, Chair
Michelle Bland
Amanda Crocker
Justin Crocker
Leila Rieder

67th Annual *Drosophila* Research Conference
March 4–8, 2026
Sheraton Grand Chicago Riverwalk
Chicago, IL

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 #TAGC24 organizers and will be available to all future Dros and TAGC organizers. We welcome feedback and input from organizers so that we can continue adding to and enhancing the Vision.

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.

To date, we've held an online session (summer 2022) and an in-person workshop (#Dros23) to pilot this effort. We are holding another workshop at #TAGC24 to help us polish the program so we can look for funding to support the work.

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

***Drosophila* Image Awards**: GSA provides design, IT, and administrative support for the *Drosophila* Image Awards and hosts the website. In preparation for the 65th 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. For the 2024 TAGC meeting, the FlyBoard elected to use approximately 5% of their reserve fund ($8800) to subsidize child care and provide travel awards for HBCU and LMIC attendees. Additional funding in the amount of $1200, was provided by the Larry Sandler Fund for these initiatives.

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 7, 2024 the balance in the *Drosophila* Reserve was $171K. Awards to recipients in the Fly Community in the amount of $36K have been made since 2021 from the reserve account.

Victoria Finnerty Fund

GSA maintains the Victoria Finnerty Fund as a restricted account for the Fly Community, from which $5K - $6K in grants 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 7, 2024 the investment account balance was $26K and there was $12K in cash, for a total of $38K.

Larry Sandler Fund

The Larry Sandler Fund is held in a custodial capacity by GSA for the Fly Community and is invested in two accounts at Vanguard. The total of the accounts has grown from $28K in

2003 to $97K as of February 7, 2024. 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, 2022, and 2023, and in support of child care and travel awards for HBCU and LMIC attendees at the TAGC conference in 2024 .

Professional Development & Other Special Programming

The Allied Genetics Conference 2024 programming

Engagement staff are organizing a robust series of professional development, networking, and mentorship events for the upcoming TAGC 2024 conference. Engagement's professional development programming will prioritize cross-community engagement and networking events, and in-depth career path information. Early- and mid-career attendees will have opportunities to attend myriad events that will make it easy to connect with researchers across multiple fields, foster scientific collaborations, explore career connections, and make new friends.

While some events are repeated from previously held activities, several are newly established programs based on survey feedback, Engagement staff ideas, and GSA's commitment to innovating approaches to community needs.

A comprehensive list of Engagement's TAGC 2024 programming is available on the conference website's professional development and networking pages, and several events are highlighted below in the "Planned Events" section.

Career tracks

As part of TAGC 2024 professional development, Engagement staff will work with Communications to develop a document that provides suggested events for an academic and non-academic career track. While some events will be unique to one path, other events are included in both paths, highlighting the many bridges between academic and non-academic careers as well as the incredible diversity of careers within each category.

Participant goals

At the end of each event, Engagement aims to ensure that participants have:

- Developed a stronger peer support network of researchers from multiple research areas and organism communities to reach out to when in need of advice, guidance, and support, or for collaborative projects.
- Gathered information to help inform their next professional step, whether that's a career transition or entering the job market.
- Gained a better understanding of the overlap between academic and non-academic careers *and* the variety of careers within and without academia, as well as an understanding that a faculty or teaching position comes in many forms.

Planned events

Planned events are listed below and have been developed in conjunction with the GSA Conferences Committee and the APC (TAGC 2024 Organizers).

3D printing in the lab and classroom: In this workshop, participants will learn how to use 3D printer software and free 3D model resources. Workshop facilitators will showcase printable educational tools, such as anatomical models of organisms and molecules. Researchers will discover types of laboratory equipment that can be printed for a fraction of the standard cost.

Accessibility in STEM: Designed for attendees to learn about the challenges of people with disabilities and to help build a welcoming and inclusive community. This free-to-attend virtual workshop will be organized and led by the ECLP Accessibility Subcommittee. The session will provide information about scientific poster accessibility in terms of text and data presentation. To encourage discussion, participants will be placed in small groups.

Capitol Hill Day: In collaboration with the Coalition for the Life Sciences, Capitol Hill Day participants will engage with policymakers and highlight the importance of fundamental discoveries. Hill Day will be held in conjunction with the Policy and Advocacy sub-committee of the ECLP, which is reviewing applications to take part in Hill Day.

Career Exploration Panel: This discussion panel of individuals representing career paths outside of academia showcases the broad options available to those with a PhD. This session is run in collaboration with the Career Development sub-committee of the ECLP.

Careers in Academia Panel: Features academic department heads and faculty who will discuss the academic job application process and provide insights into the daily life of a faculty member.

Community and career stage-specific networking events: Engage attendees within and between organisms of study and career stages. The moderated networking hotspots will focus on scientific, career, and social topics, with ~25 unique networking opportunities held across three days. Discussions will center around a range of science-based topics, such as “Cell Biology and Growth;” career-driven topics, such as “Professional Development and Careers in Science;” and social issues, such as “Diversity, Equity, and Inclusion.”

Community, Connections, and Lunch (CCL) mentorship event: Intends to facilitate interactions between early and mid-career scientists and established scientists. GSA will match mentors and mentees for a moderated, topic-based discussion. Mentees will have the opportunity to ask specific questions and receive advice aligned with their career interests and goals. GSA encourages mentors and mentees to have touchpoints after TAGC. This luncheon is organized, hosted, and sponsored by GSA. Awardees funded by GSA’s NSF grant are given priority access to this event.

Complimentary professional photographs: Allows graduate students and postdoctoral fellow attendees to receive professional photographs at no charge. The attendees may use the photograph(s) for job applications, professional social media, and more.

Education workshops: Attendees can participate in a series of 90-minute, hands-on workshops related to advancing undergraduate education. Topics include publishing education papers and course-based undergraduate research experiences.

Genetics education research session: “Towards an equitable future: Genetics engagement beyond academia” is designed in collaboration with the Personal Genetics Education Project (pgEd). Attendees will explore challenges, opportunities, and best practices for engagement with genetics in non-academic communities. Participants will engage in multidirectional conversations with educators and with public audiences on scientific, personal, and societal dimensions of genetics.

Grants and funding workshop: Provides participants with important information related to grantsmanship and funding. During the program, attendees will hear talks and discussions from experienced investigators and program officers. Workshop participants will have the opportunity to learn about the peer review process, communicating with program officers, common errors, important considerations, funding for experimental organisms, and framing significance and novelty, among other topics.

GSA Journals peer review training workshop: This two-hour workshop introduces participants to the principles and best practices of the scientific review process. The session will begin with a presentation describing the principles and purposes of peer review, peer review models, and the roles of editors and reviewers. The discussion will move on to manuscript evaluation, covering topics like evaluating scientific rigor, methodological appropriateness, clarity of presentation, strength of the conclusions, and impact on the field. The workshop will teach attendees how to write a fair, effective review, covering important aspects of review structure, summary and overall critique, fit for journal scope, and appropriate language and tone. Participants will be joined by a group of editors for a panel discussion and Q&A.

Live Twitch broadcasts: Engagement will provide a live stream of select events, including the 3D printing station and poster presentations. Poster presenters will be asked if they would like to be on stream—if they accept, they can present their poster and take questions from the live chat.

Individual Development Plan workshop: Walks early and mid-career scientists through an Individual Development Plan using free virtual tools. The workshop encourages participants to break out of the linear career path by illuminating alternative paths, practicing informational interviews, and providing a roadmap for participants to join TAGC 2024 events that highlight the rich variety of academic and non-academic careers.

Industry sessions: In addition to the keynote session, TAGC 2024 will feature three industry sessions: “Novel disease models in drug development,” “Topics in A.I. and machine learning,” and “Advances in oligonucleotide therapeutic development.” During the novel disease models session, speakers will highlight genetic disease preclinical models that offer new opportunities in drug development. The “Topics in A.I.” session will explore how artificial intelligence and machine learning are driving biotech and pharmaceutical drug discovery efforts. Speakers at the oligonucleotide therapeutics session will discuss recent advancements and limitations in oligo chemistry and delivery methods for a range of therapeutic indications.

Scientific writing workshop: Science writer Carolyn Beans will lead a workshop on how to kick-start the manuscript writing process by tackling participant abstracts. After covering abstract structure and style, participants will write their own abstracts with step-by-step instructions from Carolyn. Participants will also learn how to edit their work for clarity, brevity, and voice and how to produce clear and engaging academic writing for abstracts

and beyond. Those who have already drafted a rough abstract will be encouraged to bring it and receive peer feedback.

2024 Annual Drosophila Research Conference as part of The Allied Genetics Conference

Melissa Harrison (chair), Amanda Larracuente, Daniel McKay, Blake Riggs

The organizing committee was established in Spring 2023. Harmit Malik reached out to Melissa in January 2023, and Melissa subsequently invited Dan, Blake and Amanda to join the organizing committee. Together the group geographically spans the country, reflects the breadth of scientific research areas encompassed in this meeting, and represents the diversity of universities, approaches and people that attend this conference. The organizers communicated through nearly monthly Zoom meetings, e-mail and Google documents.

Organization of this conference differed significantly from the annual conferences that were not part of the larger TAGC meeting. The similarities and differences will be reflected in this meeting report.

