Agenda for Dros22 Board meeting, 1-4 pm PST, April 6th 2022
*Room **Palm 1-2 or*** https://cuboulder.zoom.us/j/93268041060 (password = Drosophila)

Table of Contents of reports for the 2022 Fly Board meeting (April 6, 2022)

Report from the 2021 Drosophila Board Elections Committee (Mark Peifer)

The 2021 Elections Board Committee included three members from the previous year: **Iswar Hariharan, Tina Toole and Erika Geisbrecht**. **Alissa Armstrong** agreed to serve as a new member. We held our initial meeting on September 3, discussing alternative approaches to involve the community and ensure a diverse slate of nominees across many axes of diversity. After considering the instant-runoff approach used the previous year versus an approach of two candidates for each seat, we settled on the latter. We divided the responsibilities among the committee as follows: Erika-Latin America, Tina-Asia, Alissa-Mid Atlantic, Iswar-California/ Hawaii, Mark-Europe and President.

In late-September the following email soliciting community nominations was sent to the Drosophila community by the GSA and also posted by Fly Base. We also publicized the call for nominations via Twitter and Fly Slack. This process was repeated over the next six weeks.

Dear Colleagues
It is once again time to choose candidates who will serve on the Fly Board and your input is needed to ensure we have a diverse and engaged slate of candidates!

What is the Fly Board? *This is a group of your peers who carry out a number of important functions for the Drosophila Research Community. These functions include (1) advocating for the Drosophila research community by representing your best interests to funding agencies, other scientific organizations, and the general public; (2) facilitating an open and productive relationship between the research community and resources such as FlyBase, the Drosophila Genome Resource Center, groups heading efforts to develop better tools and information resources, and the directors of the stock centers; (3) insuring a successful annual North American Drosophila Research Conference; (4) administrating our meeting funds; and (5) administrating awards, such as the Larry Sandler Memorial Lecture Award, undergraduate travel awards, and the Image Award.*

The Fly Board has made a strong commitment to truly represent the diverse community of researchers who work on Drosophila. *To that end, we are encouraging suggestions from the community for all elected positions on the Fly Board. We invite you to suggest people who you think would do a great job representing the fly community—feel free to suggest yourself or a colleague who fits this description.* ***We especially encourage suggestions of individuals from groups that have been historically underrepresented on the Fly Board, and faculty at any career stage are eligible.*** *Although you must live and work in or near the region you represent, you can nominate individuals for any region and you can vote for representatives from all regions in the final elections. Please send any of us names and a brief description (just a few lines, but this part is optional) of why the person you suggested would be good for the job by* ***October 10, 2021****.*

Who are we electing this year?
Every year, we elect a future ***President*** *of the Fly Board. The President serves for one year as President elect and for one year as President. To ensure long-term memory of the Board, the*

President will serve in an advisory role to the Fly Board for three additional years after their term ends. (See https://wiki.flybase.org/wiki/FlyBase:Fly_Board -

***Responsibilities of the Drosophila Board Presidents** for complete job details).*
*Every year, we also elect other representatives, including **Regional Representatives** and a representative from Primarily Undergraduate Institutions in the US. This is a three-year commitment to Fly Board, with a subset of representatives turning over every year. (See https://wiki.flybase.org/wiki/FlyBase:Fly_Board -**Responsibilities of the***

***Regional Representatives** for complete job details).*
This year, we will be electing representatives who will serve from 2022 through 2024 for the following regions:
Mid-Atlantic (Downstate New York, New Jersey, Eastern Pennsylvania, Delaware, West Virginia, Washington D.C., Maryland, Virginia) Current Erika Bach

California (California, Hawaii) - Current Leanne Jones

Asia - Current Tatsushi Igaki

Europe - Current Nic Tapon

Latin America – Current Helena Araujo

We look forward to engaging each member of the fly community in electing a Fly Board that will be truly representative of all of us and will help advance the shared goals of our community.

Thanks,
The 2021 Elections Board

Mark Peifer (peifer@unc.edu), Iswar Hariharan (ikh@berkeley.edu), Tina Tootle (tina-tootle@uiowa.edu), Erika Geisbrecht (geisbrechte@ksu.edu), Alissa Armstrong (ARMSTRAR@mailbox.sc.edu).

This resulted in multiple nominations. The committee then met to choose candidates in cases where more than two nominations emerged for a position, and to identify additional candidates, in the one case where fewer than two had been brought forward. Potential candidates were then contacted to determine whether they were willing to stand for office, and if needed additional potential candidates were contacted. By November 2021 we had the full slate identified and requested from each candidate their election statement. These were assembled into a single PDF (see copy below, along with election results), Brian Calvi and FlyBase then set up a process for community members to vote via SurveyMonkey and the ballot went public in the first week of December. The following email, with the candidate profiles attached, was sent by the GSA and posted by Flybase, announcing the election. It was also publicized on Twitter.

Dear Drosophila researcher,

It is time to cast your vote for new members of the National Drosophila Board of Directors. The Board plays an important role in the Drosophila research community, so please take a few moments to learn about the Board and, importantly, participate in this election. The Board's duties include overseeing community resource centers and addressing other research and resource issues that affect the fly community. The Board also administers the finances for the annual North America Drosophila Research Conference and its associated awards, and it chooses the organizers and the site of the annual meeting. The Board consists of 13 regional representatives: Eight from the U.S. and one each from Canada, Latin America, Europe, Asia and Australia/Oceania, and one representative for primarily undergraduate institutions, all of whom serve 3-year terms. The Board is led by three elected officers: a President, a President-Elect and a Treasurer. In addition, the Board has ex officio members, including past-Presidents, meeting organizers and representatives of the Drosophila community resource centers.

This year we are electing the President-elect, who will serve as President starting with the Fly meeting in 2023. We are also electing regional representatives from Europe, Asia, Latin America, California, and the Mid-Atlantic.

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

Balloting will end ***January 22nd, 20202***

Thank you,

The 2021 Drosophila Board Election Committee:

Alisa Armstrong, Erika Geisbrecht, Tina Tootle, Iswar Hariharan, and Mark Peifer

Reminders were sent out in January, encouraging community members to vote. On January 25, results were tabulated. Full results are on the PDF that follows.

Harmit Malik was elected future president. He ran against **Elizabeth Chan**. 875 people voted for President Elect.

Daria Siekhaus was elected as future European representative. She ran against **Sofia Araújo**. 761 people voted.

Hakeem Lawal was elected future MidAtlantic representative. He ran against **Fernando Vonhof.** 733 people voted.

Mousumi Mutsuddi was elected future Asian representative. She ran against **Yan Yan**.. 1179 people voted.

John Ewer was elected future Latin American representative. He ran against **Marcos Túlio Oliveira**. 737 people voted.

Blake Riggs was elected California/Hawaii representative. He ran against **Naoki Yamanaka**. 733 people voted.

We're grateful to all of the folks who helped along the way—those who nominated candidates, those who agreed to run, Tracey Depellegrin and Jacqueline Treboschi of the GSA, Brian Calvi and FlyBase, and all who voted!

The 2021 Drosophila Board Election Committee:

Alisa Armstrong, Erika Geisbrecht, Tina Tootle, Iswar Hariharan, and Mark Peifer

Treasurer's Report 2022 (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
6/28/18	opening Vanguard account 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			(8,379.00)			208,449.24

2022 award amount was for 5 awards of ~$2000 each, funded jointly from the Larry Sandler Fund and the *Drosophila* Reserve Fund. Following the new Trainee Awards Policy, we used approximately 5% of the value of the Reserve Fund.

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
1/2022		1,500			(1,500)	104,173

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

2021 and 2022 Fly Board Awards funded jointly with the Drosophila Reserve Fund.

No travel expenses for 2020 or 2021

	Vicky Finnerty Memorial Fund (Wellington Fund)					
	Contributions	Investment Income	Fees	Transfers from Meetings	Awards	Fund Balance
2011	3,726			-		3,726
2012	4,102			6,000	5,178	8,650
2013	-			6,000	7,150	7,500
2014	3,960			6,000	8,940	8,520
2015	1,324			6,000	4,705	11,139
2016	886			6,000	3,795	14,230
2017	1,500			6,000	3,844	17,886
2018	2,560			6,000	4,945	21,501
2019	2,121			6,000	4,800	24,822
2020	1,730	1,562	323	-	-	28,114
2021	500	4,099	385	6,000	941	37,063
2022					5,989	31,074

Investment account established October 2020
2022 Awards: 15, totaling $5,989

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. This year, the representatives were Kieran Harvey (for a second year), Rachel Smith-Bolton and Brian Lazzaro. In addition, this year's committee included a trainee representative, Lydia Grmai. At the first meeting, the committee decided on what type of awards to make. It was felt that last year's awards for outreach efforts to get students, including those from under-represented groups, involved in fly research, had been successful, and could potentially be more transformative than travel awards. The committee favored repeating this approach to gain additional data and experience. We placed the following ad on FlyBase in October:

Funding Opportunity for Outreach Efforts

The *Drosophila* Board invites applications for funding to support efforts to increase trainee participation, equity and diversity in the *Drosophila* research community. Non-profit programs that introduce middle school, high school or college students to *Drosophila* research are eligible to apply. Please provide the following:

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

The number of students that can be reached through the proposed program and financial need of the applicant organization will be considered in selecting proposals for awards.
Applications are due by Dec. 31st 2021 to Nancy.Rodriguez@nyulangone.org.

Seven applications were received, significantly fewer than the sixteen received in 2021. The committee met virtually to discuss them and the members were in good agreement that the top five were worthy of funding, although the small number of applications was a cause for some concern. Next year, we may want to find additional ways to advertise the opportunity, or consider another type of award.

The winners were:

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

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

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

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

Karla Yotoko for a course to train undergraduates at the Federal University of Viçosa, Brazil, to collect and molecularly characterize wild *Drosophila* strains. The students will also visit local high schools to discuss *Drosophila* species diversity and its relevance to genetics, ecology and evolution, and will invite the five best students (giving preference to under-represented minorities) to a workshop at the university.

The 2021 winners were asked to provide a progress report:

Genomics Education Partnership was given an award for translation into Spanish of their "Understanding Eukaryotic Genes" modules on manual gene annotation for undergraduates, and creation of accompanying Spanish-language videos that will enable them to reach ESL students.

GEP offered paid internships to 8 Spanish-speaking students who translated the walkthrough/protocol documents for all the modules, as well as the English captions on the video walkthroughs. The materials are now being piloted with GEP Puerto Rico before their official release.

eCLOSE Institute was funded for a summer camp program for high school students in Philadelphia, more than 60% of whom are under-represented minorities. Due to Covid-19, the current hybrid format ships students a "lab in a box" that they use to investigate the influence of diet on fly development, guided by online instructors. Fly Board funding will support 7 students.

We have not yet received the formal report, but heard informally that the 7 students had an amazing experience. In addition, eCLOSE received a large grant from a pharmaceutical company to carry out similar activities this summer.

Discovering *Drosophila* Development received an award for reagents for a summer research experience using *Drosophila* for 10-15 undergraduates, held at UNC-Chapel Hill in collaboration with Durham Technical Community College, with the goal of micropublications and the hope that DTCC students will transfer to UNC.

The two-week course enrolled 8 DTCC students, who learned how to do embryo preparation and antibody staining, although the time they needed to acquire these lab skills meant that the micropublication goal was not achieved. One student is transferring to UNC and seeking out a fly lab.

Drosophila Research and Training Centre received an award for outreach to 10 public and private secondary schools in Ibadan, Nigeria to introduce students to *Drosophila* research. Researchers will first visit the schools to discuss the importance of fly research and demonstrate fly handling and microscopy, and two students from each school will then visit the DRTC for further training.

The DRTC carried out 10 outreach events to secondary schools, and at least 30 students participated in each event, which included both lectures and hands-on lab experience. Two students from each of the schools then visited the DRTC for further practical training and a virtual lecture from Dr. Hammed Badmos about the importance of *Drosophila* in cancer research.

Science Education for Youngsters was funded to hold an event for 50 secondary school students in Osogbo, Nigeria to introduce the *Drosophila* model system, demonstrate lab equipment and carry out hands-on training using Foldscope microscopes.

This group has had challenges with Covid and their bank account set up in Nigeria, and has requested an extension so that they can carry out the event in 2022, so this award has not yet been paid out.

Finnerty Undergraduate Travel Award Report to the 2022 Fly Board

Justin DiAngelo, Finnerty Undergraduate Travel Award Committee Chair

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

This year we received 43 applications for the Victoria Finnerty (VF) Undergraduate Travel Award. Following an initial round of evaluation, 15 applications were moved to a second round of consideration and were all recommended for funding. In order to maximize the number of students who received funding, money was awarded on a sliding scale, according to their ranking, with the highest amount being $599 so that the students wouldn't have to pay taxes on their award. In total, we awarded $5989 for Finnerty Undergraduate Travel Awards this year.

The awardees are:

Saron Akalu, UC Berkeley, $599
Caroline Pritchard, Lehigh University, $500
Sequioa Smith, Sam Houston State University, $500
Alani Perkin, Harris-Stowe State University, $500
Gonzalo Morales, University of New Mexico, $500
Megan Butler, UNC Chapel Hill, $375
Collin Louis, Grand Valley State University, $375
Joanatta Shapiro, Rutgers University, $375
Sherif Negm, University of Rochester, $375
Manisha Persaud, Rutgers University, $375
Heidi Pipkin, Bemidji State University, $375
Christopher Petit, Loyola University Chicago, $375
Shanzeh Sayied, Brown University, $375
Paulo Belato, University of Connecticut, $165
Caroline Pitton, Wesleyan University, $225

Image Award (Nasser Rusan)

This year Irene Miguel-Aliaga and Toshie Kai rotated off the Image Award committee and two new members were added - **Amy Kiger** from UCSD and **Julie Brill** from the Hospital for Sick Children, Toronto, maintaining the total committee members of 6 (including Nasser Rusan, Rachel Smith-Bolton and Dan Bergstralh). Committee members are asked to serve 2 year terms, which will allow for steady turnover.

New chair

This year is the fifth and final year that I (Nasser Rusan) will serve as the chair of the Drosophila Image award. Amy Kiger and Julie Brill were added to the committee this year with the possibility of one of them serving as the next chair. If they are unable to do so, I will work with the current committee and the GSA to determine the best way forward. The committee and I welcome any advice from the Fly Board related changing the image award leadership and improving/expanding its content.

Results of the 2022 competition

This year, we have maintained our Twitter presence, especially leading up to the submission deadline.

50 total submissions: 31 images and 19 videos. That is a 37% decrease from last year.

The winners:

Image award

Yuan Tian, Yuxuan Yan, and Jingyan Fu,
China Agricultural University, Beijing, China

Centrosome Biogenesis under Sub-Diffraction Resolution
https://rupress.org/jcb/article/220/4/e202005103/211748

Video award

Ke Yang
School of Life Sciences, Tsinghua University, Beijing, China

High resolution imaging of the ER-Golgi interface through FIB-SEM
https://www.sciencedirect.com/science/article/pii/S2211124721011542

Report on 2022 Larry Sandler Award

2022 Committee:
Alissa Armstrong (Chair, University of South Carolina, Columbia, SC)
Sofia Araújo (Universitat de Barcelona, Barcelona, Spain)
Amanda Larracuente (University of Rochester, Rochester, NY)
Timothy Mosca (Thomas Jefferson University, Philadelphia, PA)
Luciano Matzkin (University of Arizona, Tucson, AZ)

Process:
The committee received **17 nominations**. Different from the previous year, applications were submitted online. As a result, advisor letters were more streamlined compared to the previous year. Based on recommendations from the previous committee to focus on diversity, equity, and inclusion, an attempt was made at collecting demographic information (see "Comments and suggestions on selection process" section below).

To come up with a shortlist, each committee member scored all applicants on the following three criteria – **significance** (a clear description of why the work is important and how it advanced the field), **originality** (did the project use a new approach? an old approach applied in a new way (organism, to address a different question, etc)? asking an entirely new question? addressing assumptions made in the field but that have never been examined experimentally?), and **clarity of abstract** (are the dissertation questions, approaches, and major findings clearly written and able to be understood by most Drosophila-ists?). Committee members scored on a 1-10 (unacceptable – outstanding) range. Additionally, scores for each category had an accompanying score of our own confidence/familiarity with the field. The committee chair then added scores for each candidate and identified those with the highest total score. For each committee member, this ranged from 6-10 applicants. In summary, there was one candidate who ranked in the top for all committee members, two who ranked in the top for four committee members, one who ranked in the top for three committee members, four who ranked in the top for two committee members, and five who ranked in the top for one committee member.

We then met via Zoom to discuss and find a consensus short list of 4 outstanding candidates quickly emerged. These 4 finalists were invited to submit their theses for the committee to read. We then again met by Zoom and after brief discussion, we settled on a unanimous winner. Because of the outstanding quality of the candidates we decided to leave the other 3 as co-runner-ups.

2022 winner: **Dr. Lianna Wat**, Ph.D. University of British Columbia (mentor Dr. Elizabeth Rideout)

Student supplied abstract:

Sex-specific regulation of fat metabolism in *Drosophila*

Maintaining energy homeostasis is essential for survival in a changing environment. When dietary energy is abundant, animals store excess energy and when dietary energy is scarce, animals mobilize energy stores to support biological functions. In most animals, fat is the main form of stored energy. One important factor that regulates fat metabolism is biological sex. In many animals, females store more fat and have decreased fat breakdown compared with males. Several studies have investigated how sex chromosomes and hormones establish the male-female differences in fat metabolism; however, the metabolic effectors acting downstream of sex chromosomes and hormones are understudied. To better understand the sex-specific regulation of fat metabolism, I used Drosophila as a model to identify metabolic genes and pathways which contribute to sex differences in fat metabolism.

In Chapter 2, I identified male-biased regulation of the triglyceride lipase brummer (bmm) and showed how this regulation contributes to the male-female differences in fat storage and breakdown. Further, I found that bmm functions in the neurons and somatic cells of the gonads to influence these sex differences. However, sex-specific regulation of bmm does not fully account for the male-female differences in fat metabolism. Therefore, in Chapter 3, I investigated the role of sex determination gene transformer (tra) in establishing the male-female differences in fat storage and breakdown. I demonstrated that tra establishes the sex difference in fat storage via the sex-specific regulation of the adipokinetic hormone (Akh) signaling pathway, a major lipolytic pathway. In Chapter 4, I explored the role of the Akh pathway in regulating fat breakdown in females and males. Here, I demonstrated that Akh pathway activity poststarvation has differential effects on fat breakdown in females and males.

By investigating the role of metabolic effectors in both sexes, I identified sex limited effects on fat metabolism in both males and females, highlighting the importance of considering both sexes in experimental design and execution. Overall, my work sets the foundation for future studies aimed at identifying conserved mechanisms underlying sex-specific regulation of fat metabolism, and thus allow for a more comprehensive understanding of fat metabolism and metabolic diseases associated with dysregulated fat metabolism.

2022 co-runner-ups:
Cheng Lyu, The Rockefeller University (PI: Gaby Maimon)
Luis Hernandez-Nuñez, Harvard University, (PI: Aravinthan Samuel)
Maureen Lamb, University of Iowa, (PI: Tina Tootle)

Comments and suggestions on selection process:
The process ran similarly to previous years, although the closing date for the nomination was bit later than other years (late December instead of early December, which caused a slight delay). The Committee all felt that the process ran smoothly, and it was easy to

find consensus on the finalists and winner. The quality of the applicants overall was outstanding which made it a challenge to rank. Prior to distributing the package of completed applications we held a meeting to discuss our methodology. Although we employed a simple numerical scoring system, we focused on an iterative consensus building based process using a list of top candidates generated by each committee members. This process worked well and we reached consensus with no major difficulty.

A topic of discussion was diversity, equity and inclusion with regard to gender identity, race and ethnicity, university prestige, new versus established investigator, etc. **A key suggestion for the future is that we find a better way to collect demographic information about the candidates as part of the application process.** Given that advisors submitted nominations online, they entered demographic information for themselves. Perhaps candidate information could accompany nominations by making the nominees complete a cover sheet where this information was included. The absence of this information makes it very challenging to ensure DEI best practices are followed.

Demographics:
7/17 nominees were female identified, 9/17 of nominating PIs were female identified. Without making inferences, we were unable to identify nominees from historically excluded groups. All nominating PIs identified as White or Asian.

Nominees for 2022 (Finalists are in Bold)

Nominee	Nominator
Byrns, China	Bonini, Nancy
Hanson, Mark	Lemaitre, Bruno
Hernandez-Nunez, Luis	Samuel, Aravinthan
Kiral, F. Ridvan	Heisinger, P
Lamb, Maureen	Tootle, Tina
Langmuller, Anna Maria	Schloetterer, Christian
Lyu, Cheng	Maimon, Gaby
Meng, Julia	Heckscher, Ellie
Millington, Jason	Rideout, Elizabeth
Mokashi, Sneha	Anholt, Robert
Nunez, Kavin	Kaun, Karla
Perez-Vale, Kia	Peifer, Mark
Ravenscroft, Thomas	Bellen, Hugo
Rosenthal, Justin	Quan, Yuan
Schoelz, John (Jack)	Riddle, Nicole
Wat, Lianna	Rideout, Elizabeth
Witt, Evan	Zhao, Li

Email to winner:

Dear Dr. Wat:

On behalf of the 2022 Sandler Award Committee, I am delighted to inform you that you have been selected as the recipient of the 2022 Larry Sandler Memorial Award!

As you may know, the goal for this award is to identify the "best" Ph.D. thesis in *Drosophila* research from the previous year. In this round we had 17 nominations, making the competition tight. The committee (composed of Drs. Amanda Larracuente, Tim Mosca, Luciano Matzkin, Sofia Araújo, and myself) unanimously felt that your beautiful work investigating the mechanisms that underlie sex-specific differences in fat storage and breakdown stood out as especially significant and deserving of this recognition. It also helped that we received very strong and supportive comments from your advisor, Dr. Elizabeth Rideout. Many congratulations on executing this spectacular set of experiments and on a superb thesis.

As the recipient of this award, you will have the honor of presenting your thesis work in the Larry Sandler Memorial Lecture on Wednesday, April 6, the opening night of the 63rd Annual *Drosophila* Research Conference in San Diego, CA. You will give your plenary lecture in front of the entire fly community present at the meeting. In addition to sharing your work with the field, we hope that your talk will help to inspire other students just starting or in the midst of their PhDs. Ms. Suzy Brown (cc'ed here) of the GSA will be in touch to make (and pay for) your travel arrangements to San Diego.

Again, please accept our warmest congratulations. You now join a long list of excellent scientists who have gone on to have successful careers (link for current list of recipients here).

Please don't hesitate to let me know if you have any questions as you prepare for your talk in San Diego. I look forward to meeting you in person in April. I have included both of your email addresses to make sure that you receive all communication moving forward.

Best wishes,

Alissa Armstrong (Committee Chair)
Sofia Araújo
Amanda Larracuente
Luciano Matzkin
Timothy Mosca

Email to runners-up:

Dear Dr. XYZ:

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

Although you are not the winner for this year's award, I nevertheless want to congratulate you for executing a spectacular thesis. This year's competition was intense: we received 17 nominations, most of which were truly outstanding and deserving of the Larry Sandler Award. The committee struggled to narrow this down to even a top four. We truly enjoyed reading about your work and accomplishments and have no doubt that you will continue to do superb research in the future. I should add that it is evident how supportive your advisor was of your work by their nomination. At your earliest convenience, please send me an image of yourself that I can use to highlight your work during the Larry Sandler Award presentation.

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

Best wishes,

Alissa Armstrong (Committee Chair)
Sofia Araújo
Amanda Larracuente
Luciano Matzkin
Timothy Mosca

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, and others
- At the FlyBoard's request, establishing and administering the Victoria Finnerty Fund
- Creating and maintaining the Image Award website and the Award plaque
- Managing the Larry Sandler Award Fund, making speaker arrangements (travel, registration, award presentation, lifetime GSA membership), providing registration for the runners up, producing the award plaque, and other tasks as needed
- Emailing the FlyNews and other special FlyBoard announcements to the community (a recent example is the FlyBoard election results announcement)
- Managing and publishing FlyBook

Code of Conduct for GSA Conferences

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

Professional Development & Other Special Programming

In 2021, the Engagement Department hosted four seminar series including the Multilingual Seminar Series, the pgEd and GSA collaborative "Discussing Genetics" series, the GSA Award Seminar Series, and the "Exploring gene function across humans and model organisms series.

The Early Career Leadership Program (ECLP) continued to expand. In February 2022 Engagement welcomed 32 representatives for our largest total cohort of 68 representatives. Engagement has begun offering training programs to ECLP representatives, including a science writing course offered by science writer Rachel Fairbank, and the Leadership and Management in Action Program facilitated by Molly Grisham.

In 2021 ECLP representatives made significant achievements. A sampling includes:

- Representatives Career Development Subcommittee hosted five #WorkshopWednesday seminars
- The Communication and Outreach Subcommittee published four articles in multiple outlets including *Genes to Genomes*, *The Scientist, ecrLife,* and *Frontiers for Young Minds*
- The Multimedia Subcommittee published the first two episodes of the new GSA podcast *Genetics in Your World.*
- The Accessibility Subcommittee was established, with members already making direct impact on GSA's virtual and in-person events.