Programming

Because the 2024 ADRC is part of the larger TAGC, programming was set by the APC (the organizing body of TAGC). TAGC includes both Topic sessions (see list of Topics below) and Community sessions, which are specific to ADRC and programmed by this committee. Community programming was distributed based on numbers of abstracts submitted, and, as was projected, the Drosophila Community was allocated 5 two-hour blocks of time (with the possibility of two sessions per time block). To maintain some of the familiar structure of the ADRC, we chose to use the first block of time for a set of 4 plenary talks. The remainder of the blocks were programmed to include the standard 8 15 minute talks. To select the plenary speakers, we generated a long list of potential speakers. For the final group, we focused on those who have contributed both scientifically and through service to the Fly community. We further prioritized those individuals who have not previously given plenary talks and who reflect the diversity of the Fly community. We selected:

Howard Lipshitz, University of Toronto, Canada
Alissa Armstrong, University of South Carolina, USA
Nasser Rusan, NIH, USA
Josefa González, Institut de Biologia Evolutiva, Spain

The remaining programming was distributed to individual community sessions based around the Topics listed below and time was distributed to reflect the number of abstracts submitted to a given topic.

Abstract categories and Session Topics

These were selected by the APC and included:

1. Technology, Resources, and Tools
2. Genomes and Genomics
3. Population and Evolutionary Genetics
4. Quantitative Genetics
5. Developmental Genetics
6. Intracellular Dynamics
7. Gene Regulation
8. Disease Models and Aging
9. Chromosome Biology and Genome Integrity
10. Neurogenetics
11. Initiatives in Education and Diversity, Equity and Inclusion (DEI)
12. Translational Approaches, Stem Cells, and Organoids
13. Sex Differences in Biology and Disease

14. Agriculture, Aquaculture, and Livestock Genetics
15. Ecological Genetics and Genomics
16. Evo-Devo

A subset of these 3,4,10,11 (in blue) was selected by the APC to have abstracts go directly to the APC or to go to another section of the conference Population Evolution and Quantitative Genetics (PEQG).

Chairs were selected for the 10 topics that corresponded roughly to topics from prior ADRC and that would be expected to have significant abstract submissions. Chairs were not selected for 14. Agriculture, Aquaculture, and Livestock Genetics and 12. Translational Approaches, Stem Cells and Organoids (in orange).

Selection of session co-chairs
As in prior meetings, two co-chairs were selected for each topic, and, together, they selected a junior co-chair. We encouraged them to select a postdoc or senior graduate student, but a number selected junior PIs. In selecting the senior co-chairs, we focused primarily on expertise in each topic and those who had not recently served in the position at ADRC. If a topic spanned a broad area of science, we worked to select co-chairs with complementary expertise. In our selection, we drew on the breadth of the Fly community to ensure that the co-chairs reflect the diversity of the community, including geographic diversity, diversity of institution, as well as gender and background. We came to consensus through discussion and invited co-chairs in late August.

Submitted abstracts
In total 837 abstract were submitted to the ADRC with 393 being submitted for consideration as an oral presentation. (The total number of abstracts submitted to TAGC were 1936 with *Drosophila* constituting the largest % of abstracts. 39% of total oral submissions. For comparison, last year 1074 total abstracts were submitted with 523 being submitted for consideration as an oral presentation. This was the highest number of abstracts for the last decade. Only 692 abstracts were submitted to TAGC in 2016.)

Topic/Session	Total abstracts	Oral abstracts	Programmed sessions
Technology, Resources and Tools	37	25	0.75
Genomes and Genomics	37	11	0.5
Developmental Genetics	177	86	2
Intracellular Dynamics	79	47	1
Gene Regulation	108	44	1
Disease Models and Aging	143	57	1
Chromosome Biology and Genome Integrity	46	18	0.75
Sex Differences in Biology and Disease	33	20	0.5
Evo-Devo	10	3	0.25
Ecological Genetics and Genomics	8	3	0.25

No abstracts were submitted to Agriculture, Aquaculture, and Livestock Genetics in our Community. 2 abstracts were submitted to Translational Approaches, Stem Cells, and Organoids. These were assigned to the Topic they selected as their second choice.

Selection of submitted abstracts for oral presentation

This process had similarities to prior years in that session chairs were largely responsible for the selection of abstracts for oral presentations, but differed in the fact that there were multiple "tiers" of selection.

The abstract submission deadline was initially November 9, but was subsequently extended slightly. Session chairs were contacted on November 19 and asked to select abstracts for submission to the APC. This total number was determined by the APC. For example, 20 abstracts from the Disease Models and Aging topic were passed along to the APC. It was communicated at the time that the APC would select half of these abstracts and return the remainder to the chairs for programming in the community session. The APC communicated that by requesting double the number of required abstracts this would enable them to program the strongest and most diverse Topic sessions. Abstracts that were not selected by the APC were returned to the chairs on December 20 and the final programming for the Community session were due on January 2 to the ADRC organizing committee. Final programming was sent to GSA on January 4.

Some challenges arose in this process:

1. For some topics the APC selected many more abstracts than initially told. For example, of the 20 abstracts submitted to the APC in Disease Models and Aging 17 were selected for programming in the Thematic sessions. By contrast, only 1 of 6 abstracts was selected in the Chromosome Biology and Genome Integrity session as compared to the expected 3. To address these inequities, we adjusted the number of oral presentations in the Community sessions (see above Table for final programming numbers).
2. Because the Topics were picked by the APC and a number overlapped with other platforms, like PEQG both Evo-Devo and Ecological Genetics and Genomics received far fewer abstracts than expected. (Both received only 3 abstracts for consideration for an oral presentation.) This was further complicated because some of these were promoted to the Thematic sessions. While we considered not having programming on these Topics, we were worried that this might inadvertently make members of these communities feel unwelcome in the ADRC. To address this, we programmed 2 oral presentations for each of these Topics in our community session and worked with the chairs to ensure that the programming was strong.

Once abstracts were selected for community programming by the co-chairs of each Topic, we looked at the wholistic selection. We noted that there was a disproportionate number of male speakers selected (nearly twice as many as female) and reached out to session chairs to ask if they would consider substituting one of the male presenters with a female that was listed as an alternate. We made sure to acknowledge that there are many aspects to consider when selecting presenters and that sex is only one such aspect. In many cases, the session chairs made the swap, allowing us to have slightly more aligned gender balance. Again, this process was complicated by the fact that the APC selection preceded the selection of the Community programming. As such, it was impossible to ensure that the programming of the Community sessions reflect the diversity of the abstracts submitted.

One other challenge that arose in the process was that the chairs had selected one of the junior co-chairs to speak in the session. We felt that this was not appropriate and suggested that perhaps a person from the junior co-chair's laboratory could present. However, the co-chair instead chose not to present. We feel strongly that this should be a stated policy moving forward such that the co-chair would have known to submit their abstract to another session or not selected to co-chair the session.

Community building efforts

In the hopes of maintaining a community feel despite the large size of TAGC, the organizing committee selected a few community-building activities, taking inspiration from the wonderful origami from the last meeting. To pick things that were not cost-prohibitive, we selected having people draw their mutant phenotype and posting them on a board leaving room for others to caption them. We also thought people could write Haiku poems explaining their research. Colored pencils, unlined notecards and colored lined notecards will be available. We had thought about a scavenger hunt to encourage interaction, but it sounds like the early career folks are already organizing a similar event. There will also be a community within the online app so that people can post announcements, etc.

Fundraising, workshops, poster sessions

These were organized through TAGC. All members of the organizing committee assisted with fundraising by reaching out to a subset of vendors by e-mail. In addition, the organizing committee assisted with application to the Company of Biologists for funding for the meeting.

Thinking ahead

Similar to what was reported last year, there were multiple requests as to whether session chairs were eligible for subsidized conference attendance. This is something that should continue to be considered moving forward, especially for the junior co-chairs.

The list of possible plenary speakers considered by the organizing committee has already been passed on to Todd Nystul, the chair of next year's ADRC organizing committee. Following this meeting, Melissa will also reach out to Todd to discuss the possibility of implementing rules regarding co-chair presentations in sessions and, if any, possibilities to support junior co-chair attendance at the conference.

For Fly Board consideration

We would like the Fly Board to consider implementing a rule that co-chairs (both senior and junior) cannot present in their own session. Lab members in a co-chair's lab are allowed to present, but not the co-chair themselves.

Proposal for mentor-mentee matching program – By Shefali Shefali

Goal:
The goal of this program is to support the growth of junior scientists, enabling them to excel in obtaining their career goals by fostering positive and meaningful mentor-mentee relationships. Our aim is to facilitate connections among members of the *Drosophila* community to cultivate a sense of inclusivity by helping junior scientists establish connections and collaborations beyond their host institutions/universities without being limited by any geographical constraints.

Rationale: We believe that the *Drosophila* community is a well-connected and supportive community. Despite that, junior members (particularly those from marginalized backgrounds) are not exposed to the breadth of resources the *Drosophila* community has to offer due to lack of access to established investigators who are outside of their host institution. The mentor-mentee matching program provides junior scientists the opportunity to seek out mentors beyond their immediate network and will be an additional resource in helping them achieve their professional and personal goals. A similar program was recently established by the *C. elegans* community and many of the ideas in this proposal stem from their already successful efforts.

Overview and logistics for prospective mentors and mentees-

Overview
The mentor match is open to graduate students, postdoctoral fellows, and early career faculty. Mentees will be paired with one mentor. (The survey forms will open for prospective mentors first, and the list of mentors will be available for mentees to see. The mentees will then fill up their survey. Depending on the requests made by the mentees, the matching committee will finalize the mentor-mentee match – see match logistics for more details.)

We will prioritize mentees who come from under-represented communities, are experiencing extensive lack of resources in their current environment, or are facing equity challenges. The number of mentee participants will be determined by the availability of mentors.

Future year plans:

- We can make this program open for mid-career faculty as well, where they can request mentors too.
- Additionally, we can also create mentoring peer groups of scientists at similar career stages and the prospective mentees will have the opportunity to be a part of the peer group. (These next decisions can be made by the flyboard president and future grad student/post doc representatives).

Career Stage	Examples of type of mentorship (from the surveys done by wormboard)
Graduate Students	Advice on different career paths, discussion of research ideas from an outside perspective, constructive and critical feedback, etc
Postdoc	Navigating the transition of being more independent and managing your own research, advice on different career paths, job applications, discussion of research ideas from an outside perspective, constructive and critical feedback, etc

Early Career PI	Navigating the transition to being a PI, learning new mentorship and lab managerial roles, managing teaching and lab/work together, getting funding, forming newer collaborations preparing for the tenure process
	For future
Mid-career or Established PI	Transitions into new leadership roles, starting new research areas in the lab, forming bigger collaborations, etc

Match logistics

Match committee: We will have a match-committee composed of 6-10 members including two co-chairs, who can be current/past members of the flyboard. The committee will have broad representation and will turn over every ~ two years to maintain continuity. The committee will design the survey forms for the mentors/mentees, post the survey forms and list of available mentors, and match the mentees with the best suited mentor from the list. In the subsequent years, mentors and mentees who benefited from the program will be encouraged to join the committee.

In future the committee can also host a yearly virtual meeting to have discussions on topics like - career paths, peer reviewing, science policy making etc which can act as a platform for the mentees to form a community.

Prospective mentors (Action required by Dec 1): The surveys for the prospective mentors will open Nov 1st every year. The survey will collect information regarding – field of study, experience in academic and non-academic jobs, etc. Mentors should fill out a new form each year. Mentors who have an existing relationship will have an option of using their details from the previous survey.
The match committee will annually update (by 15th December of each year) a list of all potential mentors along with the necessary information for prospective mentees to access.
The prospective mentor survey can also be added as a part of yearly GSA community survey.

Prospective mentees (Action after Dec 15th): The prospective mentee survey will open ~ Dec 15th every year. The survey will collect information regarding their current position, areas and type of mentorship needed, preferences regarding a mentor, etc. They would have access to the mentor survey results and can list people they prefer in the survey.

Based on all the responses and mutual agreement, the matching committee will connect the mentors and the mentees. The match list will also be posted.

Guidelines for mentors and mentees – to which all prospective mentors and mentees must agree:

The initial commitment is for one year, but it can be extended if mutually agreeable.

There are no fixed rules about frequency and time requirements for the program, but ideally should accommodate the goals of the mentee. We would recommend having few virtual meetings every semester – but this could vary depending on what the mentee needs.

The committee, mentors and mentees MUST all agree to a general professional code of conduct. This is a non-exhaustive list, and more things can be added – (ref - wormboard)
- Respectful and safe space for communication.
- Maintenance of confidentiality and objectivity.
- Value of time commitment and deadlines
- Timely response to end-of-year mentor match survey program evaluation

Follow-up:
- The matching committee is open to feedback throughout the process and can decide to implement changes as and when needed.
- The mentors and mentees agree to participate in follow up surveys and will have an opportunity to choose to become members of the program committee in the future cycles
- If either of the parties think that the match is incompatible, they can reach out to the committee chair, who can then hold a virtual meeting to access the situation.

Timeline
1st November – MENTOR survey open
1st December – mentor info posted
15th December – MENTEE survey open
15th January – mentee survey closes
20th February – match participants notified and matches posted.
(We can also adjust the timeline closer to the Annual *Drosophila* Meeting)

Reference : A lot of these ideas were taken from the wormboard mentor-mentee matching program
(https://wiki.wormbase.org/index.php/C._elegans_Community_Mentor_Match_Program)

Feedback taken from –
Dr. Michelle Arbeitman, Past-president Flyboard, Professor, Florida State University.
Dr. Sally Horne-Badovinac, President-elect Flyboard, Professor, University of Chicago.
Dr. Harmit S. Malik, President Flyboard, Professor, Fred Hutchinson Cancer Research Center.
Dr. Shyama Nandakumar, Postdoctoral representative Flyboard
Dr. Ana-Maria Raicu, Past graduate student representative Flyboard
Dr. Jason Tennessen, Flyboard Member, Associate Professor, IU Bloomington
Dr. Lesley Weaver, Assistant Professor, IU Bloomington

BLOOMINGTON DROSOPHILA STOCK CENTER

Stock Holdings as of February 7, 2024

- 88,371 stocks with 87,726 unique genetic components

2023 Use Statistics In calendar year 2023, the 171,706 samples sent in 10,112 shipments represented a decrease of 1,262 (<1%) samples and 217 (2%) shipments from 2022.

On average, we saw 2 orders per stock. 53% of stocks were ordered at least once, 13% were ordered 5 or more times, and 6 stocks were ordered >85 times. The most popular stock was Canton-S (#64349), which was ordered 137 times. 75% of stocks available for 2021–2023 received at least one order demonstrating that the majority of the collection is being used by the fly community.

User base

- 3,984 registered user groups, 1,846 of which ordered stocks in 2023
- 8,433 registered users, 2,438 of whom ordered stocks in 2023

Growth 6,398 stocks were accessioned in 2023:

- 2,594 stocks with split-GAL4 driver combinations from Janelia Research Campus
- 1,011 Drosophila Genetic Resource Panel stocks from Trudy Mackay and colleagues
- 703 CRIMIC stocks from Hugo Bellen, Norbert Perrimon and colleagues
- 344 Drosophila Synthetic Population Resource stocks from Stuart Macdonald and colleagues
- 294 UAS-human cDNA stocks from Hugo Bellen, Sue Celniker and colleagues
- 126 stocks expressing guide RNAs for gene knockout from Michael Rosbash and colleagues
- 69 Fourth Chromosome Resource Project stocks from Stuart Newfeld, Mike O'Connor and colleagues
- 63 stocks expressing guide RNAs for gene knockout or overexpression from the Transgenic RNAi Project
- 43 stocks for RNAi knockdown from the Transgenic RNAi Project
- 1,101 assorted stocks from the community at large

We are now distributing 1,411 Drosophila Synthetic Population Resource stocks and 1,199 Drosophila Genetic Reference Panel stocks—giving the fly community unparalleled resources for determining the genetic bases of phenotypic variability.

By midyear, we will be distributing ~4,300 stocks from Janelia and the University of Cambridge with pairs of split-GAL4 drivers that are useful in manipulating specific larval and adult brain neurons. We will also be adding more than 2,000 new stocks to bring the collection of single-driver stocks to nearly 9,000. We hope the fly community will make good use of these enormous collections.

Staff 78 stockkeepers (9 full-time and 69 part-time to make 29 full-time equivalents) and 11 managers/scientists. Jason Tennessen joined us as a new Principal Investigator. Stephanie Mauthner joined us as a new staff scientist.

Funding We are in year 5 of a 5-year grant from NIH with $445,047 in direct funds contributed by OD, NIGMS and NICHD and $86,674 of supplemental direct funds from NINDS for maintenance and distribution of split-GAL4 driver stocks. Fee income covers our remaining expenses and now accounts for ~82% of our regular funding. We have applied for continued NIH funding for 2024–2029. Our impact score was excellent, but we have yet to hear if we will be funded or what the funding level will be (full funding would provide a substantial increase). HHMI has provided support for us to distribute the new driver stocks for 2024–2027. We also receive salary support for participating in consortium projects to improve stock resources (R24OD028242, R01DK136945 and R24OD031952), cryopreservation (R24OD034063) and the genetic dissection of complex traits (RO1OD034064).

New Stocks We expect to add 5,520–5,940 new stocks in 2024:

- 1,645 split-GAL4 stocks from the Janelia FlyLight Project Team
- 1,345 split-GAL4 combo and lexA stocks from Marta Zlatic

- 600–800 CRIMIC and KozakGAL4 from Hugo Bellen, Norbert Perrimon and colleagues
- 500 sgRNA and shRNA stocks from the Transgenic RNAi Project
- 250–350 TRiP knock-in stocks (split-GAL4, lex-GAD, QF2, etc.) for cell and tissue-specific expression
- 150–200 UAS-human cDNA stocks from Hugo Bellen, Sue Celniker and colleagues
- 130–200 RMCE, UAS and KO stocks from the Fourth Chromosome Resource Project
- 900 assorted stocks from the community at large

Pruning We conducted no systematic culls during 2023. 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

Vienna Drosophila Resource Center (VDRC), Vienna, Austria

The VDRC (https://shop.vbc.ac.at/vdrc_store/) 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 2023

- Moved ordering and user accounts to a new e-commerce system.
- 50 new lines acquired in "Other Resources" from the European community.
- 3000 stocks maintained in reduced copy number and staff reduced accordingly to increase cost recovery.

Usage Statistics 2023

- **27,591** stocks delivered to **601** user groups in **1,079** separate orders.
- Average orders/stock = 0.99.
- 51% of stocks were ordered at least 1x.