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

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

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

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

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

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

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

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

GSA Equity and Inclusion Committee

The E&I committee has an ongoing project focused on increasing inclusion at conferences. The committee is currently co-chaired by Andrew Arsham and Alana O'Reilly, both Drosophilists.

In 2021, we produced Guidelines for DEI Scholarship Sessions at GSA Conferences, which gives rationale for including a session focused on DEI initiatives and practices in non-competing time slots at all GSA conferences. The guidelines also include advice for planning these sessions aimed at conference organizers, as well as a list of previous DEI scholarship sessions for reference.

Currently, the committee is working on a Vision for Inclusive Conferences that 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.

This document is designed to provide guidance to governing bodies on choosing an organizing committee and (co-)chair(s), bringing organizers on board with equity and inclusion goals, and adequately preparing organizers for the work ahead. We plan to have a draft of this portion of the document ready before Dros22 for discussion by FlyBoard.

It will also provide guidance to organizing committees on setting the scientific program (to include DEI scholarship, etc.), choosing an inclusive slate of invited/keynote/plenary speakers, choosing an inclusive group of session chairs, and practicing inclusion throughout all aspects of the meeting. This section of the document is underway and will be ready mid-2022.

The committee hopes that FlyBoard will review these suggestions and consider adopting them for future fly meetings.

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.

Communications

FlyNews: GSA formatted and sent the FlyNews on behalf of the *Drosophila* Board on February 15, 2022.
***Drosophila* Image Awards:** GSA provides design, IT, and administrative support for the *Drosophila* Image Awards and hosts the website. In preparation for the 63rd Annual *Drosophila* Research Conference, the website was recently updated in the Fall of 2021.
Community Notices: GSA is able to send occasional email blasts on behalf of the FlyBoard to our distribution list, such as the recent communications on the FlyBoard election. .

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 or disburses sums at the direction of the FlyBoard. Full details for that account can be found in the Treasurer's report.

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

The GSA Finance Committee of the Board of Directors determines the registration fees for the meeting and makes 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 March 3, 2022 the balance in the *Drosophila* Reserve was $205K, an 25% increase in value over the initial investment of $164K, and takes into account a total of $15K in awards to the Fly Community which were granted in 2021 and 2022.

Victoria Finnerty Fund

GSA maintains the Victoria Finnerty Fund as a restricted account for the Fly Community, from which grants approximating $5K are awarded for undergraduate travel to the *Drosophila* conference, annually.

A donation of $6K is provided by GSA from *Drosophila* Meeting 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 January 2022 the investment account balance was $26K and there was $5K in cash, for a total of $31K.

Larry Sandler Fund

The Larry Sandler Fund is held in a custodial capacity by GSA for the Fly Community and is invested in an account at Vanguard. The account has grown from $28K in 2003 to over $104K as of January 2022. In addition to covering expenses for the Larry Sandler Award winner, each cycle, the Fund (along with the *Drosophila* Reserve) has contributed to outreach awards granted by the FlyBoard in 2021 and 2022.

63rd Annual *Drosophila* Research Conference (2022)

Organizers

Erika Bach, Chair

Justin DiAngelo

Ellie Heckscher

Sally Horne-Badovinac

Artyom Kopp

2022 was another year of changes. With so much uncertainty and concern surrounding COVID-19, the GSA Board, along with the *Drosophila* Board, made the decision to plan a hybrid meeting for 2022. So while we were all hopeful to be able to meet in person, we wanted to have an option for those who could not or did not feel ready to travel. So this year is another year of experiments.

What's new for 2022?

Conference App - The conference app is an attendee's main resource. There will be no printed book this year (although one is available online for those who wish to print it). Once you download the App there is no need to connect to the internet except to download updates. You'll be able to send direct messages to other attendees, leave questions for speakers, view abstracts, make a personal schedule, and so much more.

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

An online audience - Nearly 500 people will be attending #DROS22 online. They join over 1,000 people attending in person.

Recordings - All plenary and platform sessions will be recorded and made available through the conference app through May 11.

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. If the author included their personal scheduling link, people will be able to set up a time to talk to the author. All in-person authors will display and present their poster during a specific timeframe then take their poster down so the next group can display their posters. With this year's special circumstances, and to allow for a little more room between posters, each poster will be displayed on a single 8' board rather than sharing a board with another poster. Authors have been asked to utilize 3'8" of space (the same as in past years) on the board to naturally create space between boards.

Health and Safety

Our top priority is the safety of our attendees. In-person attendees are required to wear the most protective masks they can access, ideally N95s or KN95s, while attending the conference. If you do not have access to a high-quality mask, a limited supply of complimentary masks are available at the Registration Desk in the Town & Country Ballroom foyer.

All rooms will be set with maximum seating so that attendees can sit at the spacing with which they are comfortable. The large keynote and plenary sessions will be held in Town & Country A and streamed in Town & Country B for those who want to spread out a little more. And of course, in-person attendees can also opt to participate online through the App.

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

All in-person attendees are required to be fully vaccinated, boosted, and show proof of a negative COVID-19 test taken within 72 hours of their arrival at the conference. Onsite PCR testing will be available for a fee and by appointment for in-person attendees who need or want to be tested for COVID-19 (e.g., to comply with international travel regulations).

All in-person attendees have been asked to daily self monitor for any symptoms (fever or chills, cough, shortness of breath, fatigue, muscle or body aches, headache, new loss of taste or smell, sore throat, congestion or runny nose, nausea, vomiting or diarrhea). If these symptoms appear, we can have a rapid test delivered to the guest's room (for those staying at the Town & Country). We ask that anyone experiencing symptoms not enter the meeting space.

What is Hybrid?

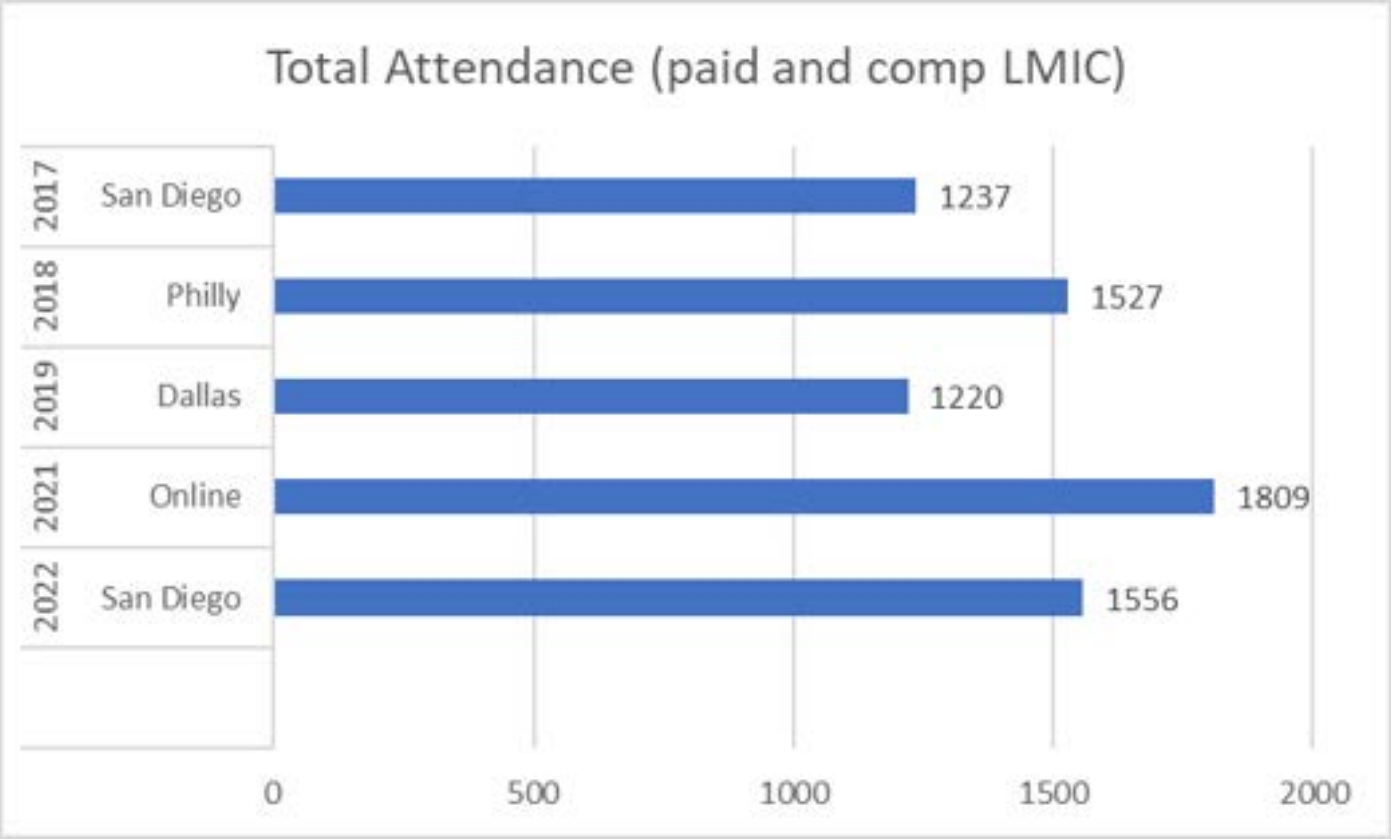
As defined by the Professional Convention Management Association (PCMA) hybrid is *a single event that serves both in-person and virtual audiences.*

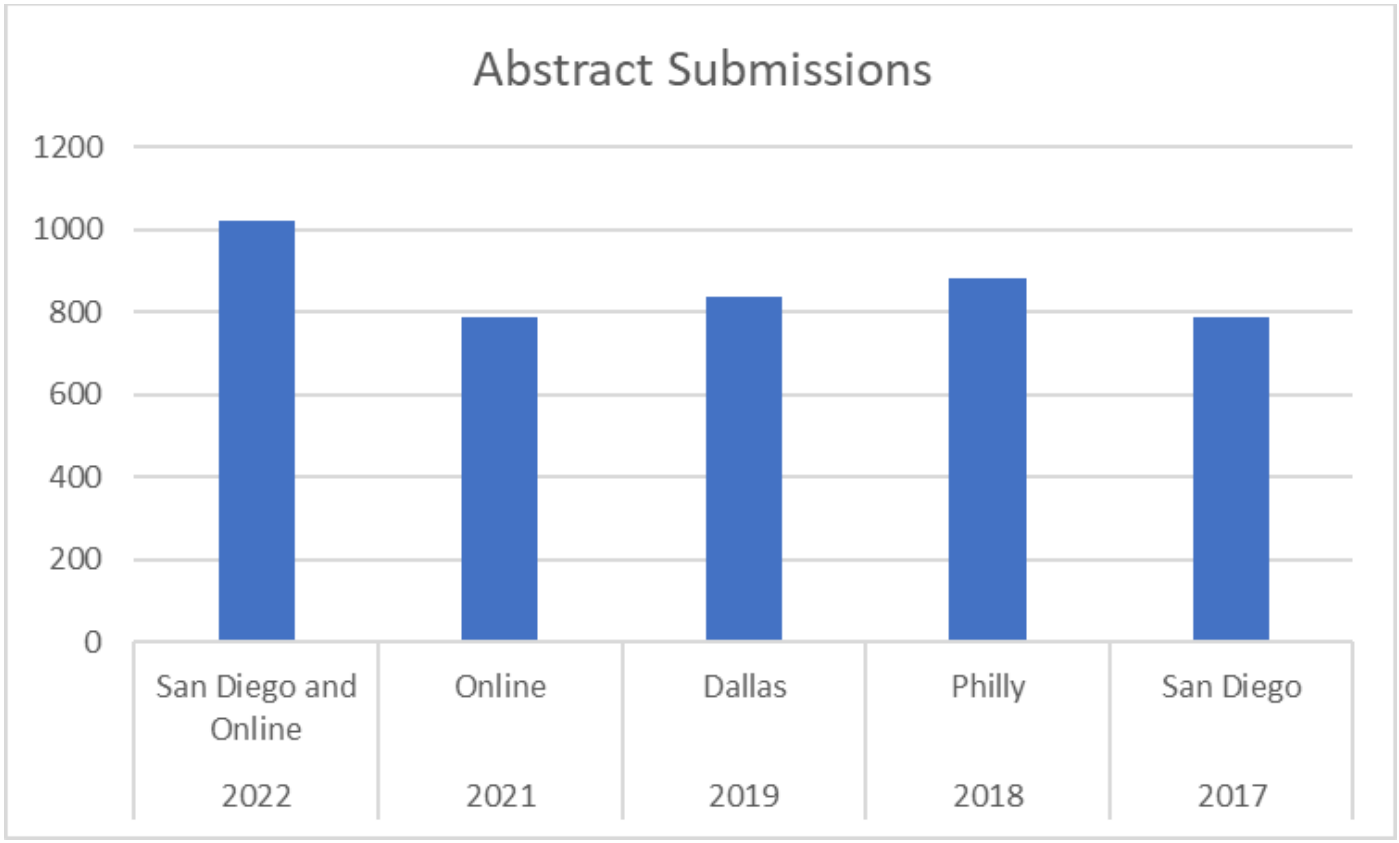
The professional development section outlines many of the conference components that are being held online and in-person. In addition, all abstract driven sessions, like the platform and plenary sessions, will be live streamed. Workshops are being held in-person and online based on the preference of the workshop organizer(s). Posters will be held in the traditional manner for those attending in person. All poster authors have the option of uploading a pdf and audio overview of their poster. Delegates can leave questions for the author in the App and, if the author provided a link to their personal scheduling program, people can set up an appointment to talk to the author.

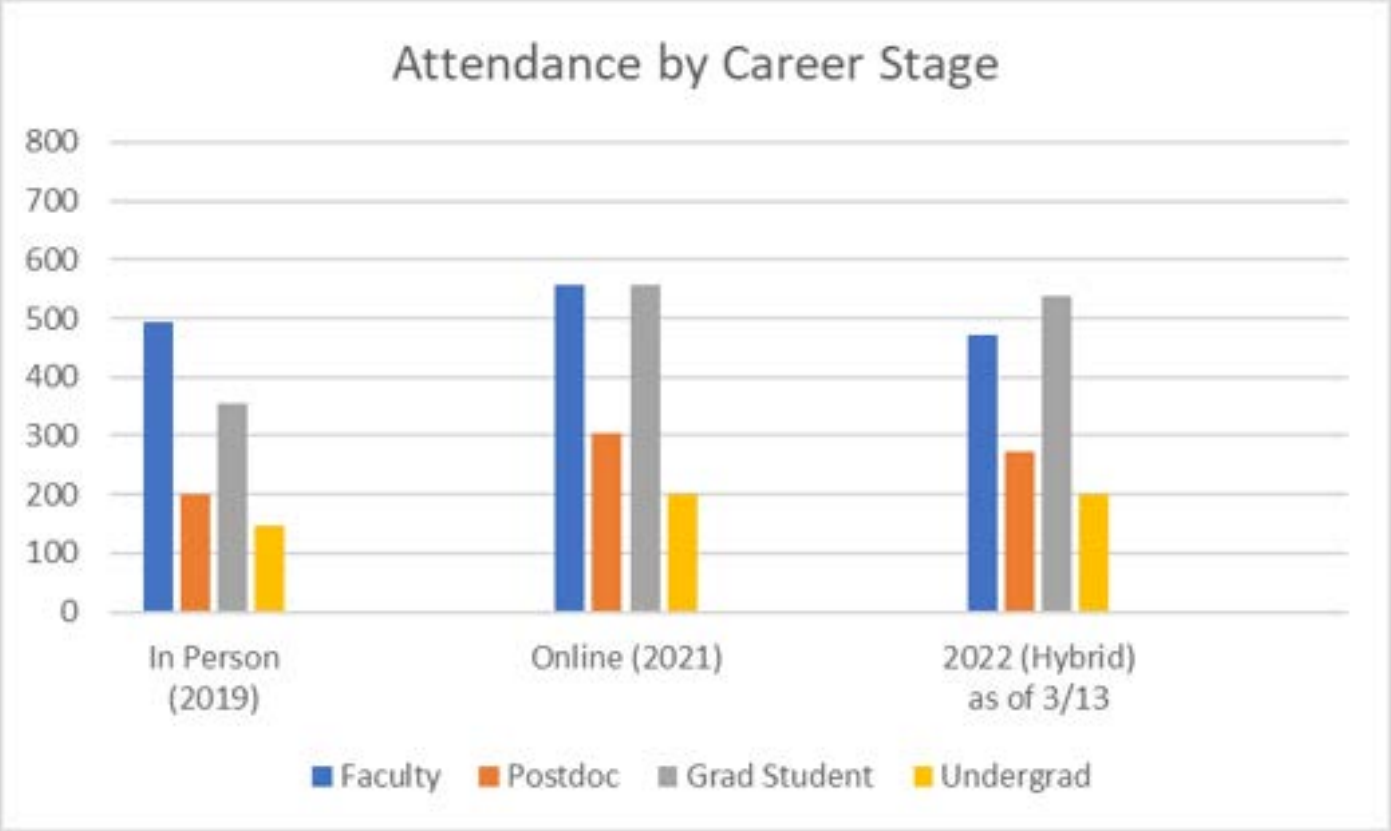
Exhibitors and Sponsors

We encourage everyone to stop by and say hello to the exhibitors. We appreciate their support. Burroughs Welcome provided funding for 46 people to attend #Dros22 online. The funding was specifically for people doing *Drosophila* research from low-income and middle-income economies.

#Dros22 by the numbers




Abstract Submissions
1200
1000
800
600
400
200
0
San Diego and Online
Online
Dallas
Philly
San Diego
2022
2021
2019
2018
2017



Future Meetings

March 1–5, 2023
64th Annual *Drosophila* Research Conference
Sheraton Grand Chicago
Chicago, IL

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

Update on the GSA Public Communications & Outreach Committee

This newly formed committee is tasked with "supporting the production of content relating to GSA's long-term public communication and engagement goals" that will "serve as a resource" for GSA members. GSA President and committee chair E. Jane Hubbard introduced the goals of this committee and related efforts in a February 2022 post in the GSA *Genes to Genomes* blog, *"You work on what?" Talking (basic) science*. Hubbard is joined on the committee by me, Elisabeth Marnik, and C. Brandon Ogbunu, and by GSA staff liaison Cristy Gelling. We have been gathering stories that connect from genetic model organism research to therapeutic treatments or other human health impacts. Big thanks to those of you who responded to inquiries from me or others last fall as we gathered stories. The committee will be sharing the stories with GSA members through posts at *Genes to Genomes*. –Stephanie E. Mohr

Report of the 2022 Fly Meeting Organizing Committee: Erika Bach (Chair), Justin DiAngelo, Ellie Heckscher, Sally Horne-Badovinac, Artyom Kopp

The 2022 Organizing Committee was assembled in 2021. Erika Bach (EB) was invited by Mariana Wolfner in August 2020 to chair the organizing committee. Erika invited Justin, Ellie, Sally, and Artyom to diversify expertise. The organizers communicated by email and monthly zoom meetings. All decisions were made by consensus following the opportunity for input from all committee members. Suzy Brown at GSA was involved at all stages of planning and participated in conference calls and group emails. In preparing this report, we have modeled it directly after the 2019 organizing committee report, to make comparisons between the last in-person meeting (2019) and this one.

Gratitude for the GSA Office

We are very grateful Suzy Brown, Tracey Depellegrin, Cristy Gelling, Sarah Bay and the rest of the GSA office for their assistance and participation in the organization of the meeting. Suzy provided timeline information, data from past meetings, valuable suggestions and points for deliberation. Suzy was very responsive to various questions and requests we made. Sarah Bay was the liaison to the GSA DEI committee.

Timeline and Overview of Meeting Organization

Discussions focused on various aspects of the meeting in the following chronological order: Keynote and Plenary speakers; platform sessions; overall program. We wanted to generate a program that would convey exciting and excellent science, with speakers representing the entire *Drosophila* community in terms of topics, gender, race, ethnicity, career stage and geographical location. The final program was decided in stages. The Keynote Speaker was set by **June 20, 2021**. Most of the Plenary speakers were set by **July 2021** with three additional plenary speakers added in **October 2021**. Platform session co-chairs were set by **Oct 2021**. The Platforms talks were set by **December 2021**. The overall timing of Events was decided by **February 2021**. The schedule and the lists of talks, posters, and abstracts are available online and through the #DROS22 Meeting mobile app or as a downloadable pdf file.

Keynote Speaker. For the opening night, there was consensus against holding a panel and preference for a single Keynote Speaker. We used a list of prior Keynote speakers as a starting point for consideration. We also considered speakers not on the list. After preliminary discussions of approximately 15 candidates, this list was narrowed down to 6, 3 males and 3 females. All of these candidates are exceptional senior scientists and excellent mentors. We also wanted to attract *Drosophila* neuroscientists back to the Fly Meeting. After a lengthy discussion, Chris Doe was selected by consensus and invited by email (EB). He accepted our invitation in **June 20, 2021**. The title of his talk is “Central Nervous System Development: Stem Cells to Circuits”.

Plenary Speakers. Through planning sessions with Suzy Brown and GSA, we initially decided to have 11 science Plenary Speakers and 3 Equity and Inclusion (E&I) Plenary Speakers. Nominations for plenary speakers were mostly restricted to those who had not previously presented in a Plenary session at the Fly Meeting in the past 10 years with a focus on mid-career or senior North American speakers and gender diversity. We used a list of prior Plenary speakers as a starting point for consideration for the science Plenary speakers. We also considered speakers not on the list. 45 candidate Plenary Speakers were initially nominated by the members of the organizing committee in **May 2021**. In **June and July 2021**, the committee had several zoom meeting where the candidates were discussed. The members of the organizing committee considered diversity of scientific subfields and geographical locations in

their discussion. We reached consensus on 11 science speakers. Invitations were sent by email on **July 5, 2021**. All invited speakers accepted and were committed with a few days' time of the invitation. In **September 2021**, a Flyboard member raised concerns that the Plenary Speaker list was not sufficiently diverse. The organizing committee obtained feedback from the Flyboard and in early **Oct 2021**, two more Plenary science speakers were chosen and they accepted within days of being invited. One Plenary science speaker cancelled her attendance at Dros22 in **Feb 2022**. The organizers decided to reduce the science Plenary session by one slot and not find a substitute at this late time. The final 12 Plenary science speakers are: Nick Baker, Michelle Bland, Heather Broihier, Melissa Harrison, Robert Johnston, Yanlan Mao, Daniel Matute, Marco Milan, Lucy O'Brien, Prashanth Rangan, Mark Rebeiz, Guy Tanentzapf.

We considered Plenary speakers for the E&I Plenary session to present scholarship on E&I topics. Based on nominations from the organizing committee, feedback from the prior organizers and the GSA DEI committee, our organizing committee unanimously chose 3 speakers - Shaila Kotadia, Marguerite Matthews, Todd Nystul – all of whom accepted by **Oct 2021**.

The organizing committee will serve as co-chairs for the science plenaries. The committee decided to select faculty with E&I expertise as co-chairs of the E&I Plenary session. The committee chose one male and one female, who both declined. The two alternates, however, accepted. The co-chairs (Andrew Arsham and Rachel Smith-Bolton) were set in **Jan 2022**.

The 2022 organizers implemented several changes to the format from the 2021 organizers who planned an entirely virtual meeting.

- We decided to return to a list of Abstract Categories and Keywords used in Fly Meetings prior to the 2021 meeting.
- We decided not to have "poster previews", also known as "lightning talks", particularly since we were planning for a hybrid meeting.

EB wanted to include a PUI faculty on the organizing committee, as the 2021 organizers did. We encourage future organizers to consider doing this. If this is not possible, perhaps the future organizers could consider liaising with the Flyboard PUI representative.

In **August-September 2021,** co-chairs for each Platform Session were nominated, discussed and decided by consensus. The co-chairs were then asked to solicit a postdoc co-chair, typically a senior postdoc in the lab of one of the faculty co-chairs. Invitations to serve as platform session co-chairs were sent on **October 1, 2022**. Nearly all faculty and postdoc co-chair positions were filled by the end of **October 2018**. In **March 2022**, two faculty co-chairs decided not to attend the 2022 Fly Meeting in person based on COVID concerns. These two sessions ("Immunity and the microbiome" and "Cell division and cell growth") will be moderated by the other faculty co-chair and the postdoc co-chair.

The abstract deadline was **November 18, 2021**. From the submitted abstracts, the Organizing Committee allocated the number of talks per Platform Session and sent the co-chairs guidelines for abstract review and talk selection. Co-chairs deliberated together to provide ranked lists of selected abstracts for talks, with the opportunity to review abstracts that listed the topic as a primary or secondary choice, by **December 15, 2021**. The Organizers reviewed the ranked lists to remove duplications across Platforms and to ensure diversity in presenter gender, career stage and individual laboratories represented. Final Platform talks were assigned by **January 6, 2022**.

2022 Fly Meeting Attendance
Attendance is **up by 22% compared to 2019** – the last in-person meeting - with 1556 attendees (1,061 in-person and the rest online) as of March 24, 2022. For historical comparison, earlier Fly Meeting attendees were: 1809 (2021, fully online), 1220 (2019), 1527 (2018) and 1237 (2017). However, the total number of in-person attendees is not greater than 2019. This is might be due to the pandemic and people electing not to attend conferences in person.

Compensation for organizers, speakers and special awards
Free conference registration was granted to the meeting Organizers (5); the Keynote (1) and Plenary Speakers (15); and the Exhibitors that purchased booths. Everyone had to cover their own lodging and travel costs. The Larry Sandler Award Winner receives complementary airfare, registration, lodging, and GSA lifetime membership. Victoria Finnerty Memorial Fund travel grants were awarded to undergraduate researchers presenting posters and these recipients are chosen by a Flyboard sub-committee.

Detailed description of program components
Opening Session and Keynote Speaker. The 2022 Meeting will follow the traditional program on the first night, with introductions and a brief historical perspective, announcements from GSA, the Sandler lecture and a Keynote lecture.

Plenary Speakers**.** The criteria for choosing Plenary Speakers were scientific importance and novelty, breadth of topics, ability to engage the audience, and a balance in gender, diversity, career stage, and foreign/domestic location. In addition, we wanted to avoid inviting people who have presented plenary talks in the past. Of the 15 plenary speakers, 13 are in North American institutions. Plenary speakers are a diverse group that we believe reflect the *Drosophila* community: (1) there was gender balance - 8 were males and 7 were females, (2) 40% are diverse (including Asian, Hispanic, and African American).

Hybrid format. The organizers and the platform session chairs did not factor in-person attendance into the decision-making for choosing abstracts for oral presentations. We believed that this is more inclusive and allows for selection of the most exciting science. As a result, some of the oral presentations will be virtual.

Abstract Categories and Keywords. The 2022 Organizers collectively made the decision to return to the abstract categories used by the 2019 Organizers and added “Diversity, equity and inclusion” from 2021. This reorganization resulted in 18 final abstract categories. As organizers, we sought to recruit two faculty co-chairs who had complementary expertise in the different sub-areas of their categories These 18 categories are also used for poster sessions. The **2022 Abstract Categories** are in **Table 1**.

Submitted abstracts. **994 abstracts** were submitted under **18 categories** and associated with keywords. Totals in recent years were 832 (2019), 889 (2018), 716 (2017), 692 (2016/TAGC), 977 (2015), 894 (2014), 966 (2013), 1005 (2012). Thus, 2022 reflects an **17% increase in abstract submissions over 2019**. There were **556 requests** in the primary category for **154 Platform talks**, which resulted in a **28% success rate.** This was lower than the 37% success rate in 2019 and might reflect in part the fact that we had fewer platform session talks because we added a stand-alone E&I Plenary session. The number of total abstracts varied across sessions (see **Table 1**). The highest number of abstracts was submitted in “Models of Human Disease”, with 96 abstracts as a primary choice. Excluding “Educational Initiatives” and “DEI”, the lowest number of abstracts was in “Signal transduction”, with 4 abstracts as a primary choice. The fraction of abstracts in a given category that requested talks also ranged widely,

from 71% in “Cell biology: Cytoskeleton, organelles and trafficking” to 44% in “Neural circuits and behavior”.

Table 1. Categories and abstracts submitted							
Received	**Request Oral**	**% Request Oral**	**Selected for Oral**	**% Selected for Oral**	**Request Poster only**	**Programmed as Poster**	**Session**
32	19	59.38%	6	31.58%	13	26	Cell Stress and Cell Death
51	27	52.94%	6	22.22%	24	45	Immunity and the microbiome
92	49	53.26%	16	32.65%	43	76	Evolution
57	29	50.88%	8	27.59%	28	49	Stem cells, regeneration and tissue injury
72	40	55.56%	8	20.00%	32	64	Reproduction and gametogenesis
67	37	55.22%	8	21.62%	30	59	Regulation of gene expression
48	27	56.25%	8	29.63%	21	40	Chromatin, epigenetics and genomics
92	53	57.61%	14	26.42%	39	78	Patterning, morphogenesis and organogenesis
4	0	0.00%	0	0.00%	4	4	Signal transduction
59	42	71.19%	14	33.33%	17	45	Cell biology
42	22	52.38%	6	27.27%	20	36	Cell division and cell growth
87	47	54.02%	14	29.79%	40	73	Physiology, metabolism and aging
79	44	55.70%	12	27.27%	35	67	Neural development and physiology
69	33	47.83%	12	36.36%	36	57	Neural circuits and behavior
96	59	61.46%	14	23.73%	37	82	Models of human disease
38	23	60.53%	8	34.78%	15	30	Techniques and technology
9	5	55.56%	0	0.00%	9	9	Educational initiatives
0	0	0.00%	0	0.00%	0	0	Diversity, equity and inclusion
994	**556**		**154**		**443**	**840**	**Total**

Platform Session organization. Eight categories that had the most abstracts were given two split sessions (I & II). “Evolution I and II” were given 16 talks, spilt into two sessions of 8 talks on separate days. “Neurodevelopment I”, Neurobehavior I” and “Neurodevelopment II/Neurobehavior II” were given a total of 24 talks across the three sessions. “Models of Human Development I and II”, “Cell Biology I and II”, “Patterning and Morphogenesis I and II”, “Physiology, Aging, and Metabolism I and II” were given 14 platform talks each, split into two sessions or 8 talks and 6 talks on different days. Four categories were assigned a single session of 8 talks: “Stem cells, regeneration and tissue injury”, “Reproduction and gametogenesis”, “Regulation of gene expression”, “Chromatin, epigenetics and genomics”.

Three categories were assigned a single session of 6 talks: “Immunity and the microbiome”, “Cell Stress and Cell Death” and “Cell division and cell growth”. “Techniques & Technology” was given 8 talks and will be held on Saturday evening as a stand-alone Platform session. All talks were selected from the abstracts. “Signal Transduction”, “Educational Initiatives” and “DEI” did not receive enough abstracts for a platform session.

Like the 2019 Organizers, the 2022 Organizing Committee designated two co-chairs to each session. The chairs were chosen for the scientific excellence but also to ensure diversity across many dimensions including gender, race, geography and institution type. The faculty co-chairs are a diverse group that we believe reflects the *Drosophila* community. Of the 30 faculty co-chairs, 57% are female, 43% are male, 10% are PUI faculty, 13% are BiPOC, 16% are Asian and 1 is transgender. The co-chairs were asked to invite a postdoc co-chair, typically a postdoctoral trainee or a new faculty, for each session. The reason for the postdoc co-chairs is to give them exposure, allow them to network and interact with more senior colleagues, and to help in judging the poster session. The 2022 **Platform Session co-chairs** who selected abstracts for Platform presentations are listed with affiliation by session in **Table 2**.

The Organizers determined the number of allocated talks to each Platform Session based on the number of submitted abstracts (see **Table 1**). The co-chairs were asked to generate a ranked list for selected talks with a target number of two more abstracts than the allocated number of talks for that session. The co-chairs were given **2.5 weeks** from November 28 to December 15, 2021 to review and submit their ranked lists of selected abstracts for Platform talks to the Organizers. The Organizers reviewed their choices and selected final talks by **January 6, 2022**. The abstracts submitted were reviewed as primary choice, but the co-chairs were instructed to carefully examine all abstracts in their session and flag abstracts more suitable for the secondary choice either as talks or posters. A few such abstracts were flagged and moved into more appropriate sessions. The Organizers ensured that there was a balance in gender and career stages of the selected abstract speakers within a session. To avoid over-representation of any individual laboratory at the Meeting, the Organizers looked through selected talks for ones from the same laboratory. We followed the rule that no one lab would present more than two platform talks, and these two talks would be in different sessions.

Poster Sessions. There are currently **840 abstracts** scheduled to be presented as posters. There were 994 abstracts submitted in total, including the 154 abstracts selected for Platform talks. Late abstracts were accepted through **January 10, 2022**. The breakdown of posters by category for the regular abstracts is shown in the **Table 1.**

Poster Awards. A total of up to six poster awards are slated to be given to the top three Graduate student posters (1st, 2nd and 3rd) and the top three Undergraduate posters (1st, 2nd and 3rd). This remains the same from the 2019 meeting. Postdoctoral poster awards will not be given, since several of the judges are the Postdoc trainees functioning as Platform Session co-chairs. Awards will be given based on merit only, so there is the option that fewer than six awards will be given. The prizes are $500 for 1st place, $300 for 2nd place and $200 for 3rd place. Based on the recommendations of the previous organizers and GSA and what was done in 2019, posters will be judged initially by the postdoc co-chairs and other postdocs who have volunteered to help judge to select the best posters in their group. To simplify judging, judges have the option to identify a short list of potential poster award winners for each category (graduate student and undergraduates) based on abstracts for review instead of the entire group in that category. The selection will be based on science and poster design, not on the poster presentation, given the time constraints of the meeting. The judges will communicate the recommended posters for each session to Erika Bach by Saturday. All five Organizers will

Table 2. Platform Session co-chairs		
Session	**Chair**	**Institution**
Cell Stress and cell death	Deepika Vasudevan	University of Pittsburgh
	Andreas Jenny	Albert Einstein College of Medicine
	Lydia Grmai*	University of Pittsburgh
Immunity and the microbiome	Will Ludington	Carnegie Institution for Science
	Nichole Broderick	Johns Hopkins
	Jessamyn Perlmutter (Jessie)*	University of Kansas
Evolution	Ana (Carolina) Llopart	University of Iowa
	Geoff Findlay	Holy Cross (PUI)
	Cécile Courret* Llewellyn Green*	University of Rochester; University of Houston
Stem cells, regeneration and tissue injury	Lesley Weaver	Indiana University
	Adrian Halme	University of Virginia School of Medicine
	Mahi Rahman*	University of Utah - Huntsman Cancer Institute
Reproduction and gametogenesis	Kari Lenhart	Drexel University
	Jenny Jemc Mierisch	Loyola University of Chicago
	Rafael Demarco *	University of California San Francisco
Regulation of gene expression	Steve Deluca	Brandeis University
	Trisha Wittkopp	University of Michigan
	Colleen Hannon*	University of California Berkeley
Chromatin, epigenetics and genomics	Julie Secombe	Albert Einstein College of Medicine
	Amanda Amodeo	Dartmouth
	Dahong Chen *	NIH
Patterning and morphogenesis	Seyeon Chung	Louisiana State University
	Todd Blankenship	University of Denver
	Raj Loganathan*	Johns Hopkins University School of Medicine
Cell biology: Cytoskeleton, organelles and trafficking	Claire Thomas	Penn State
	Blake Riggs	San Francisco State University
	Marco Monroy*	San Francisco State University
Cell division and cell growth	Sarah Siegrist	University of Virginia
	Wu-Min Deng	Tulane University
	Gary Teeters*	University of Virginia
Physiology, metabolism and aging	Ethan Greenblatt	University of British Columbia
	Laura Musselman	Binghamton University
	Juliet Girard*	University of California Los Angeles
Neural development and physiology	Xin Li	University of Illinois

	Vanessa Auld	University of British Columbia
	Yu-Chieh David Chen*	New York University
Neural circuits and behavior	Karla Kaun	Brown University
	Marie Suver	Vanderbilt
	John Hernandez*	Brown University
Models of human disease	Tirtha Kamal Das	ICAHN School of Medicine at Mount Sinai
	Daniela Zarnescu	University of Arizona
	Rebekah Keating Godfrey*	University of Arizona
Techniques and technology	Ben White	NIH
	Jonathan Zirin	Harvard Medical School
	Oguz Kanca *	Baylor College of Medicine
	* denotes postdoc co-chair	

meet Saturday to determine the poster award winners. The winners will be recognized after the Technology and Techniques Plenary session Saturday evening.

Workshops. Workshop applications and selection criteria were similar to past meetings. seven applications were received and reviewed. One application, "Understanding and modeling switch-like gene regulation in *Drosophila*", was viewed as impractical for the venue and rejected. The other six applications were approved. In addition, GSA will present several career-oriented Workshops on online prior to the start of the in-person portion of the meeting. The major Workshop Session will be Thursday night from 7:45-9:45 PM. The Ecdysone Workshop will take place at its historic pre-meeting time on Wednesday from 1:30 PM - 4:30 PM. Two workshops will be held online before the start of the in-person portion of Dros22.

Workshops listed in order of the program:
(1) Developmental Mechanics (online) - Friday, April 1
(2) Research, Teaching, and Careers at Primarily Undergraduate Institutions (PUIs) (online) Friday, April 1
(3) Ecdysone Workshop – Wednesday
(4) Everything you ever wanted to know about sex - Thursday
(5) Inter-organs communications in the era of Metabolomics - Thursday
(6) Flies on drugs – drug discovery approaches, challenges and opportunities - Thursday

Fundraising
Anne-Marie Mahoney from GSA submitted a grant to the Company of Biologists to offset registration costs for attendees from low and middle income countries (LMICs). The grant was awards in Jan 2022, and there were 55 applications for LMIC waivers so this will help cover the cost.

Planned assistance to future *Drosophila* Conference Organizing Committees
All of the material available to the 2022 organizers will be placed in a Dropbox folder, together with the information EB received from the 2021 Organizers. The chairs of future organizing committees will be invited to share the folder and will have access to all information. The information includes worksheet templates, tables listing previous speakers and session co-chairs, and templates for solicitation letters sent to potential session chairs, speakers.

BLOOMINGTON DROSOPHILA STOCK CENTER

Stock Holdings as of March 10, 2022

- 79,218 stocks with 83,463 unique genetic components
- 17,471 annotated *D. melanogaster* genes are associated with alleles, constructs, deficiencies, or duplications in the collection
- 12,620 annotated *D. melanogaster* genes are associated with alleles or constructs in the collection
- 2,372 non-fly genes (including 2,143 human genes) are associated with constructs in the collection

2021 Use Statistics We are seeing a slow but meaningful recovery from the dramatic impacts of COVID in 2020. In calendar year 2021, the 185,018 samples sent in 11,151 shipments represented an increase of 24,913 (16%) samples and 2,107 (23%) shipments from 2020. While this is a great sign that ordering activity is recovering, these increases do not fully offset the 22% decrease in samples shipped in 2020 compared to 2019.

On average, we saw 2.2 orders per stock with a range of 0 to 143. 55% of stocks were ordered at least once, 11% were ordered 6 or more times, and 4 stocks were ordered >100 times. The most popular stock was Canton-S (#64349). 76% of stocks available for 2019–2021 received at least one order demonstrating that the majority of the collection is being used by the fly community.

User base The number of BDSC users continues to grow:

- 3,711 registered user groups, 1,848 of which ordered stocks in 2021
- 8,789 registered users, 2,508 of whom ordered stocks in 2021

Growth 2,301 stocks were accessioned in 2021:

- 465 CRIMIC stocks from Hugo Bellen, Norbert Perrimon and colleagues
- 408 UAS-human cDNA stocks from Hugo Bellen, Sue Celniker and colleagues
- 154 stocks with split-GAL4 driver pairs identifying CNS cell types from Janelia Research Campus
- 112 stocks expressing tagged transcription factors from the modERN project
- 99 stocks expressing guide RNAs for gene knockout from Deepti Trivedi, Padinjat Raghu and colleagues
- 89 stocks expressing guide RNAs for gene knockout from the Transgenic RNAi Project
- 73 stocks expressing guide RNAs for gene overexpression from the Transgenic RNAi Project
- 901 assorted stocks from the community at large

Staff 62 stockkeepers (8 full-time and 54 part-time to make 25 full-time equivalents) and 9 managers/scientists.

Funding We are in year 3 of a 5-year grant from NIH with $445,973 in direct funds contributed by OD, NIGMS and NICHD and $86,855 of supplemental funds from NINDS for maintenance and distribution of split-GAL4 stocks. Fee income covers our remaining expenses and, in recent years, has accounted for ~79% of our regular funding. OD provided a $214,899 administrative supplement for 2020–2021 for upgrades to our database infrastructure. In the current grant year, OD provided a $222,187 administrative supplement to help us recover from operational setbacks caused by the COVID pandemic and a $95,543 administrative supplement to improve the media kitchen and dishwashing facility. We also receive salary support for participating in a consortium project to improve stock resources for fourth chromosome genes.

New Stocks We expect to add ~2,000 new stocks in 2022:

- 700 CRIMIC/KozakGAL4 stocks from Hugo Bellen, Norbert Perrimon and colleagues
- 300 guide RNA and RNAi stocks for SARS-CoV2 interactome genes from the Transgenic RNAi Project
- 200 miscellaneous guide RNA and RNAi stocks from the Transgenic RNAi Project
- 150–200 UAS-human cDNA stocks from Hugo Bellen, Sue Celniker, and colleagues
- 55 stocks with SARS-CoV2-related genes driven by UAS from Hugo Bellen and colleagues
- 50 CRISPR knock-in lexA and QF2 driver stocks from the Transgenic RNAi Project
- 50 stocks expressing tagged transcription factors from the modERN project

- 500 assorted stocks from the community at large

Pruning We conducted no systematic culls during 2021. We lost or discarded 249 assorted stocks.

Scientific Advisory Board

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

Intramural Advisory Board

- Justin Kumar
- Jason Tennessen

Vienna Drosophila Resource Center (VDRC), Vienna, Austria

The VDRC (**www.vdrc.at)** is part of Vienna Biocenter Core Facilities, a **non-profit** research infrastructure. Its mandate is to maintain and distribute transgenic RNAi lines and other resources to Drosophila researchers, both locally and worldwide, and to further develop and expand VDRC resources according to the emerging new technologies and community needs.
User fees are subsidized ~30% by the Austrian Federal Ministry for Science and Research and the City of Vienna.

Key changes during 2021

- 461 new UAS-sgRNA (Heidelberg, HD-CFD) lines added for CRISPR-mediated genome engineering.
- 50 new lines acquired in "Other Resources" from the European community.

Usage Statistics 2021

- **30,839** stocks delivered to **612** user groups in **1,317** separate orders.
- Average orders/stock = 1.2.
- 54% of stocks were ordered at least 1x.

Resources as of March 2022

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

- 23,416 RNAi lines (12,934 in GD, 9,679 in KK and 803 in the shRNA collection).
- 21 toolkit stocks used for the construction of the RNAi collections.
- Collectively, the GD, KK and shRNA libraries target a total 12,671 Drosophila protein-coding genes (91%). For over 8000 genes, more than one independent RNAi line is available through the VDRC.
- 1,920 UAS-sgRNA and 23 Cas9 toolkit lines for CRISPR-mediated genome engineering (Heidelberg, HD-CFD).
- 200 enhancer-GAL4 lines (VTs, Vienna Tiles). Expression patterns annotated in adult brain and embryo. Searchable databases available.
- 895 Tagged FlyFos TransgeneOme (fTRG) lines.
- A small, but growing number of plasmids and stocks made available to the community from Private Stock Collections, including mutant alleles, tagged constructs and reporters.
- 13,848 DNA constructs used for the generation of the GD collection.

Services

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

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

Future

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

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

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

KYOTO Drosophila Stock Center

TAKANO-SHIMIZU, Toshi

Organization

On April 1, 2022, Kyoto Institute of Technology has just reorganized the center into the KYOTO Drosophila Stock Center, with a renewed aim to reinforce its activities as a resource and research center.

Funding

Together with National Institute of Genetics (NIG-Fly) and Kyorin University (KYORIN-Fly), we have applied for the fifth phase of National BioResource Project (renewal from FY 2022 through 2026), which is our major funding source operated by Ministry of Education, Culture, Sports, Science and Technology (MEXT). Although it is likely that the funding will be renewed, but a reduction in funding is inescapable. Therefore, we purged 1,125 GS insertion lines in 2021 and plan to again purge further stocks in 2022.

PGC cryopreservation

We developed a cryopreservation and transplantation method for primordial germ cells (pole cells) and its paper has been published in Communications Biology (2021, DOI: https://doi.org/10.1038/s42003-021-02692-z). We are planning to launch a cryopreservation service for stocks which was or will be donated to KYOTO Stock center.

Humanized fly

In collaboration with the Bellen and Yamamoto lab at the Baylor College of Medicine and the Celniker lab at the Lawrence Berkeley National Laboratory, we made 974 UAS-human ORF stocks in FY 2021 and now, in total, 2,623 stocks are available at KYOTO stock center.

Drosophila Genomics Resource Center (DGRC): Booth #7 Poster # 1025A

Critical Changes to Report:

The DGRC now provides Research Resource IDentifcation (RRID) for all of our reagents.

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

We are looking to hire another research technician. Please have any candidates contacts us. dgrc@indiana.edu or visit our booth/poster

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

Funding: NIH P40OD010949 - The DGRC is entering our final year (April 1, 2022 to March 31, 2023) of our five-year cycle. We will be submitting our renewal application by May 26, 2022. We will/have been asking for letters of support from the Drosophila community. Also, the demand for DGRC reagents has returned to pre-pandemic levels.

Year	Vectors/cDNAs Shipped	Cell Lines Shipped	Products Shipped[1]
2017	2965	230	3522
2018	2357	250	3039
2019	1894	268	2995
2020	1645	171	2381
2021	1741	239	2459

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

DGRC Publications (2021):

- Mariyappa, D., Han, S. Basting, P.J., Dias, G.B., Luhur, A., Zelhof, A.C., Bergman, C.M. (2021). A novel transposable element based authentication protocol for Drosophila cell lines. G3 2021 Nov 25;jkab403 PMID: **34849844**,

- Han, S. Basting, P.J., Dias, G.B., Luhur, A., Zelhof, A.C., Bergman, C.M. (2021). Transposable element profiles reveal cell line identity and loss of heterozygosity in Drosophila cell culture. Genetics 2021 Oct 2;219(2):iyab113. PMID: **34849875**, PMCID: PMC8633141

- Mariyappa, D., Luhur, A., Overton, D., Zelhof, A.C. (2021). Generation of Drosophila attP containing cell lines using CRISPR-Cas9 G3 2021 Aug 7;11(8):jkab161. PMID: **33963853**, PMCID: PMC8496291

- Luhur, A., Mariyappa, D., Overton, D., Zelhof, A.C. (2021). Serum-free adapted Drosophila S2R+ line is amenable to RNA interference. MicroPubl Biol. 2021 Jan 29;2021:10.17912/micropub.biology.000362. PMID: **33537561**, PMCID: PMC7846936

New Product/Services added in the past year:

Services:

a. Cell authentication service – With the development of a protocol to authenticate Drosophila cell lines, we now offer the research community a service to authenticate their working cell lines for a fee.
b. Transgenic cell service – With the generation of our attP containing cell lines, we now offer to the research community a fee-based service to generate stable cell lines containing their transgenic construct of choice.

Cell Lines Added:

#	DGRC#	Cell line	NIH Award
1	315	S2R+-attP-99F8	2P40OD010949
2	316	S2-DGRC-attP-25C6	2P40OD010949
3	317	Kc167-attP-25C6	2P40OD010949
4	318	Kc167-attP-99F8	2P40OD010949
5	319	ML-DmBG2-c2-attP-25C6	2P40OD010949
6	320	ML-DmBG3-c2-attP-25C6	2P40OD010949
7	321	ML-DmBG3-c2-attP-99F8	2P40OD010949
8	322	OSC:eFH-piwi	Intramural NIDDK
9	333	Sua-5B-IE8	P41 GM132087
10	334	Sua5B-IE8-Act::Cas9-2A-Neo	P41 GM132087
11	335	NAMRU2-CQ-01-1.7	P41 GM132087
12	336	C6/36-HE8	P41 GM132087

Vector/DNA Reagents added

Reagent(s)	Originating Lab	Description (number)	NIH grant/Other funding
CRISPR vectors	Haase Lab	Vectors (4)	ZIA DK075111
Turbo ID vectors	Perrimon and Ting Labs	Vector (2)	R01 CA186568 DP2 GM119136 T32 GM007276 HHMI
CRISPR and RMCE vectors	DGRC	Vectors (7)	P40 OD010949
Nanotags and Nanobody vectors	Perrimon and Hidde Ploegh Labs	Vectors (18)	P41 GM132087 HHMI
Mosquito CRISPR/Cas9 vectors	Rice Lab	Vectors (3)	R01 AI116943 F32 AI120579
GFP-tagged nanobody vector	Stathopoulous Lab	Vectors (1)	R35 GM118146 American Heart Association
CasRx vectors	Akbari Lab	Vectors (18)	DP2 AI152071 Defense Advanced Research Project Agency
LexA WALIUM vector	Kim Lab	Vectors (1)	T32 HG000044 R01 DK107507 R01 DK108817 U01 DK123743 P30 DK116074
Other funding sources/Non-US Labs			
Nanobody vector	Vincent and McGough Labs	Vectors (1)	Non-US Lab
Auxin-inducible, GAL4 compatible vector	Southall Lab	Vectors (1)	Non-US Lab
Light-Inducible Nuclear Export System (iLEXY) vectors	Furlong Lab	Vectors (6)	Non-US Lab
Light-gated expression vector	Borst Lab	Vectors (1)	Non-US Lab
Human cDNA expression clones for Drosophila	Berkeley Drosophila Genome Project / Genome Disruption Project	Clones (1573)	R01GM067858

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

We focus on developing and improving technologies, and help other labs use them to study many topics. Specifically, we focus on cell-based and *in vivo* technologies that can be applied to study *Drosophila* and mosquitos. In addition, we use our well-established infrastructure to build large-scale *in vivo* fly stock collections, and to maintain and develop bioinformatics tools that support these technologies and others. Below, we outline what's new in the past year in our three main areas of focus: cell-based technologies, *in vivo* technologies, and bioinformatics resources. We then report on our outreach efforts and list recent preprints and publications.