Resources as of March 2024

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).
- 895 Tagged FlyFos TransgeneOme (fTRG) lines.
- 200 enhancer-GAL4 lines (VTs, Vienna Tiles). Expression patterns annotated in adult brain and embryo. Searchable databases available.
- 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.
- Fly Extract - for tissue culture.
- Fly food service - primarily for fly groups in the Vienna area.

Drosophila Genomics Resource Center (DGRC): Booth #621

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

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

Currently there are no term limits for serving on the DGRC Advisory Board and many have served for over 8 years. In discussions with our Board, we will be begin adding term limits (3 years) and begin rotating in new Board members. If you would like to serve or want to nominate someone, please send us their name.

Funding: NIH P40OD010949 - The DGRC has been on a no cost extension. Our resubmitted renewal application was scored well and we have been informed we will be funded and we are currently waiting on the official award notice and announcement of budget. The next funding period will be from April 1,2024 to March 31, 2029.

Year	Vectors/cDNAs Shipped	Cell Lines Shipped	Products Shipped[1]
2019	1894	268	2995
2020	1645	171	2381
2021	1741	239	2459
2022	1666	151	2310
2023	1353	216	2016

Table 1: Summary of items shipped over the past five years. 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 (e.g. Drosophila extract).

DGRC continues to run an online survey through Qualtrics

DGRC Publications (2023):

- Coleman-Gosser N, Hu Y, Raghuvanshi S, Stitzinger S, Chen W, Luhur A, Mariyappa D, Josifov M, Zelhof A, Mohr SE, Perrimon N, Simcox A. Continuous muscle, glial, epithelial, neuronal, and hemocyte cell lines for *Drosophila* research. Elife. 2023 Jul 20;12:e85814. doi:10.7554/eLife.85814. PMID: 37470241; PMCID: PMC10393297.

New Product/Updates in the past year:

Updates:

a. **Transgenic cell service.** – We have continued to expand the attP containing cell lines catalog. The DGRC offers the research community a fee-based service to generate stable cell lines containing their transgenic construct of choice.

Cell Lines:

Reagent(s)	Originating Lab	Description (number)	NIH grant/Other funding
15 Tissue specific lines	Amanda Simcox	DGRC #282-286 #323-332	R24 OD019847 P40OD010949 P41 GM132087 IOS 1419535 HHMI (Perrimon) Women & Philantrophy OSU (Simcox)
S2-Atat-KO	Steve Rogers	DGRC #344	R21NS125795 MRC_UP_A025_1011 210711/Z/18/Z

CRISPR (KO/Knock-in/Cas9) reagents, available since 2019, have been distributed 80 times. Tissue specific lines, available since 2023, have been distributed 27 times.

Vector/DNA Reagents added

Reagent(s)	Originating Lab	Description (number)	NIH grant/Other funding
UAS attB vectors	Kim Lab	Vectors (4)	R01NS116463 P20GM103440
Split-GAL4 triple donor cassettes	Desplan Lab	Vectors (2)	R01EY013010 R01EY13012 F32EY032750

			MacCracken Program, NYU NYSTEM institutional training grant
Discs large donor vector	Mosca Lab	Vector (1)	R01NS110907 R00DC013059 Commonwealth Universal Research Enhancement (Penn. Dept. Of Health) Alfred P. Sloan Foundation, The Whitehall Foundation, The Jefferson Synaptic Biology Center, Thomas Jefferson Univ.
Other funding sources/Non-US Labs			
CRISPR-Cas9 HDR plasmids	Stern Lab	Vectors (24)	HHMI/Janelia

Outreach

DGRC had a booth at the ADRC2023 in Chicago and also presented at the Midwest Fly meeting 2023.

On 19th September 2023, DGRC hosted the first biannual Lucy Cherbas Online Seminar Series to promote and highlight the use of Drosophila cell culture. Dr. Amanda Simcox was the guest speaker for the seminar. 116 participants from all corners of the USA, UK, Italy, Germany, Hungary, Switzerland, Sweden, France, Israel, Ghana, India, and Japan. We had a total of 166 views of the recording that we have made available online on YouTube as well as Kaltura.

DGRC also created a survey post seminar to request input on the best way for DGRC to assist labs to use Drosophila cell culture. From 12 survey responses, we identified that audiovisual protocol with written instructions topped the request, while an in-person summer course was at the bottom.

DGRC has schedule the second online seminar for 18th April 2024. Dr. Stephanie Mohr will be the guest speaker. Similarly, the seminar will be recorded and made publicly available on DGRC YouTube channel.

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 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 have been supported for the past 5 years as the NIH NIGMS P41-funded DRSC-BTRR. In January 2023, we applied for 'renewal' in the form of RM1 funding of our group as the DRSC-Biomedical Technology Development and Dissemination center (DRSC-BTDD). In fall 2023, we received an excellent score. Thus, we expect to be funded in spring 2024 as the DRSC-BTDD, which would similarly focus on cell-based and *in vivo* technologies, but with greater emphasis on technology improvement, training, and dissemination as compared with our past 5 years. **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 develop cell line and fly stock resources for the community; past NIHGRI funding of the FlyBi project; and current funding from NIH NIAID to support application of CRISPR technologies in cell lines from the Lyme vector *Ixodes scapularis*.

3. Key accomplishments & metrics of success:

- Our recent DRSC-BTRR collaborators include investigators from 14 US states (CA, IA, IL, IN, MA, MD, MI, MO, NV, PA, RI, TN, TX, UT) and several non-US countries
- In 2023, Addgene distributed ~130 plasmids we had deposited with them (for nanobodies, proximity labeling, CRISPR, etc.) and 2 copies of the full-genome pooled fly cell CRISPR knockout library
- In 2023, DGRC shipped 115 cell lines we had deposited, including 44 distributions of Cas9+ fly cells, 30 from the GFP-tagged organelles collection, 6 from the tumor suppressor gene knockout collection, 27 from the Simcox lab new RasV12-based tissue-specific cell line collection, and 8 mosquito cell lines
- We deposited new fly stocks for RNAi, CRISPR technologies, NanoTagging, and small ORF genes at the BDSC, which shipped ~60,000 TRiP-associated fly stocks to 1,299 different user groups in 41 countries in 2023 alone
- Our online resources were widely used, including ~230,000 views of our online tools in 2023 by ~67,000 users, and at least 68 publications mentioned our DIOPT resource in 2023
- Results of the multi-year, multi-PI "FlyBi" effort to generate an expanded high-confidence protein-protein interaction network for *Drosophila* were published in 2023; data available at MIST
- Results of a multi-year, multi-PI effort led by A. Simcox (Ohio State) to generate new tissue-specific *Drosophila* cell lines were published in 2023; cells available at the DGRC
- We began sunsetting our legacy arrayed RNAi screening libraries as users turn to the newer CRISPR pooled screen technology (custom small template and dsRNA reagent requests are still supported)

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

a. Cell CRISPR screens:

- We published a pooled CRISPR activation (CRISPRa) cell screening platform for *Drosophila* S2R+ cells and did a genome-wide screen (Xia et al. 2023 eLife)
- We further tested a 'version 2' of our pooled CRISPR knockout screen platform that results in improved data quality and an expanded list of genes that are essential in S2R+ cells
- Genome-wide CRISPR pooled screens in *Drosophila* and other insect cell lines are in planning, development, or screening stages at least 10 labs, based in 4 US states, Asia, and Europe

b. In vivo technologies:

- We completed a set of >80 LexA and QF tissue-specific driver lines using CRISPR/Cas9-mediated knock-in that have been sent to BDSC
- We continued building a set of LexAop and QUAS shRNA lines covering genes targeted by the most popular UAS-shRNA TRiP lines
- We generated over ~200 new fly stocks as part fly stock resource targeting fly orthologs of human genes identified as SARS-CoV-2-interactors
- We generated over 300 sgRNA and shRNA lines for the TRiP RNAi, TRiP-CRISPR-KO, and TRiP-CRISPR-OE collections, and deposited them at BDSC
- We generated both activation domain and DNA binding domain split-Gal4 lines for ligand genes to produce new highly specific driver lines
- We published a paper describing new split-intein tools for intersectional genetic labeling, and generated both activation domain and DNA binding domain split-intein-Gal4 lines to produce new tissue-specific driver lines
- With John Doench's group at the Broad Institute, we described a platform for modular vector assembly of plasmids, including for *Drosophila* cell-based and in vivo expression (preprint available; manuscript accepted at Cell Genomics)

c. Bioinformatics resources:

- We updated and improved our new online resource, 'PAthway, Network and Gene-set Enrichment Analysis' (Pangea) for gene set enrichment (all common model species)
- We updated our GuideXpress tool to include more orthologous mapping eg. from *Drosophila* to *Ixodes scapularis* and *Aedes aegypti* by DIOPT approach.
- We designed new genome-wide sgRNA collections for CRISPR knockout in *Ixodes scapularis*, *Spodoptera frugiperda* and for CRISPR activation in *Anopheles gambiae, Aedes albopictus, Aedes aegypti and Spodoptera frugiperda*; sgRNA designs for non-fly species available at GuideXpress
- We launched Fly Predictome, a new proteomic resource to allow mining of the binary protein-protein interaction prediction based on protein 3D structure from alphafold
- We added more Perrimon lab scRNAseq datasets to our scRNAseq portal, e.g., samples with perturbations (gut homeostasis vs recovery, thorax with Reptor/Foxo mutant, MT with Pvr mutant)
- We expanded DGET, our bulk RNAseq data portal, to include Simcox/DRGC/DRSC transcriptomic datasets for twelve RasV12-based cell lines generated by the Simcox lab (published in eLife)

d. Other research projects:

- We published the results of a multi-year, multi-PI project, the FlyBi project, which included all-by-all screening of 10,000 *Drosophila* ORFs and reported a new high-confidence fly PPI network

5. Outreach:

- At TAGC 2024, we will present talks and posters, including a talk on our new Pangea online resource for gene set enrichment, supporting all common model species
- On June 14, 2023, we presented technology-focused talks and posters on cell technologies, *in vivo* technologies, and bioinformatics at the Boston Area Drosophila (BAD) meeting at Brandeis University
- We presented additional technology-focused talks, posters, seminars, etc. at regional and national conferences focused on *Drosophila* research, CRISPR technology, and other topics
- We published a review article aimed at helping students, trainees, and other new-to-fly researchers navigate a wealth of online tools to gather existing information about a given fly gene
- *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:

Ah-Ram Kim, Yanhui Hu, Aram Comjean, Jonathan Rodiger, Stephanie E Mohr, Norbert Perrimon. **Enhanced Protein-Protein Interaction Discovery via AlphaFold-Multimer.** BioRxiv. doi: https://doi.org/10.1101/2024.02.19.580970

Jonathan Zirin, Barbara Jusiak, Raphael Lopes, Ben Ewen-Campen, View ORCID ProfileJustin A. Bosch, Alexandria Risbeck, Corey Forman, Christians Villalta, Yanhui Hu, Norbert Perrimon. **Expanding the *Drosophila* toolkit for dual control of gene expression.** BioRxiv. doi: https://doi.org/10.1101/2023.08.15.553399

Abby V. McGee, Yanjing V. Liu, Audrey L. Griffith, Zsofia M. Szegletes, Bronte Wen, Carolyn Kraus, Nathan W. Miller, Ryan J. Steger, Berta Escude Velasco, Justin A. Bosch, Jonathan D. Zirin, Raghuvir Viswanatha, Erik J. Sontheimer, Amy Goodale, Matthew A. Greene, Thomas M. Green, John G. Doench. **Modular vector assembly enables rapid assessment of emerging CRISPR technologies.** BioRxiv. doi: https://doi.org/10.1101/2023.10.25.564061

8. New Research Publications:

Bosch JA, Keith N, Escobedo F, Fisher WW, LaGraff JT, Rabasco J, Wan KH, Weiszmann R, Hu Y, Kondo S, Brown JB, Perrimon N, Celniker SE. **Molecular and functional characterization of the Drosophila melanogaster conserved smORFome.** Cell Rep. 2023 Nov 28;42(11):113311. doi: 10.1016/j.celrep.2023.113311. PMID: 37889754; PMCID: PMC10843857.

Coleman-Gosser N, Hu Y, Raghuvanshi S, Stitzinger S, Chen W, Luhur A, Mariyappa D, Josifov M, Zelhof A, Mohr SE, Perrimon N, Simcox A. **Continuous muscle, glial, epithelial, neuronal, and hemocyte cell lines for *Drosophila* research.** Elife. 2023 Jul 20;12:e85814. PMID: 37470241; PMCID: PMC10393297.

Ewen-Campen B, Luan, H, Xu J, Singh R, Joshi N, Thakkar T, Berger B, White BH, Perrimon N. **Split-intein Gal4 provides intersectional genetic labeling that is fully repressible by Gal80.** PNAS. 2023 Jun 13;120(24):e2304730120. PMID: 37276389 PMCID: PMC10268248.

Hu Y, Comjean A, Attrill H, Antonazzo G, Thurmond J, Chen W, Li F, Chao T, Mohr SE, Brown NH, Perrimon N. **PANGEA: a new gene set enrichment tool for *Drosophila* and common research organisms.** Nucleic Acids Res. 2023 Jul 5;51(W1):W419-W426. PMID: 37125646; PMCID: PMC10320058.

Xia B, Viswanatha R, Hu Y, Mohr SE, Perrimon N. **Pooled genome-wide CRISPR activation screening for rapamycin resistance genes in *Drosophila* cells.** Elife. 2023 Apr 20;12:e85542. doi: 10.7554/eLife.85542. PMID: 37078570; PMCID: PMC10118385.

Tang HW, Spirohn K, Hu Y, … Celniker SE, Vidal M, Perrimon N, Mohr SE. **Next-generation large-scale binary protein interaction network for *Drosophila melanogaster*.** Nat Commun. 2023 Apr 15;14(1):2162. doi: 10.1038/s41467-023-37876-0. PMID: 37061542; PMCID: PMC10105736.

9. New Review:

Mohr SE, Kim AR, Hu Y, Perrimon N. **Finding information about uncharacterized *Drosophila melanogaster* genes.** Genetics. 2023 Dec 6;225(4):iyad187. PMID: 37933691; PMCID: PMC10697813.

FlyBase Report to the Drosophila Board
26-February-2024

For the past thirty-one 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, 2024 will begin year 1 of our next 5 year grant cycle with NHGRI. Our January 2023 submission was reviewed favorably, although our projected budget will be less than 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 British Medical Research Council grant which altogether bring FlyBase's funding closer to ~60% of 2016. Finally, we continue to collect some fees from the community to cover the budget deficit. As of 01-February-2024 (nearly 7 years since fees were implemented), ~560 labs have contributed ~$725,000. It is essential we 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
- 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
- A 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
- Manage archives of designated FlyBase releases
- Maintain FTYP pipeline
- Maintain FlyBase Wiki
- Maintain 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
- Community outreach via commentaries and the FlyBase Newsletter
- Participate in Alliance of Genome Resources conference calls
- Ongoing development of a new centralized BLAST service and cloud structure at the Alliance of Genome Resources and FlyBase
- Documentation of data flow, resources, and operating procedures

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 found 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 Tweets are done regularly about new features and updates and has over 4,800 followers. We specialize in highly informative 'tweetorials', all of which have been hashtagged to enhance searchability. In addition, we maintina FlyBase Mastodon and Bluesky accounts, including involvement in instituting a Mastodon feed on the FlyBase homepage
- 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.
- **Publications** Staff contributed to 7 publications in the current reporting period.

New Data Capture and Processing Development (Curation)

- Implementation of AI pipeline for gene recognition in publications
- Continued refinement of chemical curation process
- Preliminary development of new AI triage and entity extraction software
- Expression Tool and Sequence Feature python proforma parsers added
- Updates to "Protein2Go" loading of Gene Ontology data
- Process for loading and reporting gene-to-cell_line relationships
- Process for loading RNA-Seq data from purified cell samples
- Automatic updates of REDFly cis-regulatory module data
- Automated quality checks of sequence targeting (RNAi/sgRNA) reagents
- Infrastructure to support Split-Gal4 expression curation

Significant New Data Incorporation/Submission

- DIOPT 9.0 update
- FlyAtlas2 RNA-Seq data update
- New bulk reports: scRNA-Seq, high-throughput expression, pathways, VFB pub list
- FlyCyc submission files

Alliance of Genome Resources

- DevOps support for all developers.
- Monitoring and maintenance of production and stage servers.
- Administration of Google software, Slack, GoCD, and Jira for the Alliance.
- New position of Specialist coordinator.
- New position of Orthology & Paralogy group lead.
- Addition of DIOPT Paralogy data (v9) to the Alliance website.
- Maintenance of Neo4J ETL pipeline, including the loader and file generator.
- Onboarding of all new developers to the Alliance.
- Literature Service. Database, API and UI coding
- Created pipeline for weekly FlyBase literature data submission
- 4 FlyBase data exports for the Alliance website
- 9 FlyBase data exports for the Alliance LinkML persistent database

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 have plans to improve and further optimize the production web site and release pipelines as time permits. Major near-term projects include the new BLAST service (with the Alliance) and the FBco "Combinations" FlyBase data class.

- Integrate the Alliance BLAST service into the FlyBase website
- Implement split GAL4 combination FlyBase objects in website presentations
- Synchronize Batch Download with current FB data types and report fields
- Complete Gene Toolkit upgrades to reports and data
- 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
- Enhance 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
- Migrate FlyBase emailing needs to a new client (as TinyLetter will be retired)
- Extend new expression plots API system to all datasets

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 2024. 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 continue to contribute to 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. This work is essential to: i) ensure accurate and complete submissions of FlyBase data to the Alliance; ii) specify suitable curation interfaces; and (iii) specify

optimal 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. We continue to contribute to working groups within our remit and areas of expertise.

2023 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 2018-2023, plus January 2024. In summary, the usage statistics for 2023, when compared to the same period in the previous year, indicate that our overall pageviews have increased (4.5%), while our sessions have decreased (~9%), and the number of users is also down (~9%). Fewer users and sessions coupled with more page views could be interpreted as more robot traffic.

Pageviews

Figure 1 shows FlyBase pageviews for the years 2018 through 2023. 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 2023 was ~768k, with a high of ~923k and a low of ~524k. The periodic dips in this plot correlate with expected seasonal patterns that we typically experience, except for the unusually flat pattern in the first part of 2020 due to pandemic measures. Compared to 2022, pageviews are up 4.5%.