I. DRSC: The DRSC serves as an NIH NIGMS P41-funded Biomedical Technology Research Resource (DRSC-BTRR) with a focus on technology development in *Drosophila* and mosquitos. Since our last report, the DRSC-BTRR:

- Continued to distribute dsRNA libraries for *Drosophila* cell screens and share related knowhow and reagents for functional genomics technologies
- Continued to develop new Cas types, libraries, and cell-based assays for CRISPR pooled-format screening in *Drosophila* cell lines
- Continued to develop libraries, modified cell lines, and cell-based assays for CRISPR pooled-format screening in mosquito cell lines
- Actively engaged in 18 Driving Biomedical Project (DBP) and 7 service collaborations, with labs in CA, IA, MD, MA, PA, RI, TX, NV, NY, and UT in the USA, and in the Czech Republic, France, Slovenia, and the United Kingdom
- Published research and technology-focused papers and preprints (see below)

Of note for the DRSC future: The P41 BTRR mechanism is transitioning to the RM1 Biomedical Technology Development and Dissemination Center mechanism, plus tech-focused R21s and R01s. We expect to apply in early 2023 to become the DRSC-BTDD.

II. TRiP: The TRiP remains focused primarily on building CRISPR-related fly stocks and other stocks for testing and implementing new technologies. Since our last report, we:

- Generated over 500 new fly stocks as part of the TRiP CRISPR-KO, TRiP-CRISPR-OE, and paralog double-knockout collections, and deposited 300 fly stocks to BDSC
- Began a new project to make an RNAi and CRISPR fly stock resource targeting ~300 fly orthologs of human genes identified as SARS-CoV-2-interactors
- Generated >30 LexA and QF tissue-specific driver lines using CRISPR/Cas9-mediated knock-in that will be deposited soon to BDSC
- Tested new applications and versions of CRISPR/Cas
- Deposited 16 lines to BDSC that can be used to detect any nanobody-epitope tagged protein of interest, as described in Xu et al. *eLife*
- We also note that in 2021, the BDSC sent 62,622 subcultures of TRiP stocks to 1,340 different user groups across the US and in 43 other countries

III. DRSC Bioinformatics:

- Performed routine maintenance and updates to existing tools for reagent design (e.g., Find CRISPRs 3), reagent identification (e.g., UP-TORR), and data view (e.g., RSVP)
- Add more functions and features to existing tools
    - added new species and algorithms to our ortholog prediction tool DIOPT
    - enhanced visualization and data mining at the scRNA-seq data portal
    - expanded mosquito GuildeXpress to cover more species and datasets

    - expanded DRscDB with Fly Cell Atlas datasets.
- Developed or in the process of developing new tools.
    - Launched PathOn for analysis of signaling pathways in bulk RNAseq datasets
    - Launched FlyPhoneDB for analysis of cell-cell communication in single-cell RNAseq datasets
    - Worked with Erika Larschan's group to develop and launch TIMEOR, a tool of analyzing temporal regulatory mechanisms from bulk RNAseq datasets
    - Continued to work with FlyBase on a gene set enrichment tool, which has been expanded to cover more species and more gene sets

IV. Training & Dissemination: We continue to inform the *Drosophila* community about our technologies in the following ways:

- Held DRSC/TRiP virtual 'Office Hours' in fall 2021 (view summaries here)
- Presented on technologies at the 2021 virtual Boston Area Drosophila meeting
- Presented on technologies at several other virtual conferences and workshops
- Continued to update our website with new protocols, publications, and more
- Continued to update *Drosophila* Models of Human Diseases
- Continued to update community news and events at the Fly Research Portal
- Provided modified *Drosophila* and mosquito cell lines to the DGRC
- Provided new fly stocks to BDSC

V. Recent preprints and publications from the DRSC/TRiP

New bioinformatics tools:

Conard AM, Goodman N, Hu Y, Perrimon N, Singh R, Lawrence C, Larschan E. **TIMEOR: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data.** Nucleic Acids Res. 2021 Jul 2;49(W1):W641-W653. PMID: 34125906; PMCID: PMC8262710.

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

Ding G, Xiang X, Hu Y, Xiao G, Chen Y, Binari R, Comjean A, Li J, Rushworth E, Fu Z, Mohr SE, Perrimon N, Song W. (2021) **Coordination of tumor growth and host wasting by tumor-derived Upd3.** Cell Rep. 2021 Aug 17;36(7):109553. doi:10.1016/j.celrep.2021.109553. PMID: 34407411; PMCID: PMC8410949.

Cell technologies and their applications:

Hans M. Dalton, Raghuvir Viswanatha, Ricky Brathwaite Jr., Jae Sophia Zuno, Stephanie E. Mohr, Norbert Perrimon, Clement Y. Chow (2021) **A genome-wide CRISPR screen identifies the glycosylation enzyme DPM1 as a modifier of DPAGT1 deficiency and ER stress**. bioRxiv 2021.12.03.471178; doi: https://doi.org/10.1101/2021.12.03.471178

Feng X, López Del Amo V, Mameli E, Lee M, Bishop AL, Perrimon N, Gantz VM. **Optimized CRISPR tools and site-directed transgenesis towards gene drive development in *Culex quinquefasciatus* mosquitoes.** Nat Commun. 2021 May 20;12(1):2960. doi: 10.1038/s41467-021-23239-0. PMID: 34017003; PMCID: PMC8137705.

Jiunn Song, Arda Mizrak, Chia-Wei Lee, Marcelo Cicconet, Zon Weng Lai, Chieh-Han Lu, Stephanie E. Mohr, Robert V. Farese Jr., Tobias C. Walther (2021) **Identification of two pathways mediating protein targeting from ER to lipid droplets.** bioRxiv 2021.09.14.460330; doi: https://doi.org/10.1101/2021.09.14.460330

Viswanatha R, Mameli E, Rodiger J, Merckaert P, Feitosa-Suntheimer F, Colpitts TM, Mohr SE, Hu Y, Perrimon N. **Bioinformatic and cell-based tools for pooled CRISPR knockout screening in mosquitos.** Nat Commun. 2021 Nov 24;12(1):6825. doi: 10.1038/s41467-021-27129-3. PMID: 34819517; PMCID: PMC8613219.

Nanobody-based epitope tagging (cells and in vivo):

Xu J, Kim AR, Cheloha RW, Fischer FA, Li JSS, Feng Y, Stoneburner E, Binari R, Mohr SE, Zirin J, Ploegh HL, Perrimon N. **Protein visualization and manipulation in *Drosophila* through the use of epitope tags recognized by nanobodies.** Elife. 2022 Jan 25;11:e74326. doi: 10.7554/eLife.74326. PMID: 35076390; PMCID: PMC8853664.

CRISPR-mediated gene tagging (in vivo):

Oguz Kanca, Jonathan Zirin, Yanhui Hu, Burak Tepe, Debdeep Dutta, Wen-Wen Lin, Liwen Ma, Ming Ge, Zhongyuan Zuo, Lu-Ping Liu, Robert W. Levis, Norbert Perrimon, Hugo J. Bellen (2021) **An expanded toolkit for Drosophila gene tagging using synthesized homology donor constructs for CRISPR mediated homologous recombination.** bioRxiv 2021.12.24.474112; doi: https://doi.org/10.1101/2021.12.24.474112

Technology review:

Zirin J, Bosch J, Viswanatha R, Mohr SE, Perrimon N. **State-of-the-art CRISPR for in vivo and cell-based studies in Drosophila.** Trends Genet. 2021 Dec 18:S0168-9525(21)00336-X. doi: 10.1016/j.tig.2021.11.006. PMID: 34933779.

From FlyNews released January 2022

News from the Genome Disruption Project (GDP)

The GDP is continuing to expand the collection of genes with human homologs using the CRIMIC strategy by inserting T2AGAL4 cassettes into coding introns of targeted genes. We also incorporated about 300 CRIMIC lines that were generated by Genetivision. The insertions were verified by PCR and imaging. To date the GDP CRIMIC T2AGAL4 collection includes 1864 stocks targeting 1746 unique genes. The GDP has increased the scope of the CRIMIC project to target genes that lack a suitably large intron to insert a T2AGAL4 cassette. Indeed, about 50% of the evolutionarily conserved Drosophila genes have no suitable intron. We designed a strategy in which a KozakGAL4-3XP3GFP construct replaces **typically** the whole coding sequence of the genes, from 5'UTR to 3'UTR. These insertions generate a null allele of the targeted gene in which the GAL4 is expressed under the regulatory input from the targeted locus. To date we have generated about 150 KozakGAL4 alleles. In addition, about 150 constructs are in the pipeline.

Till about a year and half ago, our efficiency from start to finish was about 50% (80% cloning success rate X 80% transgenesis success X 80% inserted in the proper location). We have therefore switched to synthesized homology donor intermediates and optimized the strategy. The new approaches allow synthesis of target specific sgRNAs together with the homology donor intermediate. The latter combined with excision of the donor construct in vivo using CAS9 have increased transgenesis efficiency from 50% to about 80%. The GDP secured funding through the Office of Research Infrastructure Programs (ORIP) through 2024 to target an additional 2300 genes with T2AGAL4 or KozakGAL4 strategies.

Human UAS-cDNA project

We are generating a collection of UAS-human cDNAs for the fly community. Starting with Gateway compatible clones that are part of a public or commercial ORFeome human collection, the team is subcloning human cDNAs corresponding to evolutionarily conserved genes into pGW-HA.attB plasmid and injecting them into VK33 or VK37 phiC31 integrase docking site to create a versatile collection. The plasmids are being shipped to DGRC for public distribution and the fly stocks are available from BDSC and/or Kyoto Stock Centers. To date, >5,000 clones have been generated and ~3,200 stocks are available from one or both of the stock centers. Please see below for information.

UAS-human cDNA lines available from BDSC (~2,000 stocks from this collection)
https://bdsc.indiana.edu/stocks/uas/uas_hsap.html
UAS-human cDNA lines available from Kyoto Stock Center (~2,000 stocks from this collection, ~700 are duplicates of lines in BDSC)
https://kyotofly.kit.jp/stocks/documents/Humanized_fly_lines.html
Plasmids available from DGRC (1,700 clones available, a total of 3.273 clones shipped and in the process of being made public)
https://dgrc.bio.indiana.edu/clones/Catalog# (see excel file under "Human ORF")
Searchable website for Human cDNA clones subcloned at Berkeley
https://www.fruitfly.org/humanfly/
Searchable website for Human cDNA transgenic lines injected at BCM
http://flypush.imgen.bcm.tmc.edu/humanfly/
Project documentation in FlyBase
http://flybase.org/reports/FBrf0237477

DIS Report (Jim Thompson)

Volume 104 (2021) of Drosophila Information Service was published on our web site (www.ou.edu/journals/dis) in early January. It continues to attract a broad range of research reports, technique articles, and teaching activities, although this issue was slightly smaller than in recent years. Research interruptions due to the pandemic may be a possible explanation. In addition, we continue to respond to other requests for assistance in locating information for researchers and graduate students. When it comes up on computer searches, our title is sometimes thought to indicate we are an open public information resource, which can invite surprising inquiries. Two current major projects are revising the organization of our web site and catching up with the publication of printed copies of the past couple of years. Printing was delayed due to some incompatibilities between some complex research images and the formatting requirements of the printing house. But we believe such issues are now resolved.

First published in 1934, DIS remains an active source for research, teaching, and technique articles relevant to our field. Most submissions occur in response to our traditional "Call for Papers", in which we are assisted by the excellent help of Josh Goodman, FlyBase, University of Indiana. We are already receiving submissions for volume 105 to be published soon after the end of December 2022. Free access to each new issue is provided on our web site soon after the issue is completed at the end of December. But submissions are accepted at any time. Manuscripts can be sent to James N. Thompson, jr., Department of Biology, University of Oklahoma, Norman, OK 73019; jthompson@ou.edu.

FlyBase Report to the Drosophila Board
22-March-2022

For the past twenty-nine 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, 2022 begins year 5 of our 5-year grant with NHGRI. Originally, our budget was set to be reduced by 25% over the 5-year period (which normalize to 35%), however, in Fall 2020 we were notified that our budget would suffer additional cuts which we have seen at a rate of about 10% per year. We submitted a 5-year renewal proposal in January 2022 in which our projected budget will be 50% of what it was in 2016. Additional funds FlyBase receives are an NHGRI supplement for the Alliance; an NSF grant; and funding from a BBSRC, Wellcome Trust and British Medical Research Council grant which altogether bring FlyBase's funding closer to 60-65% of 2016. Finally, we continue to collect some fees from the community to cover the budget deficit. As of 20-March-2022 (4 years since fees were implemented), ~650 labs have pledged to contribute ~$514,000. We plan to continue the user-fee collection to supplement FlyBase funding.

We are grateful for the strong support from our community and appreciate the support of the FlyBoard in reminding the community of this *extremely necessary* user fee collection. We have included charts of usage / fees collected by country in this report.

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. Highlights are:

- Automated triaging pipeline: We 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 up to date, and keeping pace with new physical interaction curation while addressing the backlog.
- Human disease model curation: curation effort continues, 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. Variants introduced into fly genes as analogous mutations (as transgenes or at the endogenous locus) are mapped to the genome. The next step is development of the Web presentation of these data.
- We continue allele-based curation of disease models based on the Disease Ontology (DO); which 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.
- 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. We have added graphical network representations to pathway pages. We will continue to add new pathways and update existing pathway reportsin 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 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 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 new modules and gene groups and human disease models will be maintained and updated as necessary.
- We are actively working with the Fly Cell Atlas and single Cell Atlas to annotate all Drosophila cell types and curate scRNAseq data sets.
- Continue to establish pipeline to fetch scRNAseq datasets from the EBI's Single Cell Expression Atlas, annotate them, and load the metadata into FlyBase as dataset reports.
- Continue curation of GAL4 drivers.
- Experimental tool report development continues.

FlyBase web site production and development will continue as planned with 6 releases to flybase.org each year. There are extensive ongoing activities to maintain the website include

internal and external group coordination, pipeline management and maintenance, and system administration tasks including:

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

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

- Community outreach via commentaries and the FlyBase Newsletter
- The FlyBase Community Advisory Group (FCAG) who respond to surveys, make suggestions, etc.
- Video tutorials round at the 'FlyBase TV' YouTube channel: https://www.youtube.com/c/FlyBaseTV.
- Twitter**:** We promote FlyBase using Twitter: @ FlyBaseDotrOrg https://twitter.com/flybasedotorg?lang=en
- FlyBase Help Desk: We maintain a project-wide help desk to provide support to users with data/web interface questions or suggestions.

Flybase website future development goals planned include:

- Basic Chemical reports based on ChEBI
- Move BLAST to a centralized system at the Alliance of Genome Resources
- Implement required changes required after the genotype curation overhaul
- Further tweaks and customizations to JBrowse tracks
- Stacked ribbons for summarizing gene expression and function
- Improvements to integration and display of DGRC data on FlyBase
- Optimize usability in FlyBase based on user feedback and observations
- Provide support for new FlyBase curator projects
- Continue to expand our use of cloud-based services where it makes technical and financial sense
- Evaluate open-source tools for automating cloud deployment and management

- Enhancement of public programmatic endpoints (APIs) to improve data access for external collaborations (*e.g.,* AGR) and advanced users
- Continue to coordinate with AGR development teams
- Continue security improvements for cloud and on-premise compute resources

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

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

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

2021 FlyBase Web Usage

The following are web statistics from the FlyBase website as captured by Google Analytics. Unless otherwise stated, all usage statistics in this document cover the period of Jan-Dec for the years 2015-2019 and Jan-Oct for 2021. In summary, the usage statistics for Jan-Dec 2021, when compared to the same period in the previous year, indicate that our overall pageviews have increased (11%), our sessions have increased (26%), and the number of users has increased (77%). This larger than normal increase is likely due to high levels of bots that are originating from China. In addition, data class report and tool usage has not significantly changed from previously observed and well-established patterns. NOTE: users by country, figure 4, was recalculated using google analytics 4 to filter out bots and covers period Sep 1 2021 to March 17, 2022. FlyBase had 5 million pageviews, 886 thousand sessions, and 281 thousand users in this time period. Finally, when comparing website usage for the Alliance site and FlyBase, the pageviews, sessions, and users for the Alliance are well below FlyBase levels for the same time period.

Pageviews

Figure 1 shows FlyBase pageviews for the previously mentioned time periods. A pageview is defined as a hit to an HTML page, script output or other content that does not include non-document files (CSS, images, JavaScript, etc.). The average number of pageviews for 2021 thus far is 747k, with a high of 947k and a low of 418k. The periodic dips in this plot all correlate with expected seasonal patterns that we typically experience. Compared to Jan-Oct of 2020, pageviews are up 12.9%.

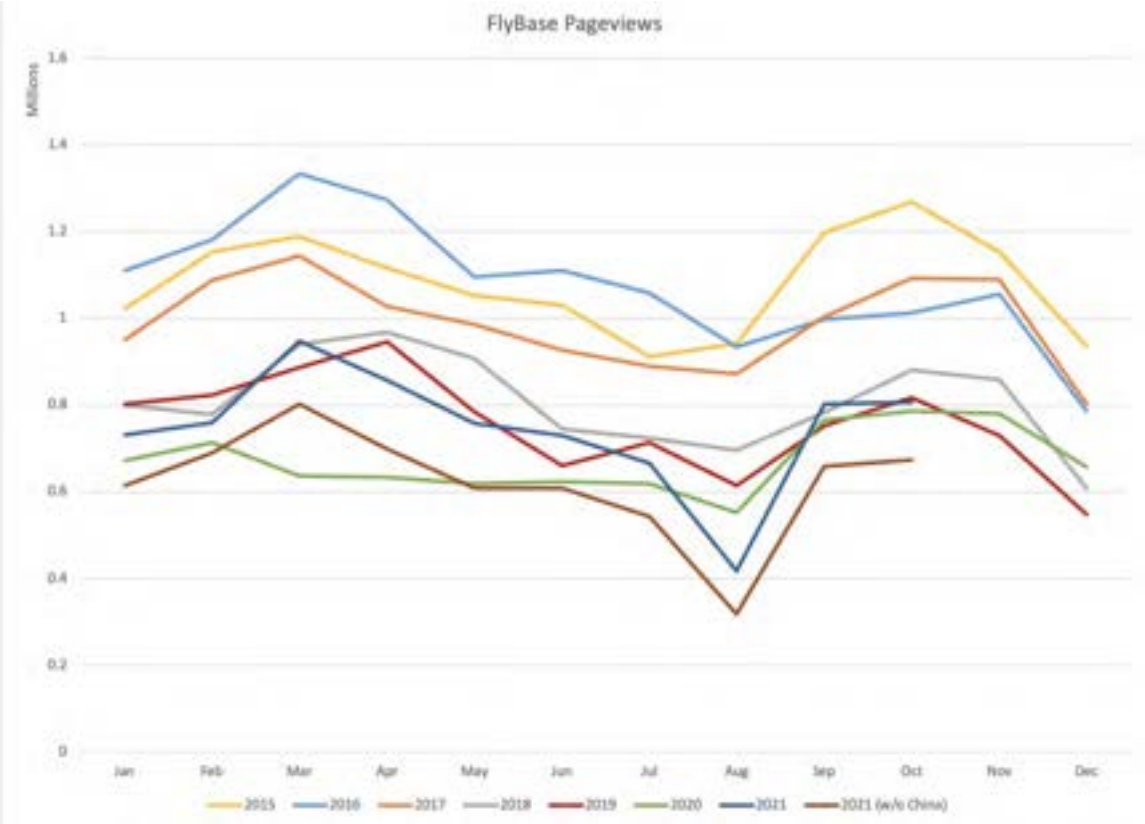


Figure 1 – FlyBase Pageviews for Jan 2015 – Oct 2021

Sessions
Figure 2 shows FlyBase sessions (visits) for the same period as pageviews. A session is defined as a period of activity by a unique web user. If no activity is recorded for 30 minutes, any subsequent activity is counted as a new session. The average number of sessions for 2021 thus far is 171k, with a high of 201k and a low of 126k. Compared to Jan-Oct of 2020, sessions are up 25.2%.

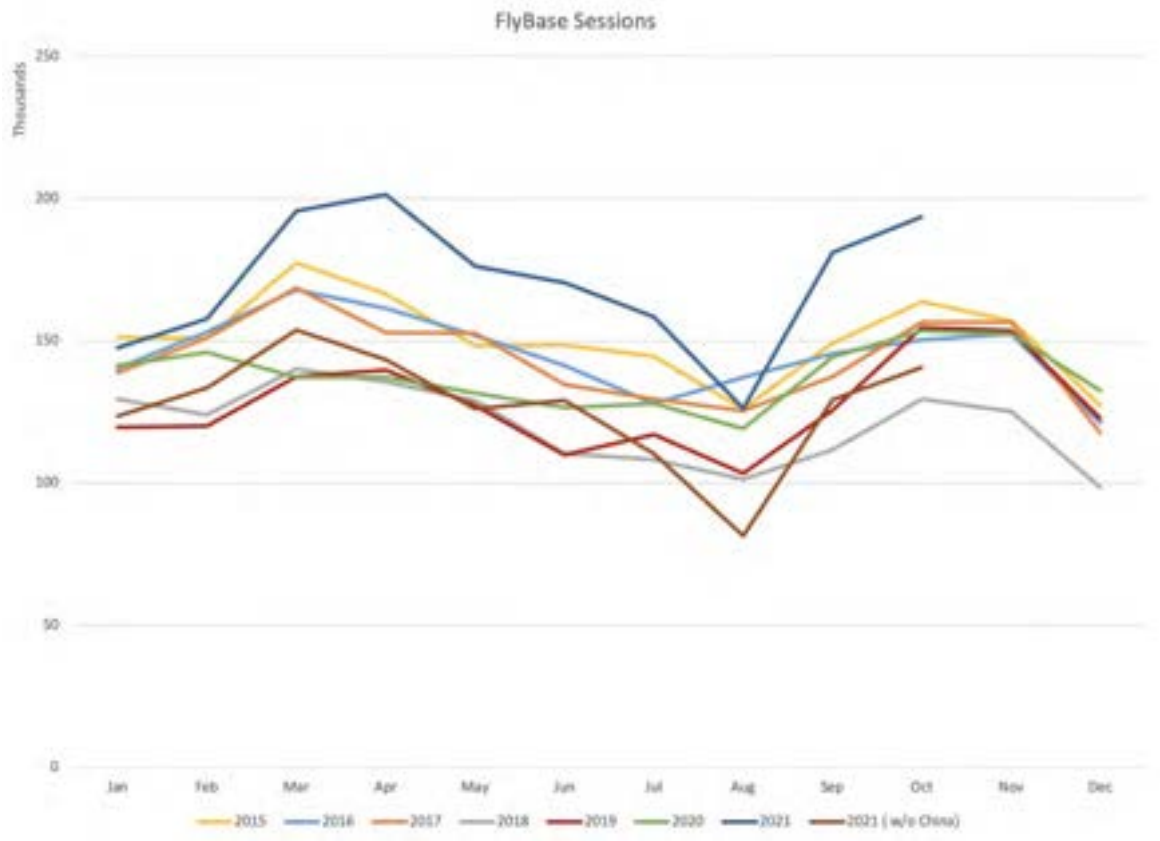


Figure 2 – FlyBase sessions for Jan 2015 – Oct 2021

Users

Figure 3 shows FlyBase users for the same period. A user is defined as a unique session ID that Google analytics generates. This value does not account for a single user using multiple computers and/or browsers in some cases (e.g. not logged into a Google account). The average number of users for 2021 thus far is 82k/month, with a high of 98k and a low of 59k. Compared to Jan-Oct of 2020, the number of FlyBase Users are up 60.2%.