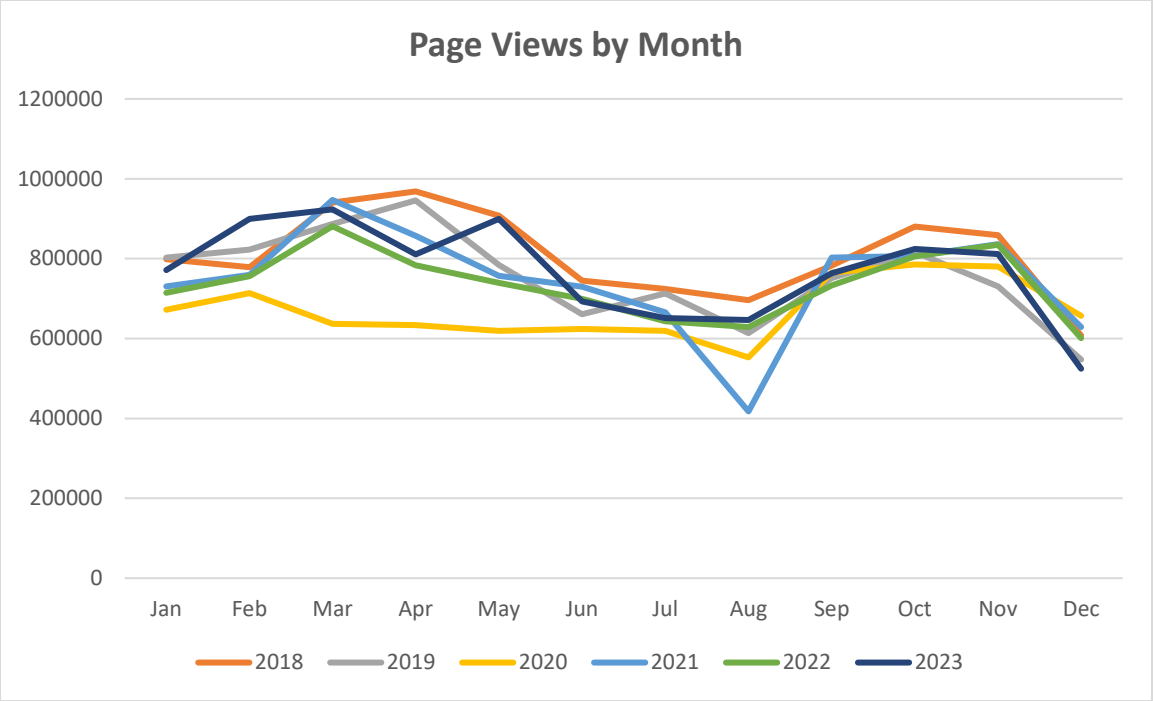


Figure 1 – FlyBase Pageviews for Jan 2018 – Dec 2023

Sessions

Figure 2 shows FlyBase sessions (visits) for the years 2017 through 2023. A session is defined as a period of activity by a unique web user. If no activity is recorded for 30 minutes, any subsequent activity is counted as a new session. The average number of sessions per month for 2023 was ~152k, with a high of ~202k and a low of ~104k. Compared to 2022, sessions are down ~9%.

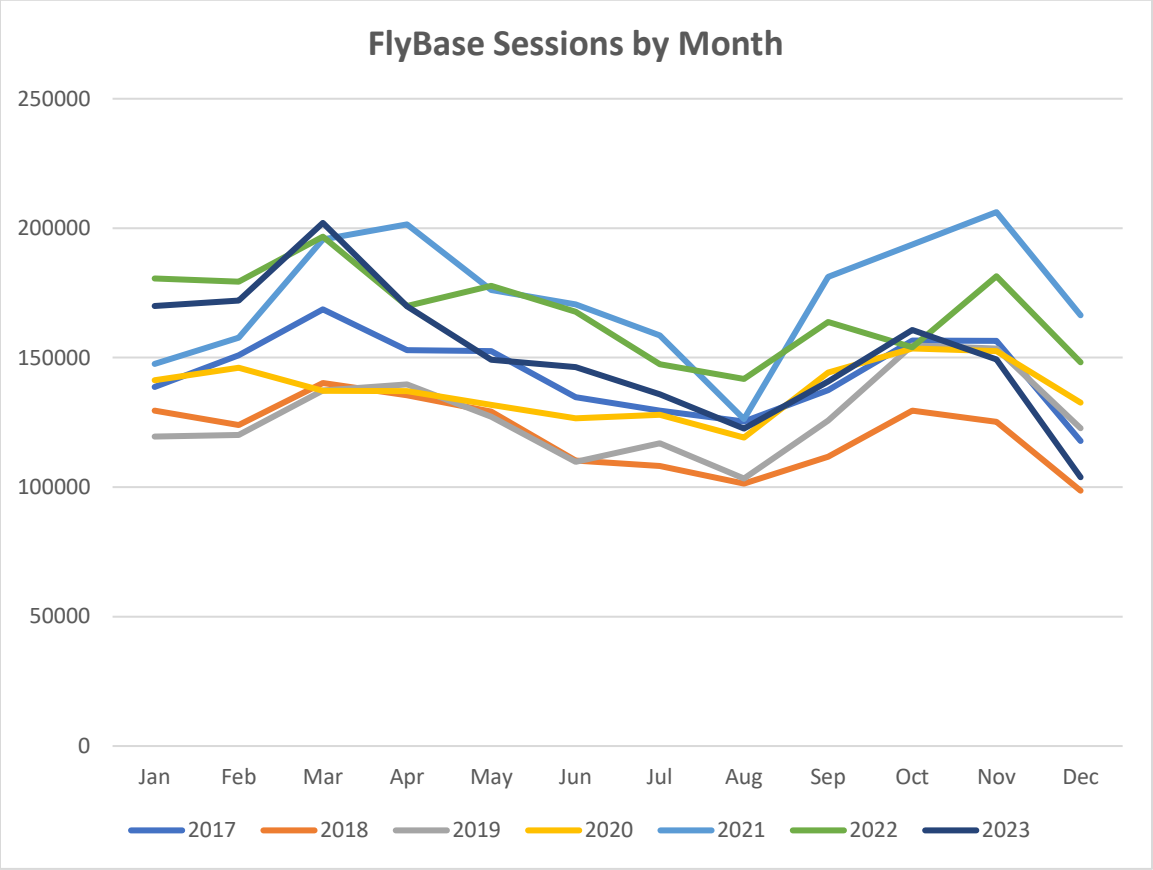


Figure 2 – FlyBase sessions for Jan 2018 – Dec 2023

Users

Figure 3 shows FlyBase users for the years 2018 through 2023. 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 2023 was ~63k/month, with a high of ~91k and a low of ~32k. Compared to 2022, the number of FlyBase Users is down by around 9%.
This statistic surged sharply in 2021, an increase we attributed to overcounting of "bots" (script-generated traffic). It is interesting that the current end-of-year dip puts this statistic back in line with pre-2021 values. The January 2024 value (34,792) is not shown on this plot, but it is much like January values from 2017 (34,120), 2018 (30,691) and 2019 (30,950).