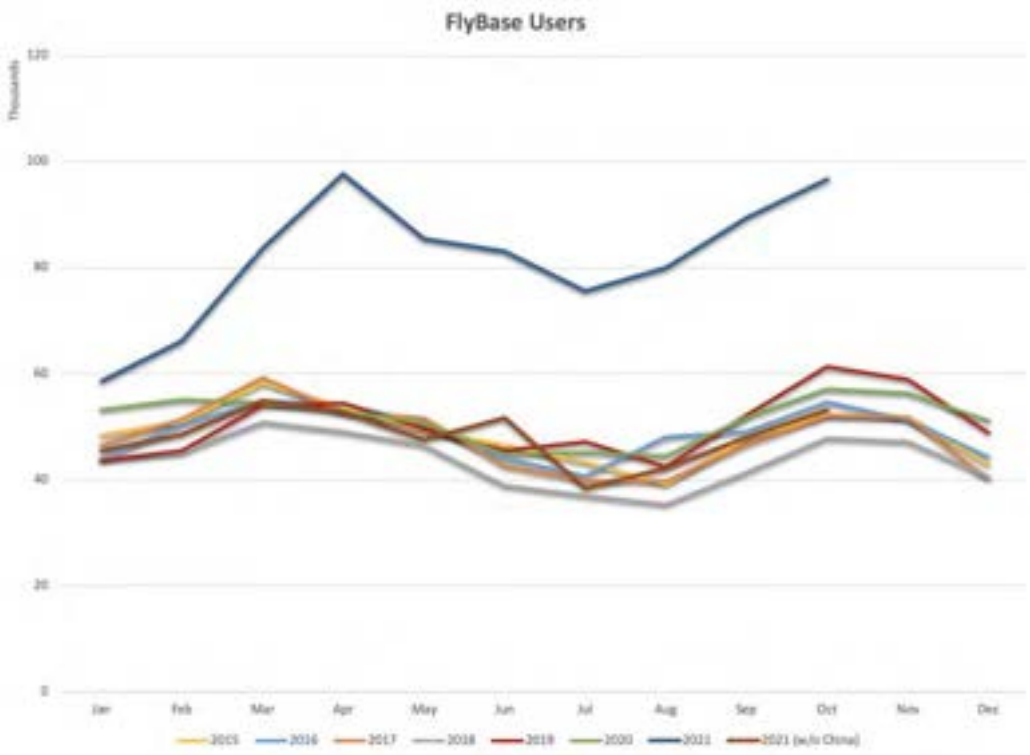


Figure 3 – FlyBase users for Jan 2015-Oct 2021

Users by Country

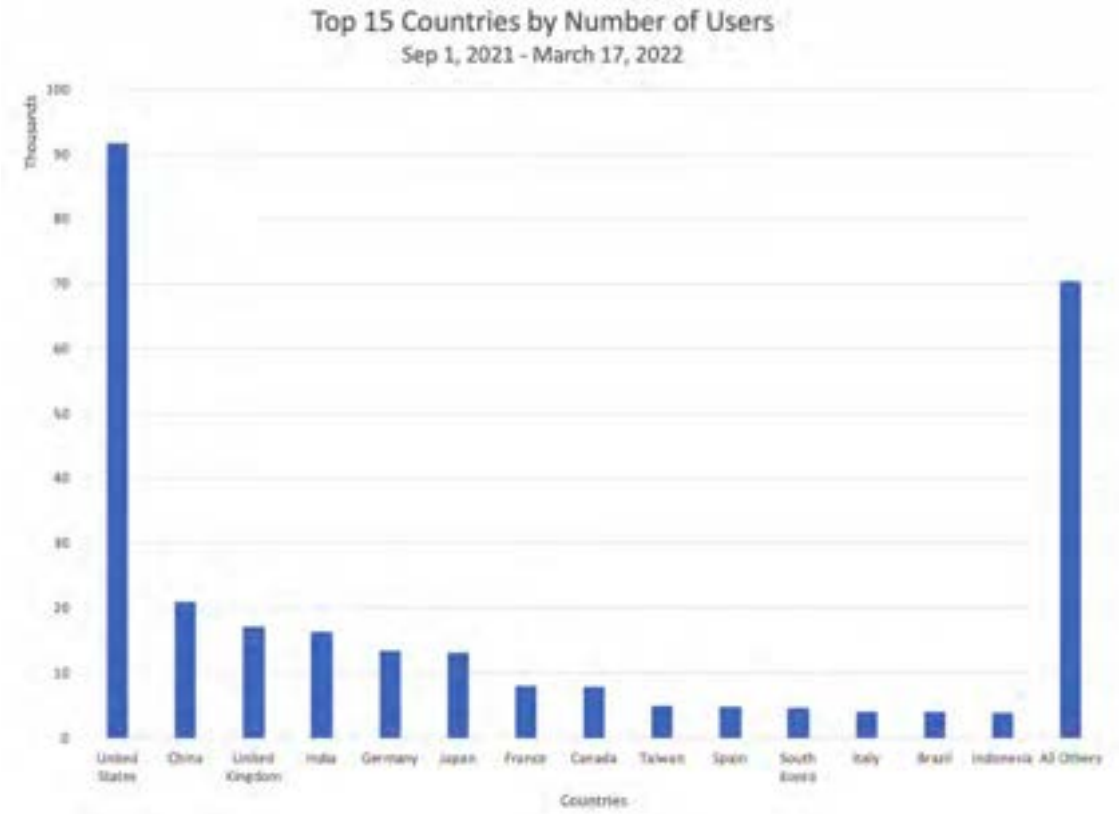


Figure 4 – FlyBase Users by Country (Sep 1 2021- March 17, 2022)

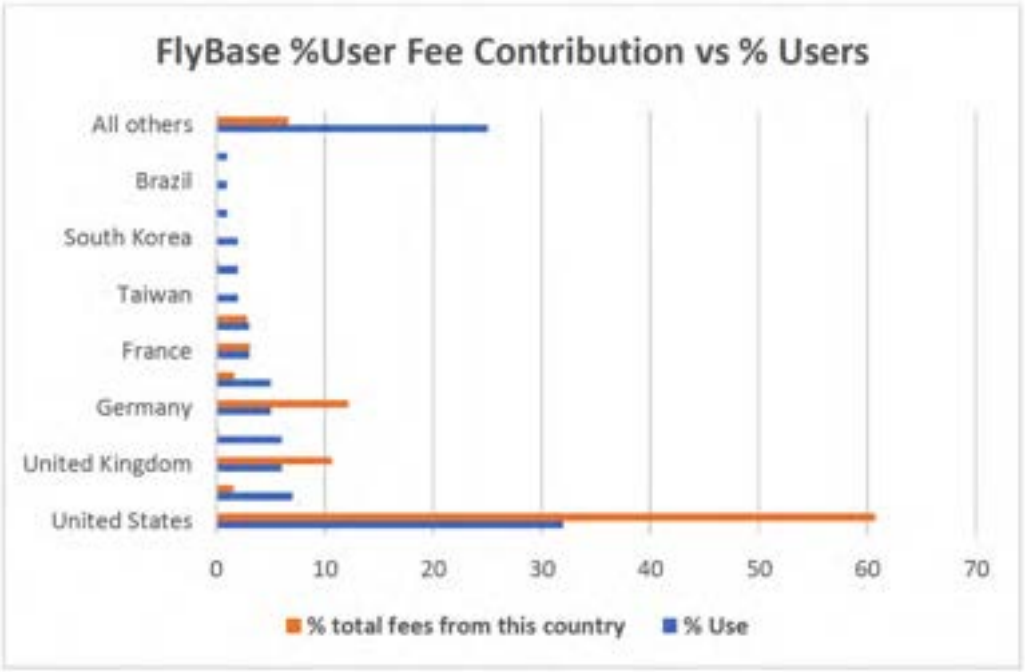


Figure 5 – % user fee contribution to date vs % users (current) fee.

Data Class Usage

Figure 6, “FlyBase Data Class Usage by Pageviews”, shows a TreeMap of total pageviews for FlyBase data class reports for Sep 2020 – Oct 2021. Genes, References, Insertions, Constructs, Alleles, and Stocks still dominate the most used spots as in years past. All other data classes remain relatively stable over the previous period aside for some minor differences.

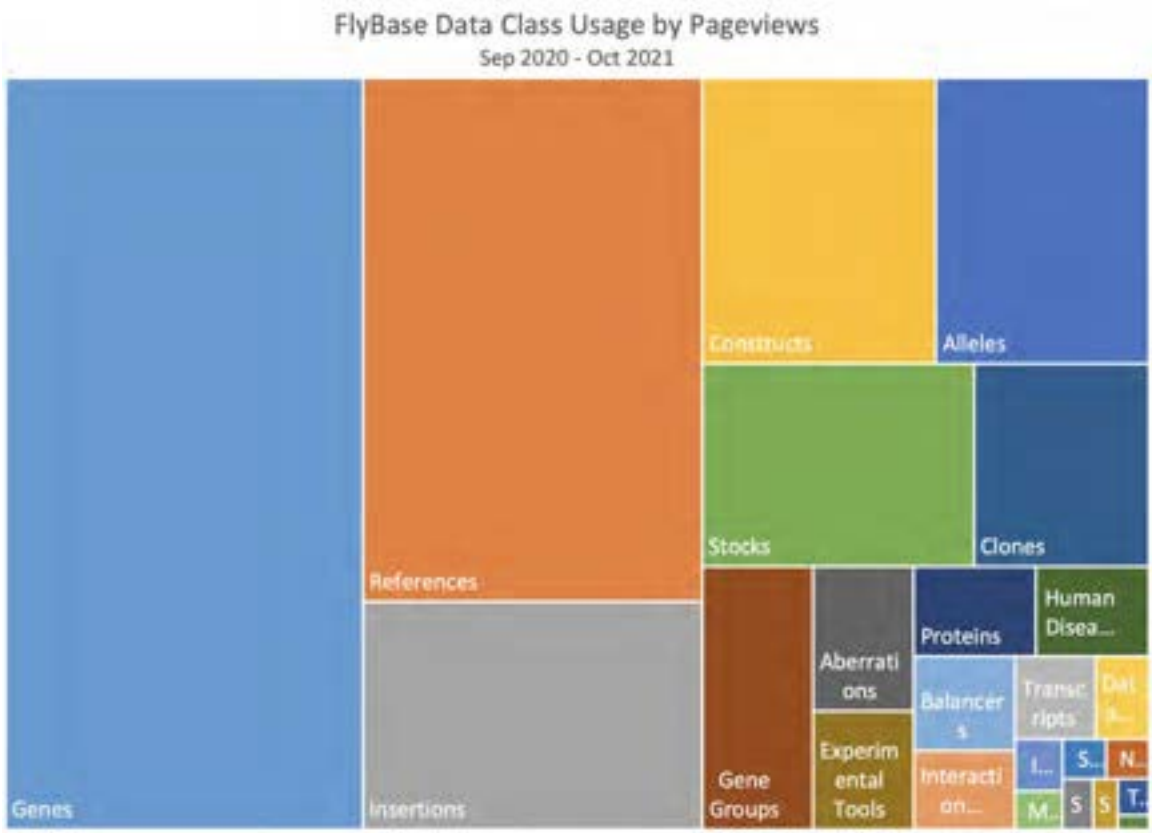


Figure 6 – Pageviews by FlyBase Data Class.

Tool Usage

Figure 7, “FlyBase Tool Usage”, shows that our top 5 tools are Simple Search, BLAST Jump to Gene, and Sequence Downloader. This is a well-established pattern with our user base and is not surprising to see. Additionally, JBrowse usage is being undercounted due to technical issues related to how it is implemented. This will be addressed by our upgrade to Google Analytics 4.

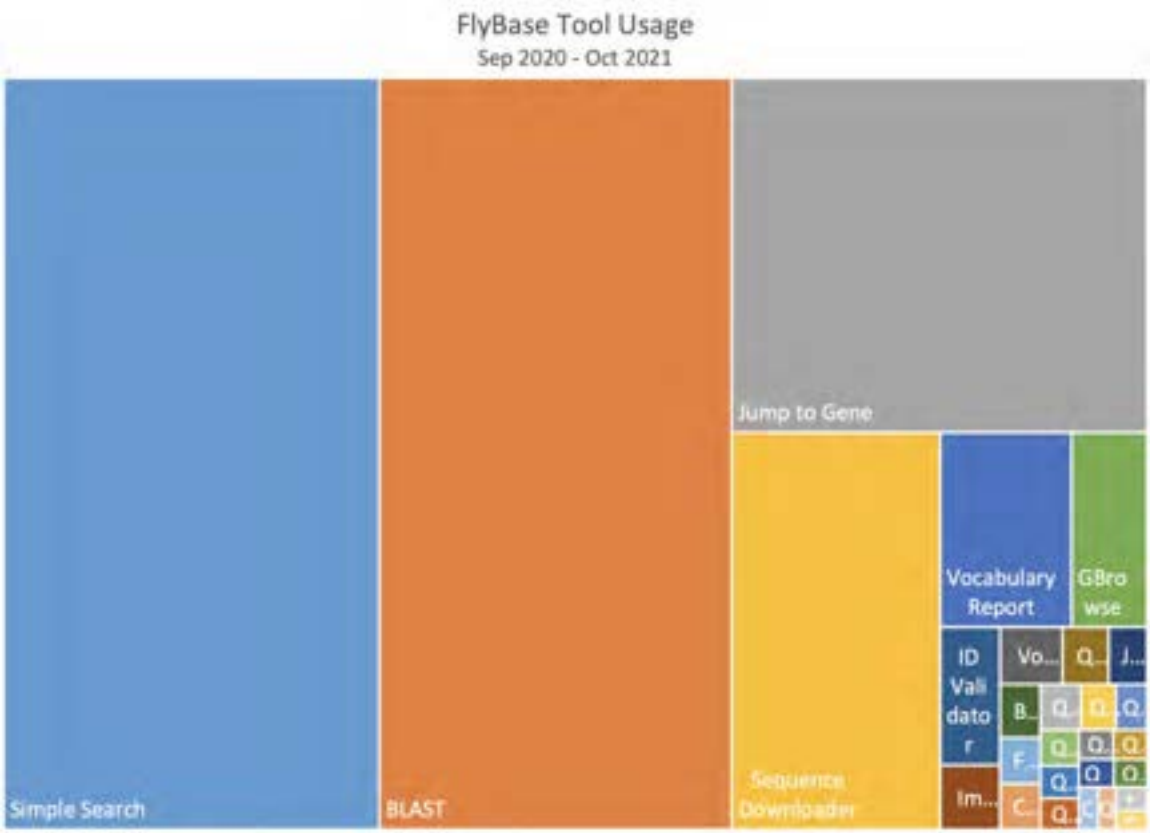


Figure 7 – FlyBase Tool Usage.

Alliance and FlyBase Usage

In Figure 8 website usage for Sep 2020 until Oct 2021 is shown for FlyBase and the Alliance. Alliance usage levels (pageviews, sessions, and users) all trail far below corresponding levels measured on FlyBase. FlyBase generated 6,320 sessions for the Alliance from FlyBase users and the Alliance generated 227 sessions for FlyBase. The traffic from FlyBase to the Alliance represents 8% of the overall referrals from external sites into the Alliance site.

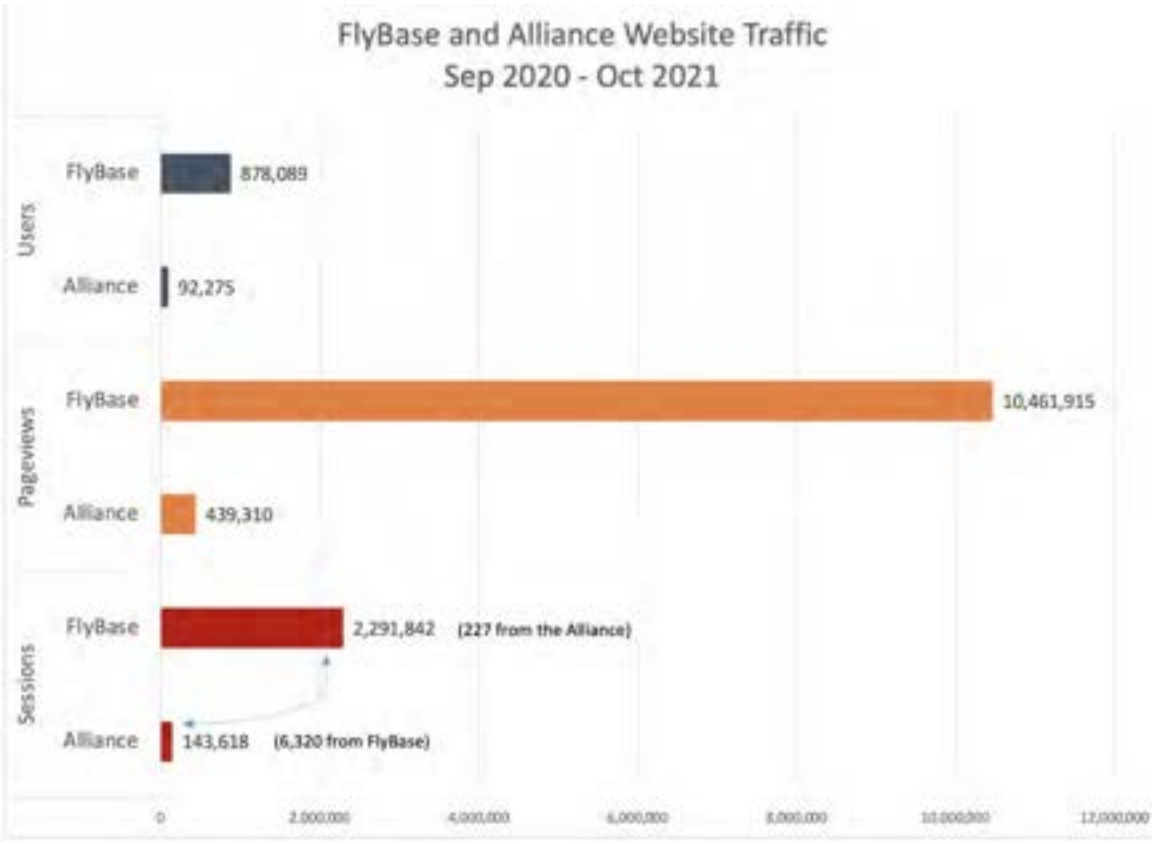


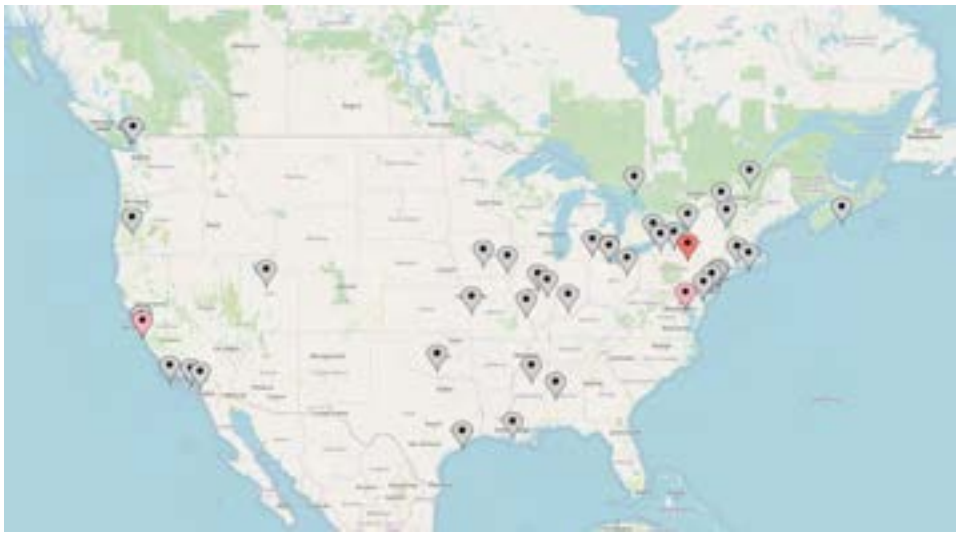
Figure 8 – FlyBase and Alliance website traffic Sep 2020 – Oct 2021. The blue arrow indicates that FlyBase was responsible for directing 6,320 new sessions to the Alliance website during this period and the Alliance generated 227 new sessions for FlyBase.

“Graduate perspectives of Drosophila use in the lab”

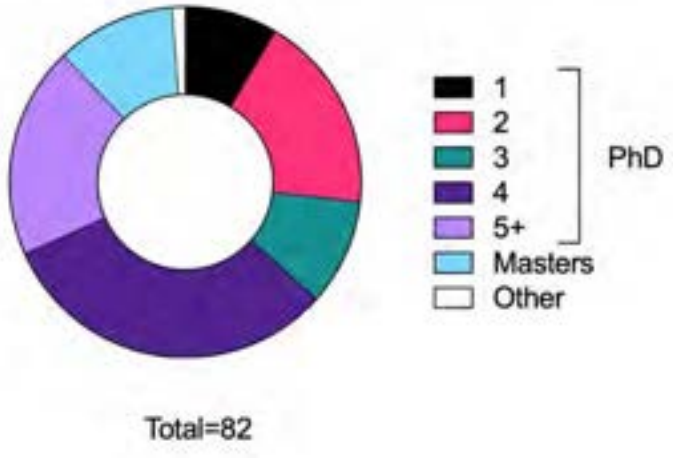
Flyboard Graduate Student Survey
Created, administered, and analyzed by Ana-Maria Raicu,
Graduate Student Trainee Representative
April 2022

Between May and July 2021, I received responses to a google survey tailored to graduate students from North America, conducting research using Drosophila. I received responses from 82 unique respondents from 42 different institutions. The survey was distributed via Twitter and email.

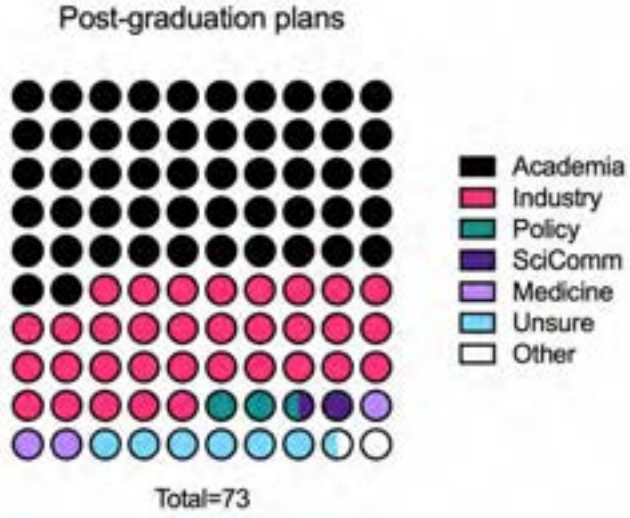
Pins on the map below indicate the location of the university the graduate student was attending when they filled out the survey (Gray: 1-5 respondents; pink: 6-10; red: 11+).



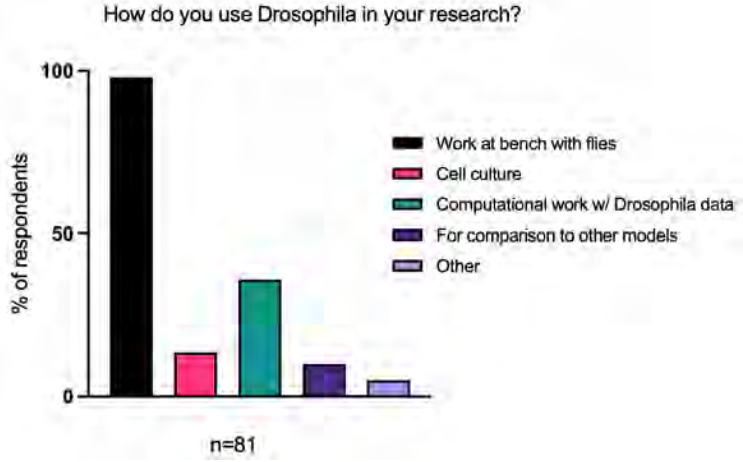
Breakdown of the year in school of the survey respondents. >50% were 4th and 5th year students.



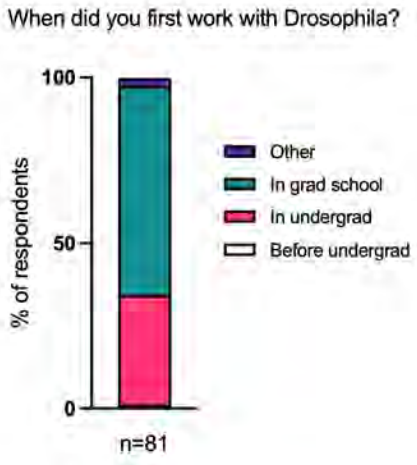
More than 50% are planning on going into academia after finishing their PhD.



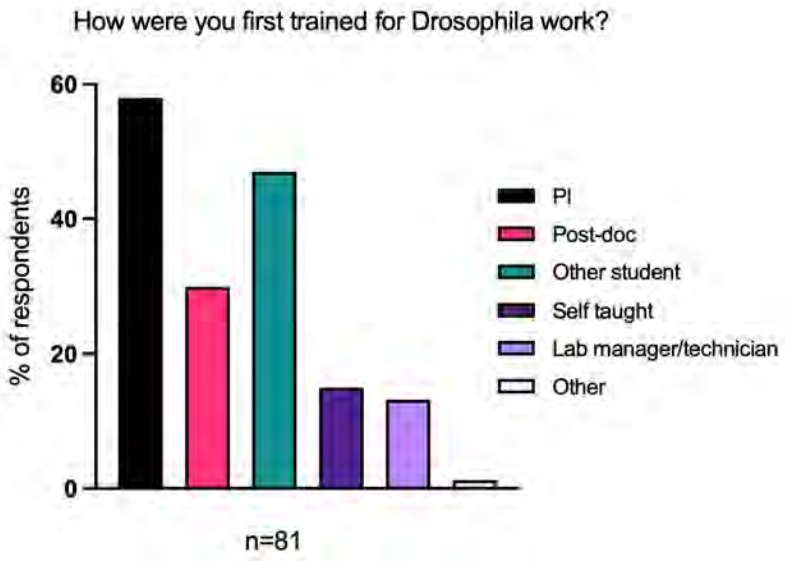
Everyone uses flies at the bench, and some also use Drosophila cell culture or Drosophila data for computational work.