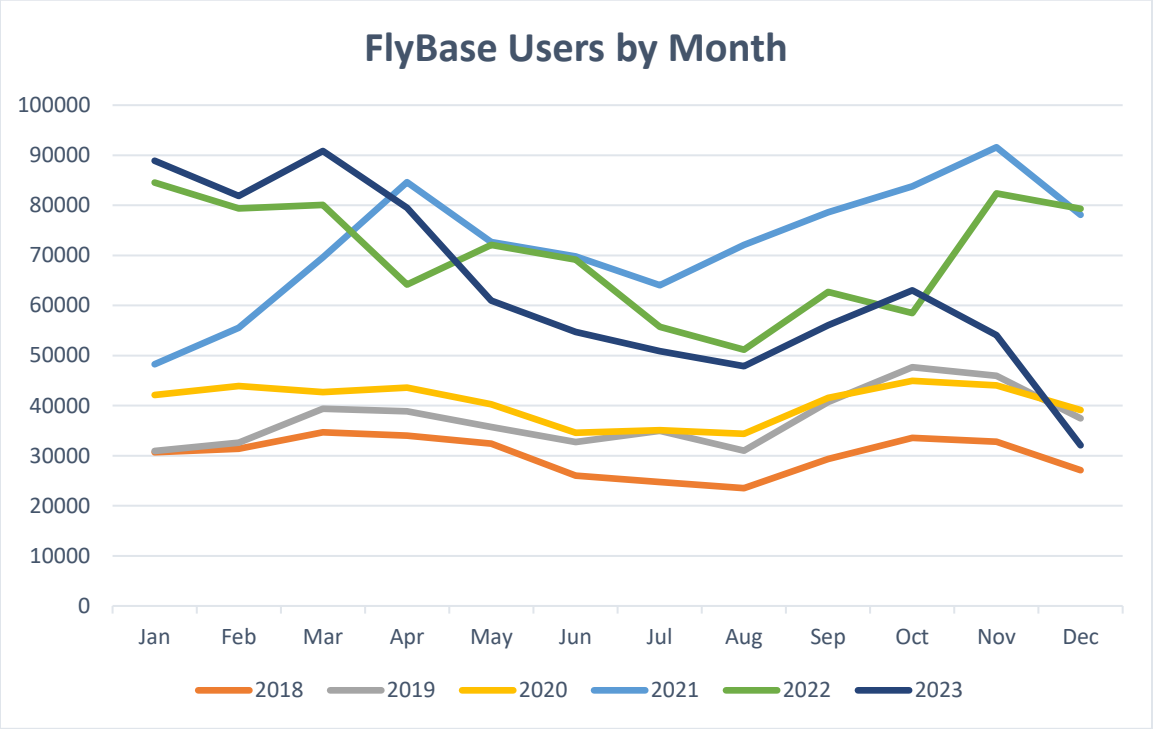
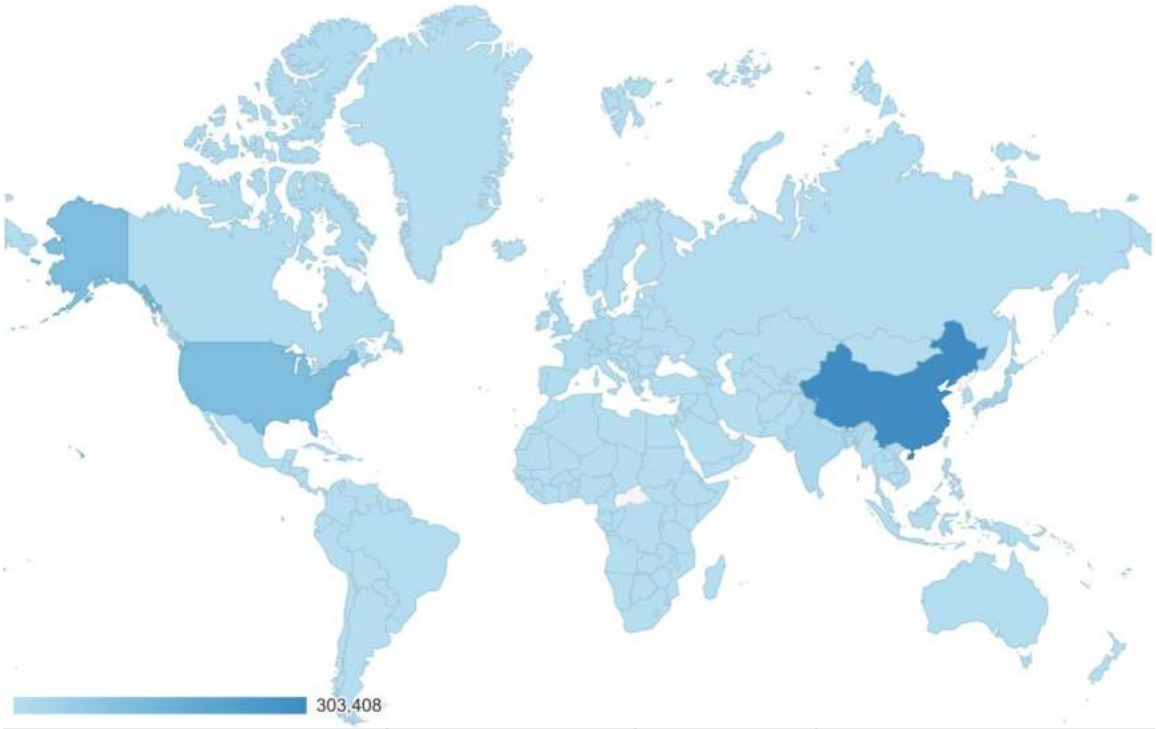


Figure 3 – FlyBase users for Jan 2018 – Dec 2023

Geographical Distribution

The majority of user traffic to FlyBase in 2023 came from the U.S. and from China, with the number of ostensible Chinese users being more than double the number from the U.S. The high Chinese traffic continues a pattern seen over the last several years. This graphic is only available using the deprecated Google Analytics 3; for the Fall meeting this graphic will change to a similar GA4 offering.



	680,817 % of Total: 100.00% (680,817)	680,817 % of Total: 100.00% (680,817)
1. China	**303,408**	44.60%
2. United States	**122,404**	17.99%
3. Japan	**31,971**	4.70%
4. India	**21,487**	3.16%
5. United Kingdom	**20,083**	2.95%
6. Germany	**19,272**	2.83%
7. Singapore	**12,903**	1.90%
8. Canada	**10,488**	1.54%
9. France	**10,182**	1.50%
10. Philippines	**9,830**	1.45%

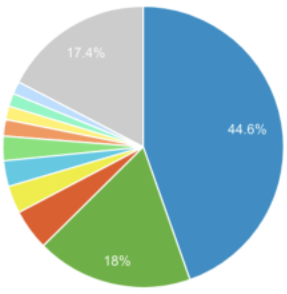
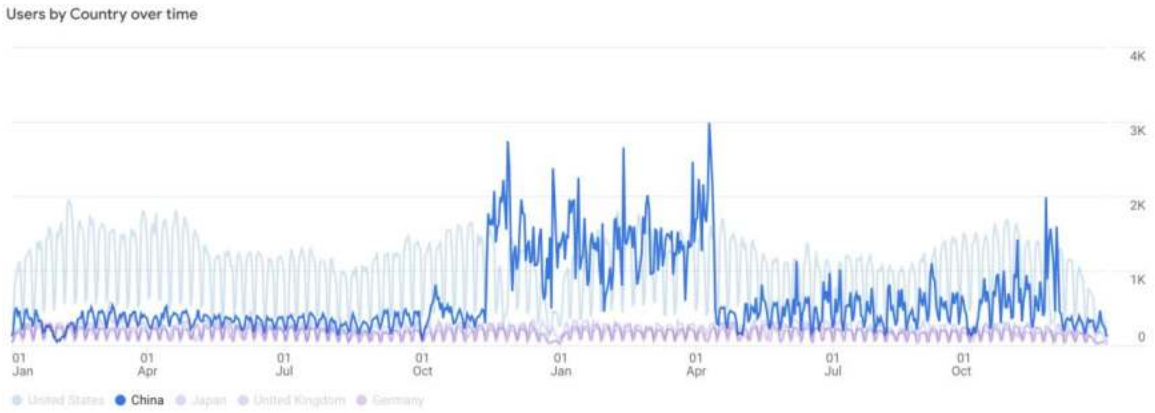


Figure 4 – FlyBase Users by Country (Jan-Dec 2023)

Usage Patterns for China

During April of 2023, usage from China (as reported by Google Analytics v4) showed a sharp decline. Exploring further I found that usage statistics from China are quite erratic:



The burst of activity during approximately November 2022 to April 2023 cannot be reasonably explained by human user activity. Instead, it seems likely that there are periods during which Chinese "bots" are implemented to gather data. This is further evidence that we must take with a grain of salt the user statistics generated by GA4 for China.

The lighter "background" traces here are for the other countries listed at the bottom of the graphic: U.S. (tall regular trace with weekly and seasonal variations), and Japan, U.K., Germany (much lower levels, but also with consistent weekly/seasonal variations). These other country traces show none of the anomalies seen in the Chinese trace.

Gene Disruption Project (Kanca, Bellen, Levis)

Update of the GDP

The GDP has been generating versatile alleles that are invaluable for gene functional annotation to empower fly researchers for > 20 years. The first strategies that the GDP employed were based on mobilizing diverse transposable elements (TE). The GDP has generated and molecularly mapped more than 200,000 TE alleles with diverse payloads to facilitate generation of mutant alleles, detection of expression patterns of genes, GAL4-inducible ectopic expression of genes or tagging the genes with epitope tags or fluorescent proteins (Bellen et al., 2004, 2011; Spradling et al., 1999). The most useful TE insertions are distributed by the Bloomington Drosophila Stock Center (BDSC) and more than 20,000 TE insertions are available and regularly requested by users. One of the most versatile transposable elements developed by the GDP is the *Minos* mediated insertion cassette (MiMIC). 17,000 MiMIC insertion stocks were created and sequenced and 7,000 are available from the BDSC. The MiMIC *Minos* TE contains an artificial exon that is spliced in the mature mRNA of a gene if it is inserted in an intron in the same orientation as the gene (Venken et al., 2011). The MiMIC screen used an artificial exon that created a gene trap, when inserted in an intron between two protein-coding exons in the proper orientation, truncating translation of the protein at the site of insertion. This artificial exon was flanked by phiC-31 attP sites. The artificial exon can be exchanged after the initial targeting event through Recombinase Mediated Cassette Exchange (RMCE) (Bateman et al., 2006; Nagarkar-Jaiswall et al., 2015), providing the means to use the same entry site to generate a variety of genetic reagents and has allowed elegant manipulations for 1,700 genes. For example, a MiMIC insert can be used to integrate a *Splice Acceptor(SA)-T2AGAL4-polyA-3XP3EGFP-polyA* artificial exon in a gene containing a MiMIC through RMCE (Diao et al., 2015; Lee et al., 2018; Nagarkar-Jaiswal et al., 2015). This cassette causes a premature transcription termination due to the presence of a polyadenylation signal. During translation the T2A ribosome skipping sequence leads to truncation of the protein and release of the nascent peptide while enabling translation of the yeast GAL4 transcription factor from the mRNA of the targeted gene. This typically leads to a severe loss of function allele. Importantly, the expression of the GAL4 recapitulates the spatial and temporal expression pattern of the targeted gene (Lee et al., 2018; Nargarkar-Jaiswall et al., 2015). This GAL4 can then be used to drive UAS-fluorescent proteins, providing a very sensitive read out of the gene expression pattern, or the UAS-cDNA of the tagged gene or its human ortholog, providing a genetic rescue paradigm for about 75% of the tagged genes. Once rescue is established, it permits structure function studies with designed mutations in the cDNA (e.g. deleting a domain) or rare genetic variants that have been observed in patients (e.g. missense mutations). The latter is one of the most powerful means to assess human variants in a model organism. Another powerful use of MiMICs is to replace the integrated cassette with an artificial exon containing the SA-GFP-Splice Donor (SD) cassette. This leads to tagging of the gene product internally with GFP. This approach has been shown to create a functional protein for 75% of the GFP-tagged genes (Nagarkar-Jaiswal et al., 2015). The GFP tag can then be used to assess the subcellular localization of the protein (e.g. mitochondria, ER, peroxisomes, lysosomes, plasma membrane, nucleus) and can be used as an epitope to pull-down the gene product and its interactors using anti-GFP antibodies and standardized protocols (Neumüller et al., 2012). The interactors can be identified using mass spectroscopy for proteins, often allowing the identification of molecular pathways.