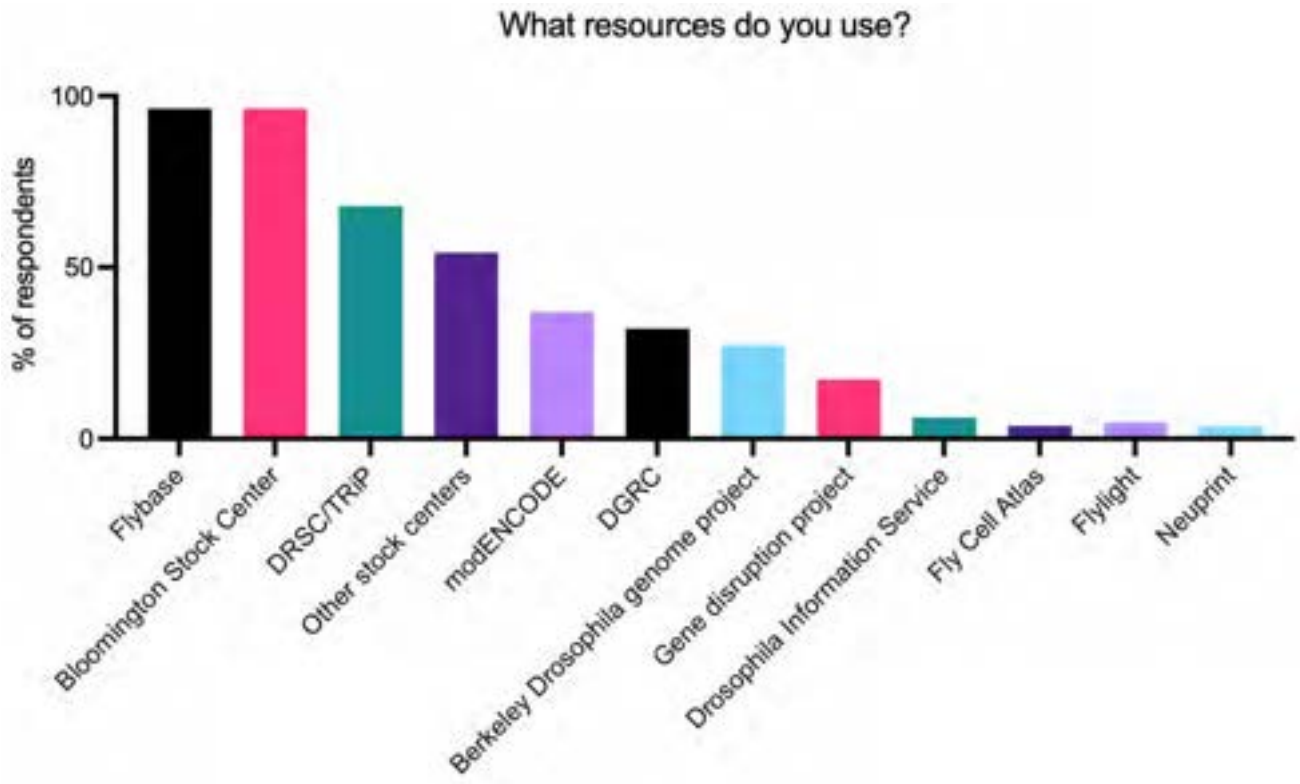
1/3 started working with Drosophila as undergrads. Perhaps they chose a Drosophila lab in graduate school due to their undergraduate fly experience. Yet, most graduate students were new to Drosophila research.



Most students were trained directly by their PI! Aside from direct training by the PI, graduate students were trained by other students in the lab or post-docs. 15% were self taught.



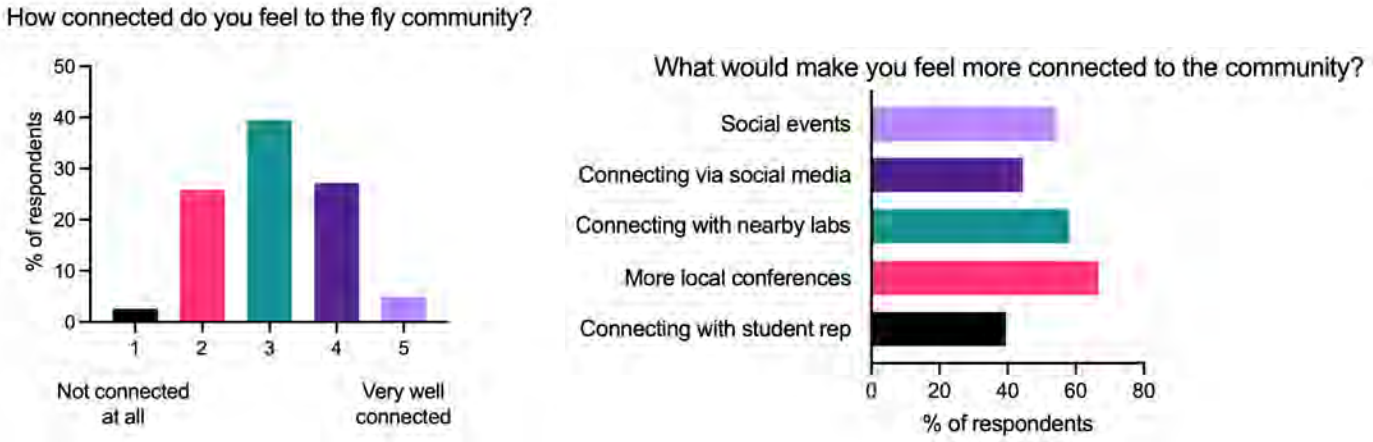
Everyone uses Flybase and orders stocks from the Bloomington stock center. This shows how important these two resources are, and that we need to continue getting funding for them. Other resources are also very valuable, and used by many graduate students, as indicated below.



What types of resources do you see are lacking in the fly community? Below are direct quotes from some respondents:

- Better resources for non-melanogaster species
- A **centralized/updated website** for all Drosophila resources available to the community
- A **troubleshooting guide** for basic experimental issues.
- I feel like it would be super cool to have a program that helped you **map out crosses** for complicated genetics.
- Community resources on **how to dissect different tissues** of Drosophila.
- A **standard set of training modules** to get students started with, standard operating procedures for cleanliness and mite prevention, accessible resources for teaching students on how to start working with flies, teaching modules for becoming acquainted with Drosophila genetics methods/vernacular
- Antibody database
- It would be really nice to have a detailed **online collection of the drosophila balancers** and their respective phenotypes
- **Job-boards/internship opportunities** for Drosophila researchers
- A **forum/website** that houses Drosophila horror stories, so newcomers know what to avoid in the lab/in the field.
- There should be a resource to know more about **all the fly labs in North America** or a global fly lab data consolidation for easier sharing of resources

Many students neither feel disconnected nor very well connected to the fly community. The majority don't think they are well connected to the community, and they would feel more connected by having local events and meeting with nearby fly labs.



What suggestions do you have for other ways to improve the graduate students' experience using Drosophila for research? Below are direct quotes from some respondents:

- More **method based videos**
- More **spaces for communication** and collaboration
- A more **centralized database of practical resources** would be awesome. eg, balancer genotypes, genetics tutorials, pictures of marker phenotypes etc.
- It would be great to have a **shared dropbox or github** where we could share protocols easily or look to see what methodologies are possible for certain questions we might have.

- More social media accounts (Twitter, discord channel)
- Youtube video will help.
- Some sort **online resource** that collects any and everything related to Drosophila in just one place. Maybe Flybase is that place, but it's also really hard to navigate that site at times.

Is there anything you wish you knew at the start of your Drosophila training that you know now?
Below are direct quotes from some respondents:

- I didn't realize **how many resources** are out there since I just find out from word of mouth or reading papers. If there was a centralized location for a student to go to (aside from flybase), that would be so useful for finding appropriate resources/books/labs
- **There are a lot of fly resources**, and I sometimes feel overwhelmed because I do not know what all of the resources do. It would be nice to have some type of tutorial or guide explaining fly resources.
- It is hard to get funding on Drosophila work from NIH
- Almost everyone is willing to share if you simply ask for help
- **How to use Flybase**, a better understanding of how to set up crosses
- I wish I knew how disjointed a lot of the community is in terms of understanding and clearly stating what each other were doing as opposed to developing so many new tools that take an inordinate amount of time to learn and you really have to find someone with a lot of experience which is rare to teach you some of the “secret tips and tricks” to working with them. Sometimes it can feel like the tools are moving faster than we can effectively use them.
- **That Flybase exists!** I worked in a lab where we didn't really focus on the genetics aspect of our work, and I joined a more genetics heavy fly lab for grad school. I was pretty lost and still am lost on how to navigate the wealth of resources when it comes to genetic nomenclature, how to follow fly genetics, etc.
- Just how to use flybase (and actually understand the names/insertions etc.)
- I wish I knew just how big the fly community is

And most importantly:

- That flies are small, and have the ability to go up your nose :)

Conclusions:

Based on these responses and suggestions, students feel that they are **lacking a centralized location for finding information**, aside from Flybase. I am proposing the creation of a website that would include best practices, shared protocols, videos of various techniques, information about current Drosophila labs, job postings etc. all in one place. Such a website would take a lot of work to put together and keep updated (and potentially would need additional funding that we are already having a difficult time getting), but as we are expanding as a community, this is a perfect opportunity to start a discussion about developing such a resource.

If you would like to contact me to discuss this survey or the suggestions, you can reach me at raicuana@msu.edu.

Thank you!

Subject: Quick European Drosophila Board discussion at Board meeting
Date: Friday, April 1, 2022 at 2:43:19 AM Mountain Daylight Time
From: Nicolas Tapon
To: Tin Tin Su
CC: Daria Siekhaus

Hi Tin Tin,

Hope all is well for you! Sorry to bring this up so late, but would it be possible to have a very quick discussion at the American Board meeting next week (maybe in the AOB part) about European/North American fly board cross-representation. If you remember, I brought this up at the last American board meeting, and we agreed cross representation would be a good thing, and that I should discuss it with my European Drosophila board (EDB) colleagues and come back with a more concrete proposal. We have just elected Daria as Euro rep (cc'ed to this mail as she is taking over from me after next week's board meeting), so there is no huge urgency to implement this as we already have her in place for a few years, but it is good to get the discussion going now.

In the meantime, the EDB set up an elections working group equivalent to its American counterpart (myself, Estee Kurant, Frank Schnorrer and Luis Teixeira). In a nutshell, this is what we propose:

Each board (North American and European) nominates one of their elected board member to act as cross-board representative. We think this makes more sense in future than electing a European rep through the American board elections, and vice versa, as each election process is more effectively targeted at their own local constituents (ie, we make efforts to maintain a good European fly researcher's list). As mentioned by Tania Reis at the last American board meeting, there is no shortage of people with European ties on the American board who would be happy to volunteer for the job of American rep to EDB.

On the American rep to EDB side, the task would not be too onerous: we plan one in-person meeting at the EDRC (every two years) and a Zoom meeting every other year. In practice, we are having more meetings right now as we are starting from scratch on issues like sorting out some sort of official charitable organisation status (alas we have no GSA to administer the EDRC!), but this will (I hope!) calm down gradually, and the American rep would not necessarily need to attend all the "inner workings" meetings, just the annual general EDB meetings. One potential issue is that the EDB term of office is 4 years (two EDRC cycles), whereas the American term is three years if I remember correctly.

Once we have a general agreement on a plan, perhaps the leads of both election committees can meet and sort out the details.

@ Daria, please let us know if you have any thoughts.

All the best,

Nic

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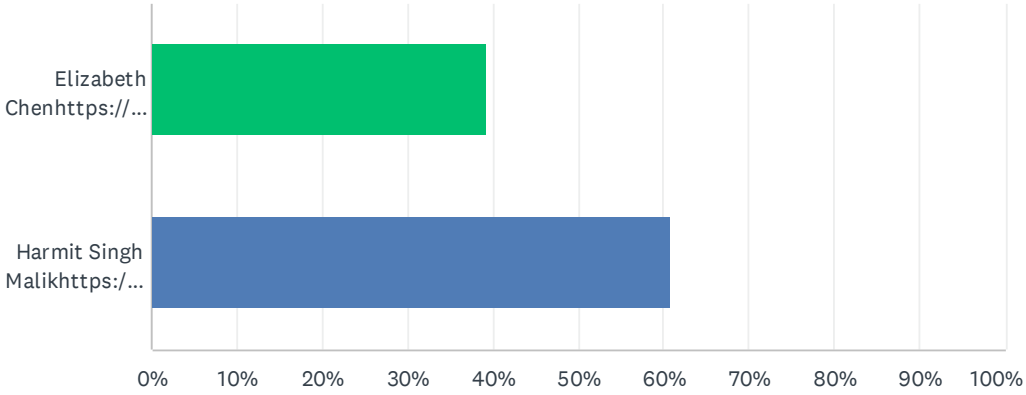
Q1 President-elect (Vote for ONE)

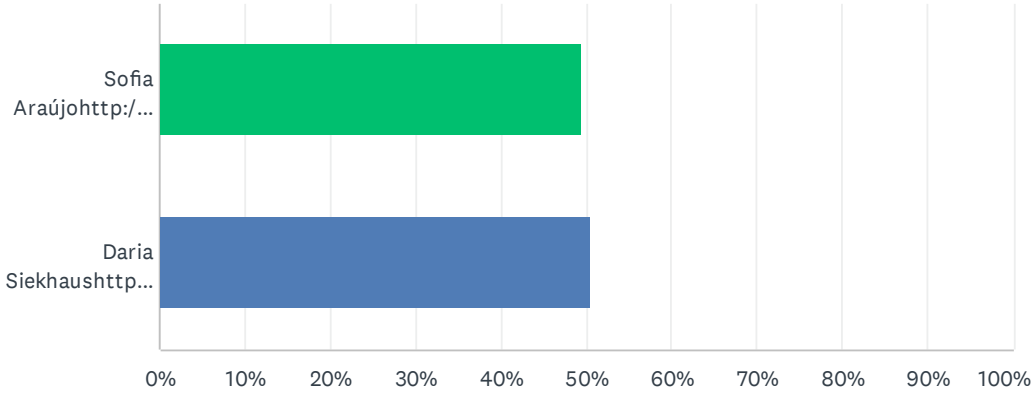
Answered: 875 Skipped: 442



ANSWER CHOICES	RESPONSES	
 Elizabeth Chenhttps://www.utsouthwestern.edu/labs/chen-elizabeth/research/ I received my undergraduate degree from Peking University in China before coming to the US to pursue my interest in life sciences. As a graduate student at Stanford, I fell in love with fly genetics and joined Bruce Baker's lab to study how the sex determination pathway integrates with other developmental pathways to generate sexually dimorphic tissues. For my postdoctoral studies, I wanted to use the powerful fly genetics to tackle the problem of cell-cell fusion. I joined Eric Olson's lab, which is primarily a mouse lab, and initiated a large-scale forward genetic screen for myoblast fusion mutants in Drosophila. Subsequent work in my own group at Johns Hopkins University (2004-2016) led to the discovery of the asymmetric fusogenic synapse, where one fusion partner extends membrane protrusion to invade the other to promote cell-cell fusion. Like many fundamental principles first discovered in Drosophila, the asymmetric fusogenic synapse has later been found to be a conserved feature underlying the fusion of vertebrate muscle and non-muscle cells. After my lab's relocation to UT Southwestern Medical Center (2016-present), we continue to use interdisciplinary (genetics, cell biology and biophysics) and cross-species (fly, zebrafish and mouse) approaches to study the mechanisms underlying cell-cell fusion, actin cytoskeletal dynamics and mechanobiology.The fly community has profoundly influenced me as a scientist. My first scientific conference was the Drosophila Research Conference, an eye-opening experience for a young graduate student. Over the years, research in my lab has benefited tremendously from colleagues in the fly community and resources at the FlyBase. As a PI, I enjoyed chairing platform sessions at fly meetings and serving on the Election Committee of the Drosophila Board (2017-19) and the Drosophila Image Award Committee (2019-20). My other service experience includes being a member of the National Institute of Arthritis and Musculoskeletal and Skin Diseases Advisory Council, the President of Society for Muscle Biology, and an organizer of international meetings in the fields of muscle biology and cell biology. It would be a great honor to continue giving back to the fly community by serving as the Fly Board President. I will continue the excellent work done by the past Boards and focus my efforts on advocating the importance of fly research; promoting interdisciplinary and cross-species studies; attracting young investigators to the field; enhancing diversity, equity and inclusion; and fundraising for the fly community.	39.31%	344
 Harmit Singh Malikhttps://research.fredhutch.org/malik/en.htmlI grew up in the city of Bombay (Mumbai), India where I got my BTech, Chemical Engineering at the Indian Institute of Technology, Mumbai. Having been enamored by biology and evolution as an undergraduate, I then moved to the US to get my PhD in Biology, at the University of Rochester, NY with Dr. Thomas Eickbush. There, I began my nearly three decades long love affair with Drosophila melanogaster, studying the genetic consequences and evolutionary strategies of retrotransposable elements, especially the R1 and R2 retrotransposons that insert into the multicopy rDNA genes. In 1999, I moved to Seattle to the Fred Hutchinson Cancer Research Center (the "Hutch"), to do my postdoc with Dr. Steve Henikoff to study the 'centromere paradox' i.e., rapid evolution of centromeric DNA and proteins despite essential function. In 2003, I started my own lab at the Hutch, where I am currently a Full Professor & co-Associate Director of the Division of Basic Sciences. In 2009, I was selected as an Early Career Scientist of the Howard Hughes Medical Institute and as a Full Investigator in 2013. My lab studies the causes and consequences of genetic conflicts that take place between different genomes (e.g., host-virus interactions, mitochondrial conflicts with nuclear genomes) or between components of the same genome (e.g., chromosomal competition at centromeric regions). We are interested in understanding these "molecular arms races" and how they drive recurrent genetic innovation, from the perspective of both evolutionary biology and disease. Much of our work focuses on Drosophila species; we use a combination of traditional genetics, genomics, and cell biology. I am most proud of the several postdocs and graduate students who have trained with us, many of whom are faculty in prestigious departments in the US and Europe and are considered leaders in their respective fields. Our work has received significant accolades for me and my lab members. Most recently, I was awarded the 2017 Eli Lilly Prize in Microbiology, the most prestigious prize awarded by the American Society of Microbiology and elected to the US National Academy of Sciences in 2019. I have been a member of GSA since graduate school. I have been a regular attendee at annual Drosophila meetings, where I have spoken several times, including as a Keynote speaker in 2021. I helped co-organize the 2019 Drosophila meeting in Dallas, TX. Previously, I was a Councilor and am currently the President of the Society of Molecular Biology & Evolution (SMBE). I also serve on the editorial boards of seven scientific journals and on the advisory board of five scientific institutes in the US, Europe, and Taiwan. I am passionate about the future success of scientific societies, model organism databases and research, and creating a scientific culture that values diversity and inclusion.	60.69%	531
TOTAL		875

Q2 Drosophila Board Europe Representative

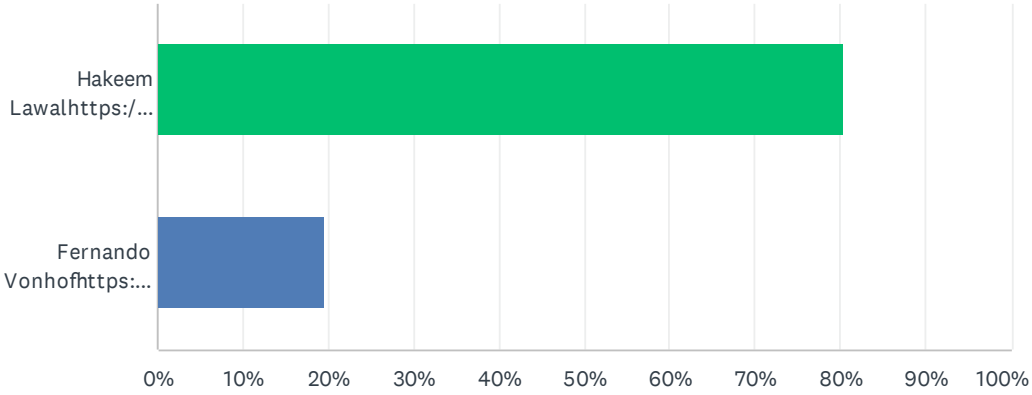
Answered: 761 Skipped: 556



ANSWER CHOICES	RESPONSES	
 Sofia Araújohttp://www.ub.edu/ibub/research-group/sofia-araujo/ I am an Associate Professor in the Division of Biomedical, Evolutionary and Developmental Genetics in the Department of Genetics Microbiology and Statistics at the University of Barcelona in Spain. The goal of my research is to better understand how cellular behaviour during development impinges on overall organismal homeostasis and behaviour. In my research lab we work towards understanding how intracellular processes govern cell migration, guidance and subcellular branching, focusing on the organelles and cytoskeleton.Drosophila became my model organism of choice, after my Ph.D. on the mechanisms of DNA damage and repair, when I recognized the power of the fly and joined Guy Tear's lab at King's College London in the UK. After that, I joined Jordi Casanova's lab at the IBMB-CSIC in Barcelona, where I later started my independent research, as a career development fellow. I worked on the mechanisms of tracheal and nervous system development, focusing on cell migration and branching. In 2016, I began my Lecturer appointment at the University of Barcelona and was promoted to Associate Professor in 2020. Since then, I have been very active not only in research and undergraduate teaching, but also in our masters and graduate programmes in Genetics. Earlier in 2021, I became the Head of the Division of Biomedical, Evolutionary and Developmental Genetics.Besides research, one of my passions is to explore new and better avenues to take science to various audiences. So, over the years, I have been involved in many SciComm activities with schoolchildren, primary and secondary school teachers and senior citizens, as well as organizing workshops and courses to help scientists communicate their research. Lately, I have also been involved in opening the doors of scientific conferences to non-scientific audiences (https://thenode.biologists.com/opening-the-doors-of-scientific-conferences-to- local-citizens/outreach).Since 2015, I have been a member of the Junior European Drosophila Investigators (aka JEDI) and co-organized our 2018 meeting in Spain. I am a board member of the Spanish Society for Developmental Biology (SEBD) and was on the scientific committee of our last meeting in 2020. I am also a member of DrosAfrica, helping to build an African Drosophila community (https://drosafrica.org). In 2017-2020 I was honoured to become and ambassador first for ASAP-Bio and then for eLife, where I could work towards better publishing policies, equity, and diversity in science. In 2021, I was appointed a member of the board of reviewing editors (BRE) of eLife.I am eager and willing to bring these motivations and skills to the Fly Board, acting as the European representative.	49.41%	376
 Daria Siekhaushttps://ist.ac.at/en/research/siekhaus-group/ I first fell in love with flies in college at Harvard during an introduction to Biology course taught by William Gelbart. After being shown the antennapedia phenotype I was hooked, and changed my major. I went on to do a Ph.D. at Stanford identifying a role for a neuropeptide processing protease in triggering hatching behavior in a project crafted as a bridge between Mark Krasnow's and Robert Fuller's group. I later worked with Ruth Lehmann, then at NYU School of Medicine, pioneering Drosophila macrophage migration as a model for tissue invasion, a process relevant for immune responses and cancer metastasis. I conducted a screen that showed that moving into and through tissues requires distinct programs from general migration. In my own lab near Vienna at IST Austria my group has used genetics, live imaging, biophysical approaches, next generation sequencing, metabolomics, and glycomics to characterize some of these programs. We like to tease out mechanisms for previously uncharacterized genes with conserved vertebrate orthologs and have identified new regulators of glycosylation and mitochondrial ATP production. We are strong advocates for the power of Drosophila and the wonders of macrophages. My lab has donated lines to Bloomington to enable easy visualization of macrophages and independent manipulation of these immune cells and surrounding tissues, which have been broadly adopted in the fly community. I have also been a co-organizer of the international Drosophila Blood Cell Meeting with attendees from the US, Europe and Asia. I also have regularly attended the European Drosophila Research conference and the Junior European Drosophila Investigator meeting, and have organized sessions at the American Drosophila Research Conference.As the European representative to the Fly Board I would seek to coordinate efforts to increase funding for Flybase from the ERC, Welcome Trust, DFG, FWF, NIH, and Asian grant administering institutions. I would also coordinate to advocate for Drosophila research with journal editors to increase attention from the larger biomedical community. I would try to bring to the other international regions a version of the European fly email lists that allow swift interaction between all European Drosophila PIs, and among their trainees, facilitating the exchange of fly lines, reagents, and advice. Finally, I would work to increase sponsorships and alliances with Drosophila representatives from other continents, including DrosAfrica, to find ways to allow at least online attendance at Drosophila conferences of students, post-docs and PIs regardless of location or funding.	50.59%	385
TOTAL		761

Q3 Drosophila Board Mid-Atlantic Representative

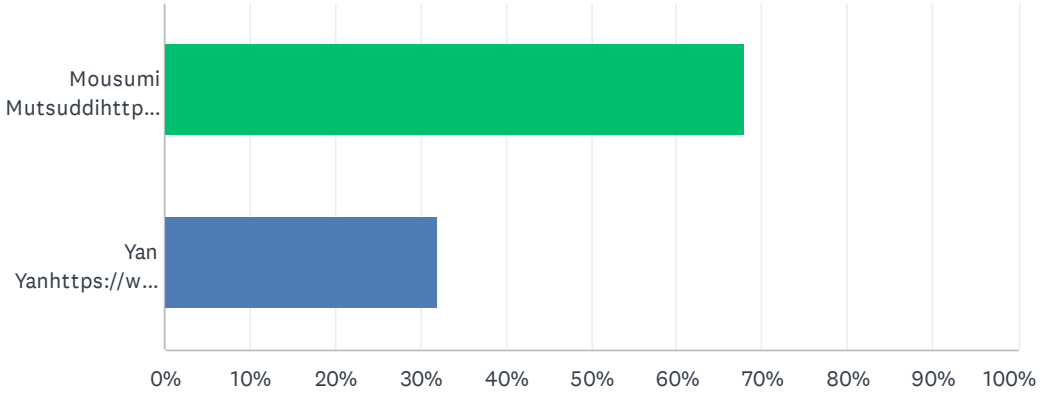
Answered: 733 Skipped: 584



ANSWER CHOICES	RESPONSES	
 Hakeem Lawalhttps://www.lawallab.org/ I am an Associate Professor and Vice Chair in the Department of Biological Science at Delaware State University and I have been a member of the Drosophila community for over eighteen years. Born and raised in Lagos, Nigeria, I obtained my Bachelor's degree in Microbiology. The era of molecular possibilities ushered in by the completion of the Human Genome Project motivated me to move to the U.S to pursue a Ph.D. in Cell and Molecular Biology at the University of Alabama, Tuscaloosa under the mentorship of Janis M. O'Donnell. My doctorate thesis was focused on using Drosophila to study the regulation of dopamine biosynthesis. I then joined the David Geffen School of Medicine at UCLA for my postdoctoral training in neuroscience in David Krantz's research lab where we used Drosophila as a model system to understand the basic biology of the vesicular monoamine transporter and its relevance to neurological disorders like Parkinson's disease. I moved cross-country once again, this time to start my research lab at Delaware State University where I have been a faculty since 2013. My lab uses Drosophila to elucidate the biology of central synaptic neurotransmission and its relevance to normal and pathological aging. The U.S faces a deep and sustained challenge of under-representation of minorities at all levels in STEM and I have resolved to use my position to help address this issue. Drosophila as a neuroscience resource has allowed my lab to successfully train students, including those from under-represented backgrounds at all levels from high school through doctorate education.I have two goals for moving the community forward; and if elected to the Fly Board, I will work on advancing them. First, I will push for increased funding for critical fly resources like FlyBase, Drosophila Genome Resource Center, and Bloomington Drosophila Stock Center (BDSC) such that they remain as free or subsidized and accessible as possible. Second, I will support further investments in the careers of young Drosophila research trainees and the identification and promotion of those early stage individuals from under-represented backgrounds so that we can build talent from the ground up. As a member of the Drosophila research community, I have benefited tremendously from the use of beloved community resources like the BDSC. I have also served on the volunteer leadership at the Society for Neuroscience (2013-2019), and on several merit review panels at both NSF and NIH. Together, these experiences position me to help identify the needs of the community and help advocate for them on the board.	80.35%	589
 Fernando Vonhofhttps://vonhofflab.umbc.edu/ I'm honored to be nominated as the potential Fly Board Representative of the Mid-Atlantic Region. I have worked with Drosophila for 15 years, starting as an undergraduate at the Free University in Berlin, Germany, working in Carsten Duch's lab. In 2007 his lab moved to Arizona State University, where I completed my PhD in Neuroscience. In 2012, I started as a postdoctoral fellow in the lab of Haig Keshishian at Yale University. I started my independent lab at the University of Maryland Baltimore County (UMBC) in 2017, where I am currently an Assistant Professor. Throughout my entire career I have studied activity-dependent molecular mechanisms regulating neuronal connectivity, ranging from fundamental processes to neurological diseases. If elected to the Fly Board, my top priority would be to address the concerning fact that certain racial and ethnic groups are underrepresented in STEM relative to their representation in the US population. It still feels for me like a dream come true to be one of the few tenure-track faculty members from an underrepresented background at UMBC, an institution with a strong commitment to promote diversity and inclusion, as evidenced by the Meyerhoff program, which has produced most of the African American M.D.-Ph.D. degree-earners nationwide in the last years.Overall, the scientific community has become more aware of this problem and more programs exist to help minority scientists stay resilient. However, both racial and ethnic underrepresentation as well as gender inequality are still improving at an extremely slow pace. Although my contribution may be modest, I'm determined to continue working with this group of bright minds in the Drosophila research community aiming at forging long-term commitments to promote diversity, equity, and inclusion in the scientific community. Serving on the Fly Board, I believe, it is the best way for me to inspire the next generation of inclusive scientists while also helping build and sustain a more diverse, innovative, and humane scientific enterprise. I'm honored to be nominated as the potential Fly Board Representative of the Mid-Atlantic Region. I have worked with Drosophila for 15 years, starting as an undergraduate at the Free University in Berlin, Germany, working in Carsten Duch's lab. In 2007 his lab moved to Arizona State University, where I completed my PhD in Neuroscience. In 2012, I started as a postdoctoral fellow in the lab of Haig Keshishian at Yale University. I started my independent lab at the University of Maryland Baltimore County (UMBC) in 2017, where I am currently an Assistant Professor. Throughout my entire career I have studied activity-dependent molecular mechanisms regulating neuronal connectivity, ranging from fundamental processes to neurological diseases. If elected to the Fly Board, my top priority would be to address the concerning fact that certain racial	19.65%	144
TOTAL		733

Q4 Drosophila Board Asia Representative

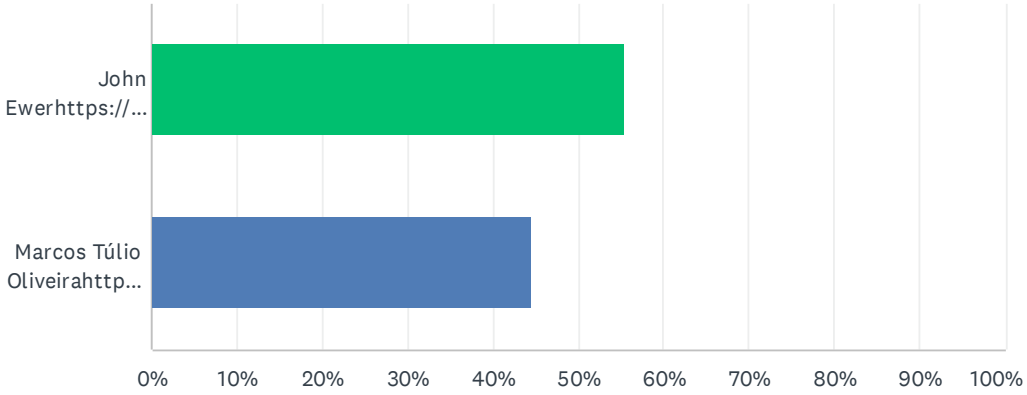
Answered: 1,179 Skipped: 138



ANSWER CHOICES	RESPONSES	
 Mousumi Mutsuddihttps://new.bhu.ac.in/Site/FacultyProfile/1_157?FA001189 Having over two decades of experience using flies for my research, I have actively engaged with the national and international research communities to advance the field of Genetics in academic and applied industrial research. After garnering a fulfilling post-doctorate experience from Whitehead Institute and as a Scientist at Broad Institute, Massachusetts Institute of Technology, USA, I moved to India in 2006 to establish my laboratory at the Department of Molecular and Human Genetics, Banaras Hindu University. The main goal of my research is to advance our understanding of the genetic and molecular mechanisms underlying neuronal development and neurodegenerative diseases. My laboratory first characterized Maheshvara, as a modulator of Notch signaling and apoptosis in Drosophila. My laboratory has also identified a rare variant affecting retinal neurons in families with hereditary ocular diseases, specifically in the North Indian population encompassing Eastern Uttar Pradesh and Western Bihar. Our lab is harnessing the power of Drosophila to bridge gaps in our understanding of traditional Indian medicine (Ayurveda). On the other hand, we strive to apply mechanistic insights from Drosophila studies in modern medicine to develop novel therapeutic strategies for neurodegenerative disorders.As one of the first Indian Drosophila Flyboard members from 2014-2017, I have gained enormous benefits in various avenues of my professional career. Hence, I would like to spread the word about the Flyboard mission within my professional network. As a former executive body member of the Indian Society for Cell Biology , I advocated formulating strategies to integrate basic biology research for undergraduate students across colleges in rural India that did not have access to state-of-the-art infrastructure. I have partnered with academic publishers such as Springer Nature India to conduct workshops to help Ph.D. students develop outreach, networking, scientific writing, and undergraduate teaching and mentoring skills. Recent work from our lab is an excellent example of how working on a simple developmental behavior using Drosophila model systems can lead to potential therapeutic applications. It is the need of the hour for the scientists working with the model systems to integrate industry and academic research. My experience as one of the early career researchers of South Asian descent in the United States and at the vibrant, diverse Banaras Hindu University has been phenomenal. Hence, the commitment to diversity, equity, and inclusion in science is routine practice in my laboratory. The Flyboard will be a suitable platform to propagate these ideas, develop new ones, and expand a strong network within the region.	68.11%	803
 Yan Yanhttps://www.yanlab.ust.hk I received my PhD degree in 2010 from the Department of Molecular Biology at Princeton University. With Professor Trudi Schupbach as my thesis adviser, I performed a genetic screening for mutants affecting Drosophila follicle epithelial morphogenesis and proliferation. My thesis work was to elucidate the functions of a number of novel regulators in the Notch and Hippo signaling pathways. I received postdoctoral training in the laboratory of Professor Chris Doe where I investigated how Drosophila embryonic neuroblasts emerge from neuroepithelia. These training experiences were a starting point for me to learn that cell polarity, and more broadly cell structural proteins, are essential for determining organ size and shape. This became a major research interest in my group after I took an independent position in Hong Kong University of Science and Technology. My laboratory studies organ formation processes including organ size control and morphogenesis through a combination of Drosophila genetics and quantitative biology methods. Over many years I have received many generous help and suggestions from the fly community. I would therefore very much like to contribute to the fly community of which I consider myself as a proud member. I have served as a board member for the Asia Pacific Drosophila Conference since 2014. I helped with recruiting fly researchers to Hong Kong and the broader bay area in China. I think I will be able to facilitate liaison with the fly community in Asia Pacific region effectively as a fly board member.	31.89%	376
TOTAL		1,179

Q5 Drosophila Board Latin America Representative

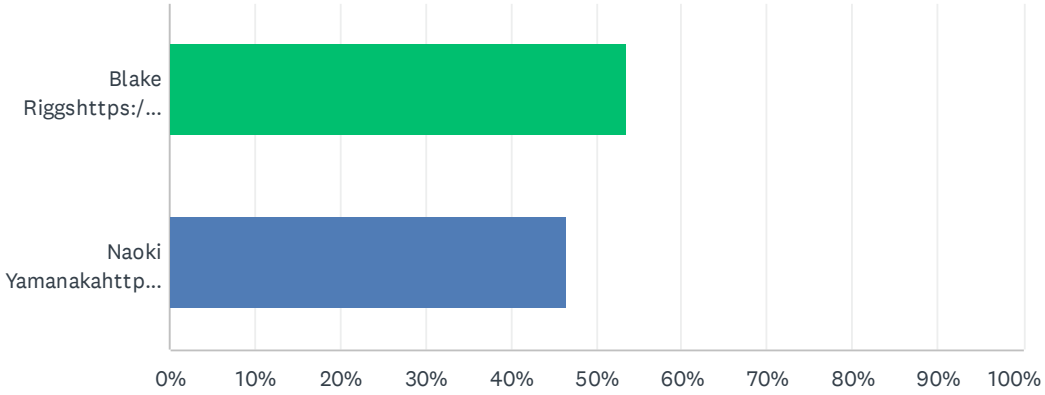
Answered: 737 Skipped: 580



ANSWER CHOICES	RESPONSES	
 John Ewerhttps://www.ewerlab.org/ I have used Drosophila for my research (and also in developmental biology teaching labs) starting in Graduate school in Jeff Hall's lab (Brandeis University); this amounts to 36 years! Part of this time was spent in the USA, including as Assistant, then Associate Professor, at Cornell University (Entomology Department), returning to Chile in 2006. Thus, I have experienced the use of Drosophila in the USA, where it is firmly established as a useful research organism, and can contrast this with the situation in Chile, where it is not widely used. But Chile is not an outlier in the region; quite the contrary, it has one of the highest number of fly labs in Latin America. However these total less than 10. This situation is odd, considering what a great organism this little fly is for doing sophisticated experiments essentially on a shoestring. Just contrast the cost of making a transgenic fly vs. a transgenic mouse; not to mention space, maintenance costs, etc. Add to this the well established and observed tradition of respecting the dictum "if it's published it's public"--which means the latest super fly is only a courier away, and you have a really appealing system in which to ask any number of very diverse biological questions using very sophisticated tools. Yet, many Latin American researchers opt to use the mouse for their research. In order to try to revert this tendency, since 2010 I have co-organized a very successful practical course ("Small Brains Big Ideas", http://smallbrains.org/) aimed at showing how Drosophila (as well as C. elegans and bees) can be used to carry out the best research in neuroscience and biomedicine. We now have students of alumni taking the course, so the word is (slowly...) spreading. One of my missions as regional representative would be to work to enlist the help of the GSA to strengthen the use of Drosophila as a research organism in Latin America.You can find information on my research at https://www.ewerlab.org/ We're at the Universidad de Valparaiso, in the port of Valparaiso, described by Lonely Planet as "Syncopated, dilapidated, colorful and poetic, Valparaíso is a wonderful mess." Come visit!	55.36%	408
 Marcos Túlio Oliveirahttps://www.fcav.unesp.br/#!/mtoliveira It is an honor to be a candidate for a position as FlyBoard Representative from Latin America. For a Drosophila researcher in North America or Europe, it may sound inconceivable to hear that the simple shipment of an order of fly lines takes more than 6 weeks to arrive, and that the flies very often arrive dead. But this is the reality of Drosophilists in South America, who must rely on stock centers that are too far away in other continents, and count on inefficient international courier and customs services. If elected, I would like to work towards finding efficient ways to deliver flies to labs in South America, which in my view would be one of the most important aspects for the promotion of Drosophila research "down here". Creating a local stock center with the help of Bloomington and the international Fly community would be the ideal scenario.After doing my BS and MSc studies in the State University of Campinas, Brazil, I conducted my PhD work in Dr. Laurie Kaguni's lab at Michigan State University, USA, on the mechanisms of mitochondrial DNA replication in humans and flies. My post-doctoral research was developed in Dr. Howy Jacobs's lab at Tampere University, Finland, with the focus on understanding the biochemical and physiological impact of the ectopic expression of the mitochondrial alternative oxidase on Drosophila. Since 2013, I have been an assistant professor of biochemistry and molecular biology at the Sao Paulo State University-Jaboticabal campus, Brazil, and have continued with these two lines of mitochondrial research, always using flies as models. Our fly work has been financed primarily by the Sao Paulo Research Foundation, and by minor grants from the Brazilian National Council for Scientific and Technological Development, and our lab has currently four graduate and four undergraduate students, who are passionate about what we do. By being far from centers of strong fly research in North America and Europe, I would like to believe some local colleagues and I have created our own fly community with the passion of our students.	44.64%	329
TOTAL		737

Q6 Drosophila Board California Representative

Answered: 733 Skipped: 584



ANSWER CHOICES	RESPONSES	
 Blake Riggshttps://biology.sfsu.edu/faculty/riggs The first time I saw a cell divide, I was hooked. Cell biology and microscopy became a passion for me, as I was fascinated that I could view the dynamics of a cell, the fundamental unit of life. As a young undergraduate, I joined Bill Sullivan's research group investigating the mechanisms involved in cytokinesis. Strangely to me, the Sullivan lab studied this question in the fruit fly embryo. I never thought that we could learn anything about human health and development from an insect that would buzz around my kitchen. I was fascinated that many of the genes found in the fruit fly could also contribute to our understanding of human development. Understanding the inner workings of the cell captivated me and the reality that there are so many unanswered questions involving the cell. Thinking of models involving cell division, I hypothesized that intracellular membrane contributed to cytokinetic furrow formation and discovered that Rab11 is involved in metaphase furrow formation in the syncytial Drosophila embryo (Riggs et al. 2003).Completing my PhD, I joined the research group of Rebecca Heald at UC Berkeley to continue my study of mitosis and cell division, specifically focusing on the organization and contribution of membrane organelles during mitosis. Finding difficulties in exploring my models using in vitro Xenopus egg extracts, I was able to show that endoplasmic reticulum (ER) membrane surrounds the mitotic spindle, but does not contribute to bipolar spindle formation (Riggs et al. 2012). In starting my own research group, we asked a simple question, "are organelles inherited during cell division?" Moving back to the Drosophila embryo, we found that ER membrane is reorganized during mitosis and is in frame with the cell cycle (Bergman et al. 2015). Surprisingly, we also saw that the ER is asymmetrically partitioned in a small percentage of cells at gastrulation prior to cell fate determination (Eritano et al. 2017). Currently, my laboratory investigates the role of ER in the correct partitioning of cell fate determinates to generate cell diversity during development. Throughout my career, I have been an advocate for efforts involving greater diversity, equity and inclusion in STEM (Science Technology Engineering and Math). As scientist, we are tasked to answer questions involving human health and natural phenomenon that impact the lives of our nation, however we are not accessing our rich talent in this country. There is an extreme need for different viewpoints and approaches in research and increasing diversity and inclusion is necessary to achieve the next scientific discoveries. As a member of the Flyboard, I will push for greater inclusion of all institutions and viewpoints to move our community into this new era of equity and inclusion.	53.62%	393
 Naoki Yamanakahttps://www.yamanakalab.com I received my Ph.D. (Biological Sciences) from the University of Tokyo in 2007 for my work on neuropeptides that control insect molting and metamorphosis. I was trained as a fly geneticist when I was working as a postdoc from 2007 to 2014 under the supervision of Mike O'Connor at the University of Minnesota, where I studied molecular mechanisms regulating production and secretion of the steroid hormone ecdysone during Drosophila development. In my own lab in the Department of Entomology at UC Riverside, we work on ecdysone and other lipophilic hormones/lipid mediators that control insect physiology. Through our recent work on Ecdysone Importer (EcI), we are proposing the facilitated diffusion model of lipophilic hormone transport across cellular membranes as compared to the traditional simple diffusion model.I believe that my background in entomology and endocrinology research can bring a new perspective to the Drosophila community, where issues related to "inter-organ communication" are becoming more important than ever before. In the past few years, I have been involved in organizing workshops and conferences on insect hormones, such as the Ecdysone Workshop at the Fly Meeting 2019 and the International Insect Hormone Virtual Workshop this year. I have also been actively engaged in multiple outreach activities in our Entomology Department; in the Junior Entomologist Summer Camp Program led by our graduate students, for example, I teach 4-6th graders how to genotype fruit fly mutants by using PCR. I would like to leverage my experience in these outreach activities to benefit the entire fly community and beyond.	46.38%	340
TOTAL		733

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

A. Introduction

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

B. Reference Genome sequence

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

C. Reference Microbiome Genome sequence

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

D. cDNA Clone Resources

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

Table 1. Summary of Human Expression Clones.

Collection	Vector	Promoter	C-term Tag	System	Started in 2021 -still in process	Finished this past year (3/2021-3/2022)	Total Finished
hGUHO	pGW-HA.attB	UAS	3xHA	Gal4-UAS	1536	641	6157

D. Embryonic Gene Expression

We continue to collect embryonic spatiotemporal gene expression data from high throughput *in situ* hybridizations using the Gold Collection clones as templates for RNA probes. Annotations assigned by stage to each gene are now included in the FlyBase gene reports. In addition to the wild type gene patterns, we are collecting expression patterns for selected CRM-driven reporter constructs from the Rubin/Janelia collection and additional constructs generated as part of our collaboration with the Berkeley Drosophila Transcription Network Project. We incorporate the CRM experiments into the public database (http://insitu.fruitfly.org) with links to the FlyBase sequence feature reports for these constructs. Our homepage includes a separate browse tab for the CRM experiments to improve accessibility. Our improved gene reports include graphical summaries of the stage specific organ system annotations and a graphical representation of the associated modENCODE RNA-seq data. The updated version also allows searches by all known gene name synonyms and human ortholog names. We continue to add new search and discovery tools based on computational image and annotation analysis. We published an advanced method for modeling spatially local gene interactions and networks with our dataset. An interactive viewer based on the annotated patterns of 708 site-specific transcription factor genes, using self-organizing maps to show relationships among transcription factor expression patterns in the context of organ system development, can be accessed at http://insitu.fruitfly.org/som. We are active participants in the development of image analysis within the open-source image analysis platform FIJI (fiji.sc). We are starting to use our recently finished open-source microscope automation software for automated slide loading and imaging with commodity hardware. We have updated our manual imaging tools away from proprietary products to use a prosumer Nikon D5100 camera with open-source Micro-Manager software. The newer camera and open-source software allow us to take high quality images while using well-maintained software that runs on modern operating systems. To date we have completed and annotated experiments for 8558 genes and 336 CRMs documented with over 182,991 images. We have begun projects to image new sets of genes, including Kinases, smORFs (103 imaged), and lncRNAs (41 imaged)

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

The modERN (model organism Encyclopedia of Regulatory Networks) project is an independent R01 submitted to complete the study of fly and worm transcription factors (those defined as having a currently recognized DNA-binding domain) determining their genomic DNA binding sites in animals using the ChiP-Seq assay as was perfected in ENCODE. To date the Celniker lab has produced 401 transgenic GFP tagged-TF fly lines. All but the most recent are deposited at the Bloomington Stock Center. The White Lab intends to perform ChiP-Seq for a total of 597 lines having already completed 502 datasets for 486 lines. The data is being processed through the ENCODE pipeline and is being distributed through the ENCODE DCC. In addition, we produced TF knock down RNAi followed by RNA-seq experiments for a number of TFs [54 sequenced (~324 RNA samples)]. The validated RNA-seq files have been submitted to the ENCODE DCC and are in their process to be made available to the community. We hope to have a manuscript soon describing the putative targets of these TFs.

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

A RO1, "Systematic, Genome-Scale Functional Characterization Of Conserved smORFs" was funded in 2017 to functionally characterize genes that may or may not be coding proteins that have small open reading frames (<100 aa) and are conserved from flies to humans. We have two manuscripts ready for submission.