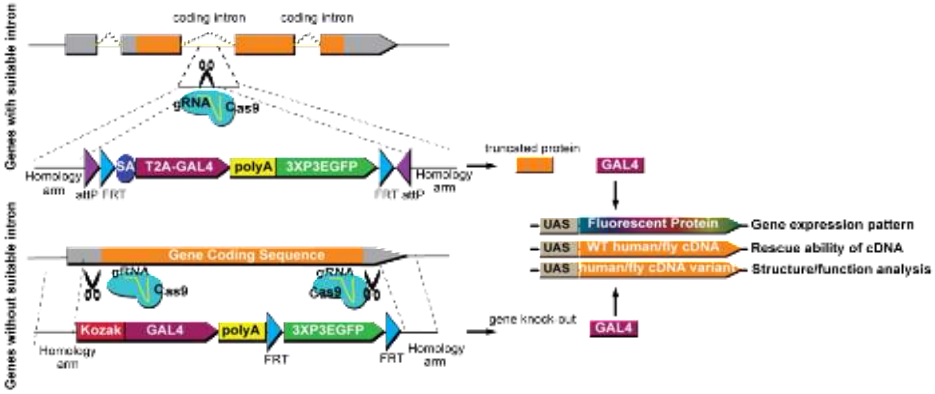


Figure 1. T2AGAL4 and Kozak GAL4 alleles generate GAL4 transcription factor in the expression domain of the targeted gene and can be used to drive a variety UAS constructs.

With the advent of CRISPR-based techniques, the GDP has adapted its strategies to disrupt the genes in a targeted manner through CRISPR-mediated homologous recombination (CRIMIC). The first CRIMIC alleles aimed to create a landing site in the targeted gene that can be used to functionalize the insert as a

protein trap or gene trap through RMCE, similar to MiMIC. The strategy quickly evolved into direct integration of *attP-FRT-SA-T2AGAL4-polyA-3XP3EGFP-polyA-FRT-attP* in coding introns (CRIMIC-T2AGAL4) or *KozakGAL4-polyA-FRT-3XP3EGFP-FRT* to replace the whole coding region of the targeted gene with KozakGAL4 (CRIMIC-KozakGAL4) collectively known as CRIMIC-GAL4 alleles (Figure 1).

The first homologous recombination strategies relied on using homology donor constructs containing large homology arms (>1kb) cloned on either side of an exchangeable cassette. However, this approach was not very efficient as the success rate was about 50% because of molecular cloning issues and the integration efficiency of these large constructs (~ 5kb) in the genes of interest was low and labor intensive. We have explored multiple alternative strategies to decrease the homology arm size and discovered that short homology arms can lead to insertion of large constructs if the homology donor construct is linearized *in vivo* by the action of Cas9. Short homology arms make it feasible to synthesize a homology donor intermediate that can be used to generate a homology donor vector with a single straightforward and effective cloning step. This is a cheap option as it only cost $100 to design the intermediate construct. This intermediate only requires a single straightforward directional cloning step to prepare the homology donor construct for injection and the cloning succeeds nearly 100% of the time (Kanca et al., 2019). In our design, we flanked the to-be-inserted DNA with two sgRNA target sequences that are only present in the vector and are not found in the genome and that can be cut by a specific sgRNA (sgRNA^{1}). We therefore injected three plasmids: 1) the sgRNA^{1} encoding plasmid; 2) the target specific sgRNA (sgRNA^{locus}) encoding plasmid; 3) the homology donor construct containing the exon *attP-FRT-Splice Acceptor (SA)-T2AGAL4-polyA-3XP3EGFP-polyA-FRT-attP* to target a gene. This approach was successful but tedious and we obtained integrants in about 65% of the cases. In the past two years we revised our targeting strategy to include the U6 promoter-sgRNA^{1} in the vector backbone followed by a partial tRNA sequence that is complemented by the synthesized fragment followed by sgRNA^{locus}. Hence, both sgRNAs are produced as a transcriptional unit containing the sgRNA^{1} and sgRNA^{locus} (Figure 2). This 'improved Drop-in' strategy decreases the workload to target a gene by obviating the requirement of cloning, prepping and injecting the separate plasmids encoding sgRNAs. Importantly, it ensures co-delivery of all the components required for homologous recombination in a single plasmid at equimolar ratios. This strategy substantially decreases the labor of cloning and simultaneously increases the transgenesis rate by about 25%. Hence, we now typically obtain an 85% to 90% success rate upon the first injection. We shared our findings in an open access publication and included a detailed protocol to help other laboratories use our methods (Kanca et al., 2022). This innovative strategy leads to generation of a library of homology donor intermediate plasmids that have all the components required for homologous recombination, which can be repurposed to insert new payloads in targeted genes. Currently, we are testing repurposing homology donor intermediates to knock in different payloads *like SA-GFP-SD-Scarless DsRed* artificial exon to generate GFP tagged protein trap alleles or *SA-T2A-human cDNA-polyA-DsRed* to knock-in human orthologous gene in the locus of the fly gene. The stocks that we generate are deposited in the BDSC where they are distributed to fly researchers all over the world. More than a million stocks generated by the GDP have been distributed by the BDSC. In conclusion, the GDP continues to be a driving force for developing and implementing gene targeting strategies to empower Drosophila. In the last year, we have generated 455 new alleles and sent 539

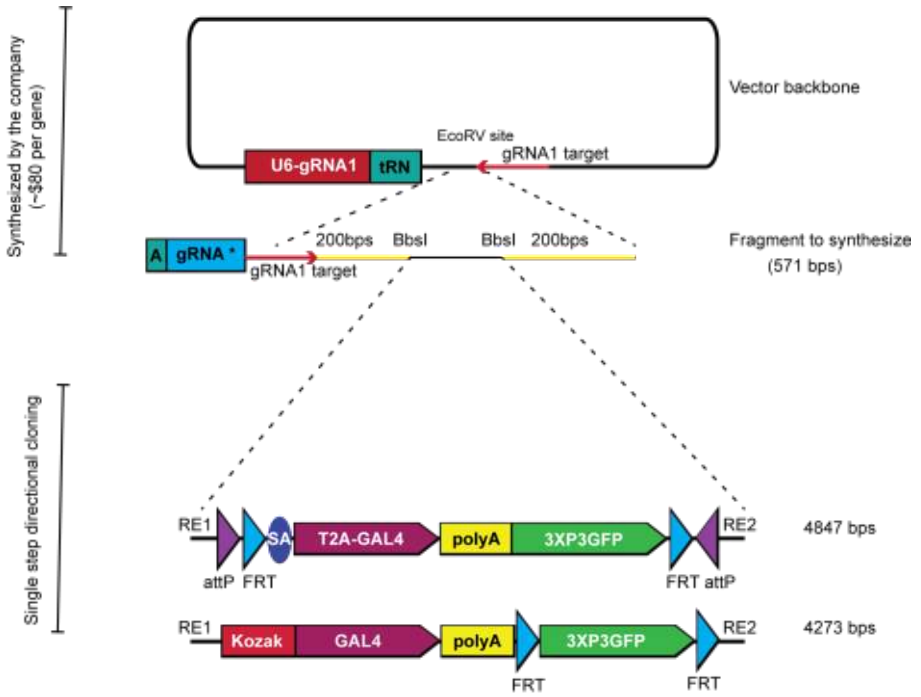


Figure 2. New Drop-in design allows combining all components for homologous recombination in homology donor in one vector. Inclusion of a tRNA after the sgRNA^{1} permits multiple sgRNAs to be expressed from the U6 promoter and sgRNA^{locus} to be included in synthesis.

alleles to the BDSC. In addition, in collaboration with the UAS-human cDNA project and Bier lab, we have also built a Drosophila COVID-19 resource (DCR) where we generated GAL4 alleles for 313 fly orthologs of human host interactors of the SARS-CoV-2 proteome. Additionally, we supported the Fourth Chromosome Resource Project led by Stuart Newfeld and Michael O'Connor to help generate GAL4 alleles and GFP protein traps of the genes on the 4th chromosome (Stinchfield et al., 2024). To date, the GDP has generated GAL4 alleles for over 3,000 genes by converting MiMICs through RMCE or CRISPR mediated homologous recombination to insert a SA-T2AGAL4 cassette in a coding intron or through replacing the coding region of the targeted genes with a KozakGAL4 cassette. These have been sent to the BDSC. We are currently funded by the Office of Research Infrastructure Programs (ORIP) until 2025. We applied for renewal of our grant support to continue the project to the year 2029 and increase the scope of imaging the expression pattern of the generated GAL4 alleles.

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