G. Other Resources

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

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

H. Technology

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

I. Funding

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

Reference for Drosophila microbiome

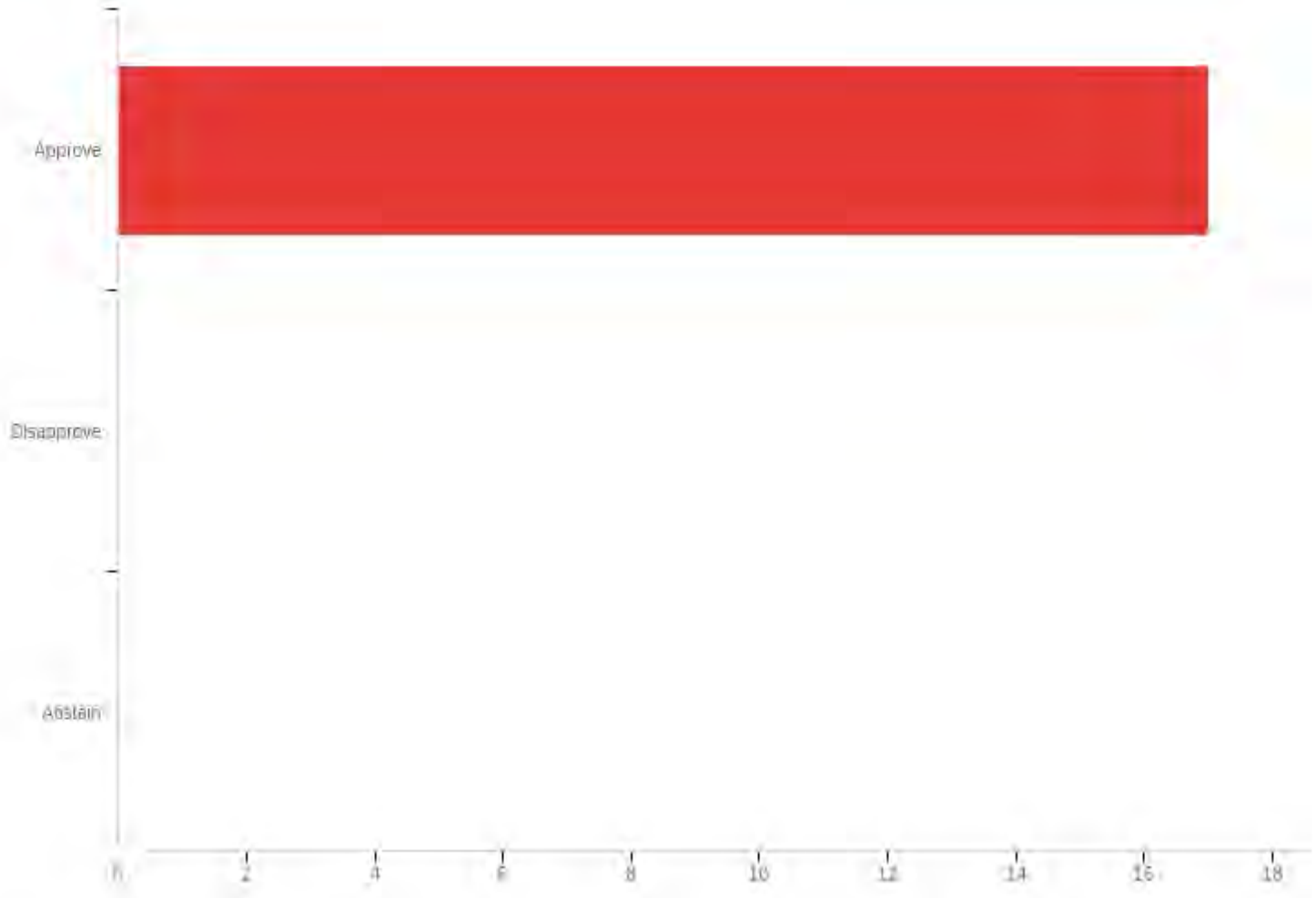
An integrated host-microbiome response to atrazine exposure mediates toxicity in Drosophila.
Brown JB, Langley SA, Snijders AM, Wan KH, Morris SNS, Booth BW, Fisher WW, Hammonds AS, Park S, Weiszmann R, Yu C, Kirwan JA, Weber RJM, Viant MR, Mao JH, Celniker SE. Commun Biol. 2021 Nov 24;4(1):1324. doi: 10.1038/s42003-021-02847-y. PMID: 34819611

Voting Report

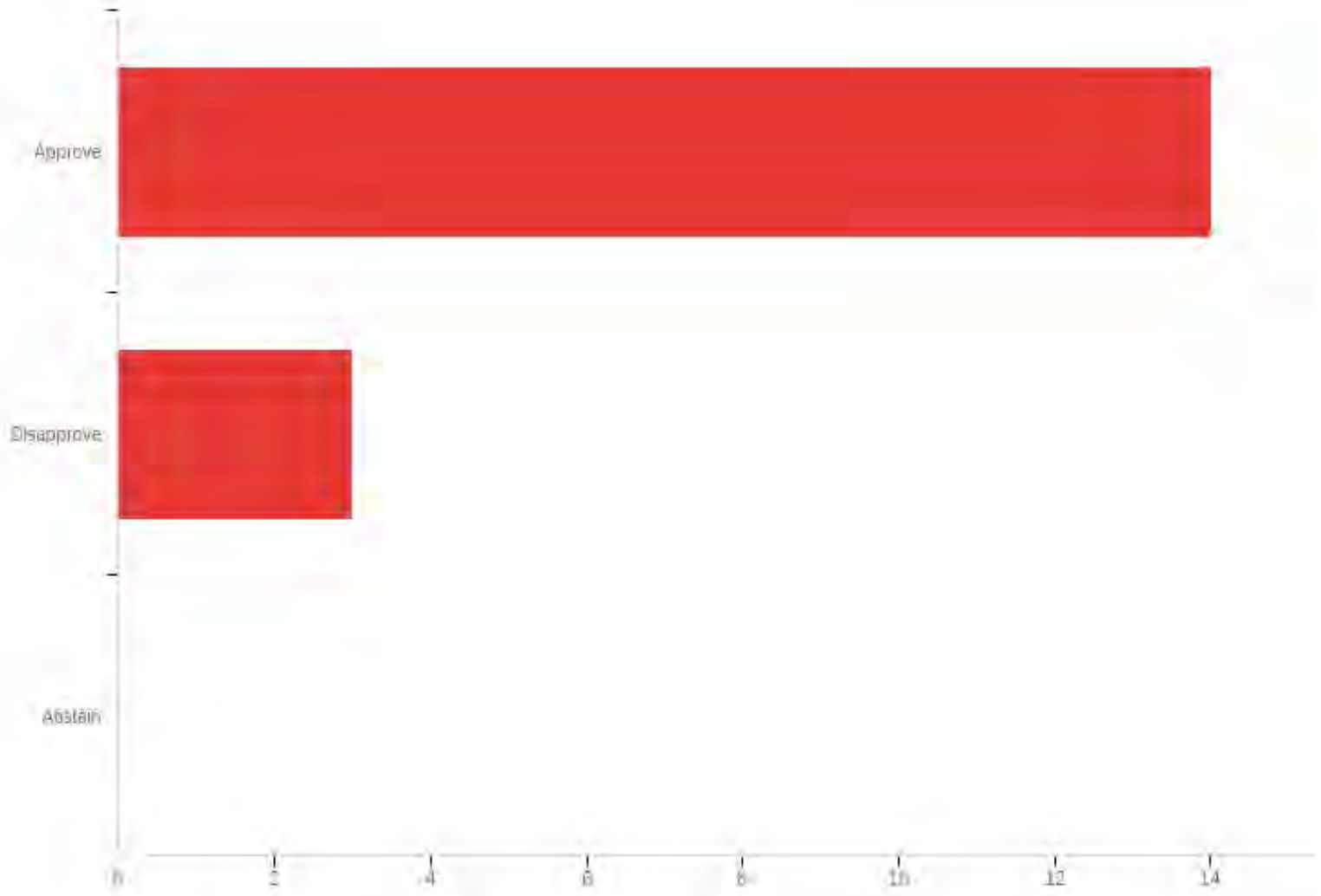
Fly Board Feb-March 2022

February 28th 2022, 12:25 pm MST

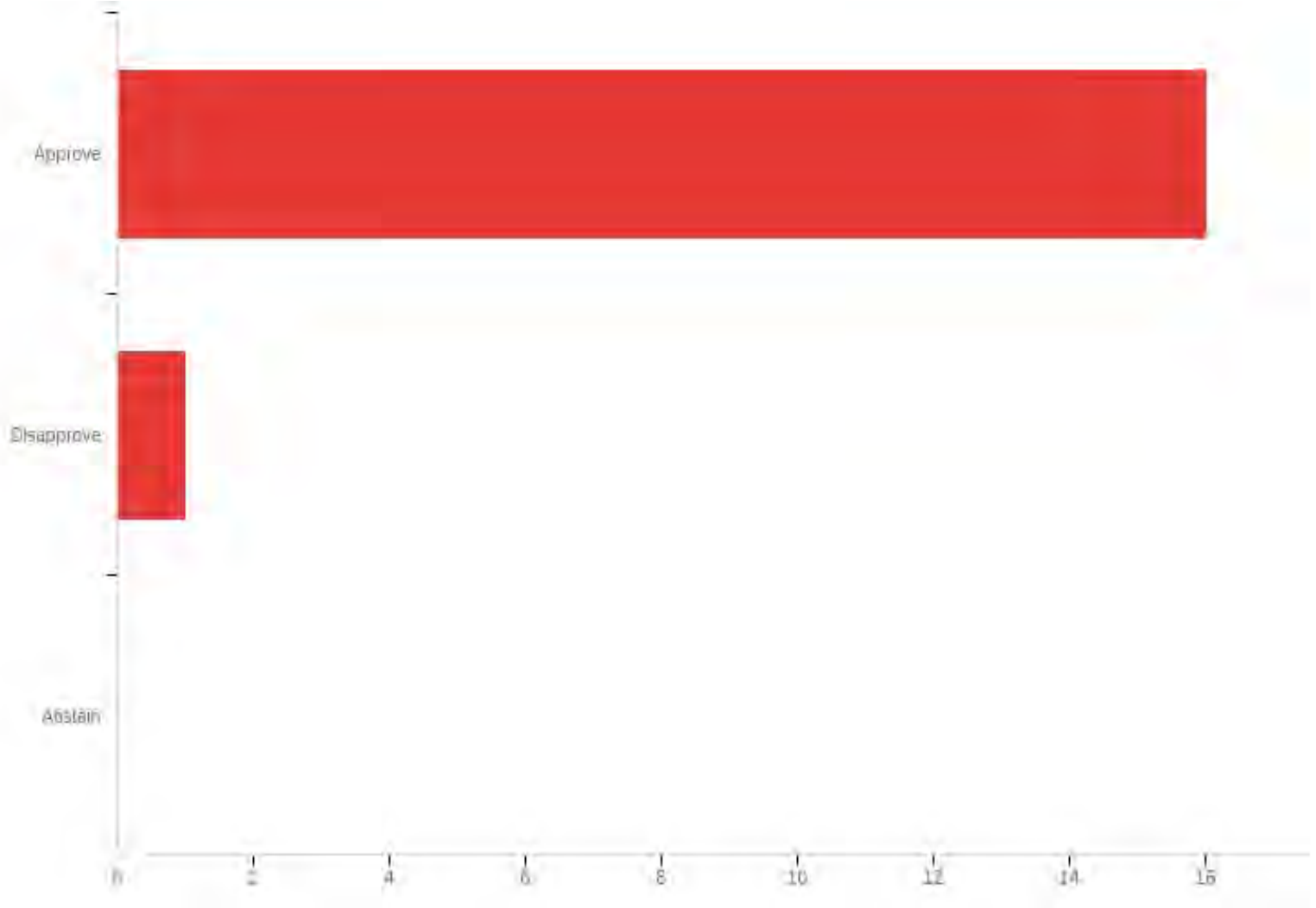
Q1 - In 2022, Fly Board will conduct a survey with the assistance of the Genetics Society of America. This survey has three goals: 1) build an email database of fly community members; 2) ask community members if they would be willing to volunteer for Fly Board and ADRC-related groups; and 3) to build an opt-in database of Drosophila colleagues from all backgrounds so that we can ensure committees, organizers, and speakers reflect the full diversity of our community.



Q2 - Add to the Fly Board one member to represent minority-serving institutions and community colleges. Election of this representative will first occur with the Fall 2022 regular Fly Board elections. The appointment will cycle every three years, similar to the regional representative's service to the Fly Board.

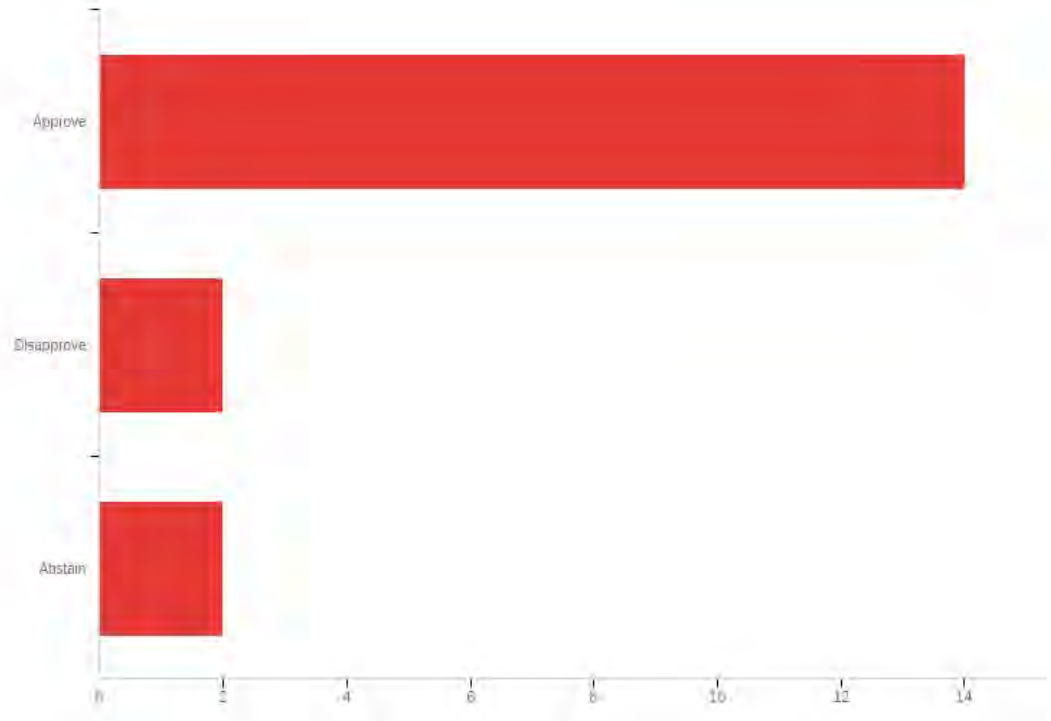


Q3 - Develop a mechanism for orderly transfer of information for each committee from one year to the next (Sandler, Finnerty award, Trainee award, Image award, Elections committee, Communications committee), including a timeline that each committee should follow and best practices. (This information will be accessible via a link from Fly Board wiki, much like meeting minutes.)



Q4 - Fly Board encourages the organizers of ADRC to:1. Consider all demographic groups when selecting speakers and session chairs, especially from groups that have been historically underrepresented in these roles. 2. Develop a broadly advertised and accessible process to nominate speakers, including self-nomination. 3. Be creative and flexible about the format of the meeting from year to year.

Designate an ADRC committee member as the DEI representative for the group and devote part of each ADRC committee meeting to considering how the group is proceeding with respect to DEI.4. Consider Flyboard and GSA as a resource to support ADRC committee efforts, for example, by getting feedback on speaker choices throughout the process.5. Consider making a land acknowledgement statement that is coupled with a statement about concrete DEI actions.6. Provide the next set of organizers with a timeline and notes about best practices to help to ensure consistency across years in having a diverse, equitable and inclusive meeting.



Minutes From 2022 Drosophila Board Meeting at Annual Drosophila Conference, April 5, 2022 in San Diego, California.

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

2. Approval of the minutes from 2021 meetings: The minutes from the previous North American Drosophila Board meetings were approved, including minutes from two additional Zoom meetings that occurred in July and October of 2021.

3. Vote on Service Award: Michelle Arbeitman presented the policy for a new Service Award. The committee members that worked on the policy were Kevin Cook, Nadia Singh, and Michelle Arbeitman (chair). The Service Award policy was approved by the Drosophila Board.
    - The chair of the Service Award committee has the option of working with the GSA DEI committee to help pick members of the committee that will decide on the recipients of Service Award.

4. Brief Reports
    a) *Fly Board elections:* Mark Peifer presented the results of the Fly Board Elections. The Elections committee included Iswar Hariharan, Tina Toole, and Erika Geisbrecht. Alissa Armstrong agreed to serve as a new member. Voting this year was between two candidates for each seat. The Report from the committee includes the email used to solicit nominations.
        - It was noted that not all people that vote do so for all candidates. It is not clear why this is the case.
        - It was suggested that voting could be tied to early registration for the Fly meeting, as a way of publicizing the election to the community. The goal is to get more people to vote.
        - A suggestion to add a question about career stage to the ballot to get an idea of who is/isn't voting.

    b) *Treasurer's report*: Jessica Treisman presented the Treasurer's report. The funds in the Vicky Finnerty Memorial Fund were invested in the stock market (Wellington Fund). There was discussion about use of the Drosophila Trainee Fund (also called Reserve Fund) and the Sandler Award Fund for trainee awards. A committee that included Jessica Treisman (chair), and three regional representatives, Kieran Harvey, Rachel Smith-Bolton, and Brain Lazzaro, decided to make a call for awards for outreach efforts, rather than travel awards. A call for applications for these Trainee Awards was made in October with an advertisement on Flybase. Seven applications were received.

- It was noted that there were significantly fewer applications this year than the previous year.
- The committee found five applications that were meritorious of funding.
- There was discussion regarding how to find additional ways to advertise the award to have a larger pool of candidates.
- There was discussion that even though there were fewer candidates that this was a great use of money, with many worthy proposals.
- Is there a way to evaluate impact without overburdening recipients? A short questionnaire was suggested. It was mentioned by several individuals that monitoring outcomes could be an issue because of the time it takes and potential parental consent issues, if awardees work with minors.
- It was suggested that the GSA blog would highlight the awardees. It was also suggested that colleagues can reach out to science journalists to expand outreach.

c) *Sandler Report*: Alissa Armstrong (chair) presented on the Sandler Award Committee process. They had 17 nominations with a submitted abstract that each member ranked on a scale from 1-10 for significance, originality, and clarity. Four finalists were identified and invited to submit their theses. A unanimous winner was chosen and three co-runner-ups.

- The committee used an iterative consensus building process that they thought worked well.
- It was suggested that the call for nominations be done in early December, with a clear due date. It was also noted that the letters were longer than what fit in the box—make the process clearer.
- Is there a way to broaden the pool of nominees? Can there be a self-nomination process? There is an awards task force that Sarah Bay is working with to ensure DEI is considered for all awards.
- The committee discussed DEI and suggested that in the future there is a better way to collect demographic information about the candidates as part of the process.
- The winner will be announced before the ADRC meeting in future, as it is thought that it could be a draw to attend the meeting.

d) Genetics Society of America Report:

i) GSA reports from several individuals: Tracey Depellegrin's report shows the range of services GSA provides to the Droosphila community. She also reported that the 2022 ADRC meeting is the second largest ADRC meeting, with ~1,100 in-person attendees and ~1,600 total. All GSA meetings are currently being held in the hybrid format. Suzy Brown reported that extra efforts were made to minimize contact between people, with printable badges. Hugo Bellen spoke about additional measures to ensure safety with covid testing and vaccination requirements. N95 masks were provided. Meeting rooms with extra space was also available. All talks were live-streamed and recorded. Posters were online with an audio application for questions. In-person posters had 1 person per 8-foot board. It was announced that the next 2023 ADRC will be in March in Chicago.

The 2024 meeting will be in March in Washington DC and will be an Allied Genetics Conference. Hugo Bellen provided information about the current administration at GSA. He commented that Tracey Depellegrin and her team have done a great job and that GSA is in good financial health.

- There was a brief discussion regarding whether there were any concerns that needed to be addressed about the hybrid format. The format has been successful, and no concerns need to be addressed by the Fly Board, at this time. It was mentioned that the GSA will keep evaluating the responses and consider if meetings going forward will be hybrid.
- Hybrid meetings provide opportunities to be more inclusive.
- The technology is evolving and will likely be less costly going forward.

ii) Equity and Inclusion Committee: Sarah Bay and Andrew Arsham are members of the committee that provided updates. They made clear that the DEI committee is working in collaboration with the model system community partners. The GSA DEI committee was formed in 2019. A public commitment to have DEI scholarship as a plenary session was established, with the first meeting having this session in 2021. The GSA DEI will assist ADRC meeting committees with the process of selecting speakers. The GSA DEI committee will provide guidelines for ensuring a diverse and equitable meeting, to support the Fly Board and meeting organizers. The GSA DEI committee presented a Draft of their vision for best practices for choosing Chairs and organizing committees. This will go to the GSA board for approval. It will then go to model system boards for feedback. The document will be ready for the 2023 meeting planning process.

iii) GSA public engagement and communication: Stephanie Mohr reported on the committee's activities. Jane Hubbard is the chair of the GSA committee. The goal is to promote the numerous GSA success stories. For example, studies that go from model system research to therapies. The GSA Blog will describe these stories. The plan is to make this an iterative process and get feedback for future years.

e) ADRC organization

i) 2022 ADRC Committee Report: Erika Bach (chair) self-nominated for the role of chair and then invited additional colleagues to fill-out different areas of expertise. Erika detailed the committee's process and expressed appreciation for Suzy Brown (GSA) efforts to keep their committee on track. One goal of the committee was to invite a diverse set of speakers. Chris Doe was chosen for the keynote address, given his outstanding science and that he also may be a strong draw to have Drosophila neuroscience colleagues attend the meeting. This year there were more plenary speakers, which left less time for platform talks. Andy Arsham and Racheal Smith-Bolton chaired the DEI session. Faculty were invited to be platform chairs by the ADRC committee, and they reached out to post-docs to work with them. The committee accepted nearly all the platform talk recommendations, except if the person spoke in the previous year. Erika discussed that they used the keyword categories from previous years and noted some categories had very few submissions, so should be evaluated

further. For the 2022 ADRC meeting, there were fewer workshop applications than typical, with two held online the Friday before the meeting. Due to Covid, posters were hung and then removed after the session, so there was more space.

ii) Tin Tin Su announced that Savraj Grewal will be the chair of the 2023 ADRC committee.

f) Resource centers

i) BDSC: Kevin Cook commented that BDSC survived the impact of the pandemic, though use numbers are still down. There were some concerns about covering costs. It was noted that solutions may be higher fees, the need for more grant support, or some stocks will be culled. It was noted that there is difficulty shipping outside of the USA. Additionally, independent of the pandemic some stocks, like transposon insertion alleles, are likely not being ordered due to the ability to use CRISPR-based strategies to make alleles of interests.

ii) VDRC: Lisa Meadows commented that VDRC also has fewer orders than pre-pandemic. They are missing some of the large orders/full collection requests. They are considering which lines to keep, given they need to reduce costs. They are also asking colleagues to donate stocks, especially those in Europe.

- There was discussion about keeping DNA from retired stocks, to gain sequence information.
- The protocol for freezing stocks was discussed. At this time, it is not a mature technology.

iii) DGRC: Andy Zelhof discussed that ordering has returned to pre-covid levels. He was appreciative of Drosophila community members for donating reagents. The DGRC is in their final year of a grant award. They will request letters from different community members. The DGRC catalog now has RRID numbers to aid in paper submission.

iv) DRSC/TRIP: Stephanie Mohr indicated that TRIP has NIGMS funding and will be applying for additional grants. Many of the services provided rely on bioinformatic tools. The DRSC/TRIP has made significant improvements to these computational tools. There are also several additional screening platforms, including mosquito, in vivo tools and protein technologies. The DRSC continues to do outreach and training. The DRSC/TRIP efforts have also made good progress on biomedical sciences partnerships and they will apply for further funding in January, 2023.

v) GDP: Hugo Bellen discussed the three main projects. One is the gene disruption project that is focused on developing T2A-Gal4 and Kozak-Gal4 lines. A second project is the Human cDNA project that focuses on genes that contribute to human disease. This effort is in collaboration with several additional groups (Kyoto and Berkeley). The group also obtained covid grant supplements to make transgenes for genes that contribute to Covid.

g) Flybase

i) Flybase: Susan Russo Gelbart reported that Flybase had a good year, with several new features implemented. The Flybase effort is in year 5 of a 5-year grant. There is a new 2023-2028 proposal, with a drop in funding to 50% of the current level. The fees Drosophila

researchers have been paying are very helpful, though dropped off recently. Harvard has streamlined the process for payment.

- Discussion about how much labs should pay for undergraduates that use Flybase. It was suggested that colleagues pay what they feel is appropriate.

ii) The Alliance: Brian Calvi discussed the Alliance Genome Resources that is a database for multiple model systems. They are funded by a U24 (2019-2024), with Flybase colleagues putting a lot of effort into the grant. There are only 2 FTE supported by the U24. Drosophila colleagues are encouraged to use to the website.

iii) Flybase was approached about gene names that might be offensive, including *hunchback*, *Kruppel* and Gypsy.

- There was a discussion about renaming genes. Flybase will make sure that all synonyms are listed. Flybase did not feel that it was in their purview to change names. A committee will be formed by Fly Board president to further evaluate this issue.

h) Graduate student survey. Ana-Maria Raicu presented the results of the graduate student survey, with 82 people responding. One issue that was discussed was having a centralized place for electronic resources. This would include materials for people new to Drosophila research, resources for dissections, and troubleshooting guides. It was also noted that people do not feel strongly connected to the Drosophila community.

- Discussion about social events, especially local events ensued. Can we help newcomers understand the fly community through more web based resources, including a map with all fly labs.
- There was discussion about Flybase having a link to resources, including wiki-pages, youtube videos with the idea that it would help people new to Drosophila research.
- It was discussed that some of the "outreach funds/reserve funds" could be used for this Flybase effort. The Treasurer, Jessica Treisman, called for a vote on this proposal. A vote about whether Flybase could apply to obtain an outreach/trainee award to enable making this web-based resource occurred and was approved (13 people raised their hand, seven of which were on Zoom). The issue being decided was whether this would be an appropriate application-type, under the current language.

5) Updates and Announcements

a) *Mission Statement*: Bruce Edgar chaired a committee that drafted a mission statement for the Drosophila Board. The goal is to communicate the goals of the Fly board. The mission stated is now posted on the wiki-page.

b) *European Drosophila Society*: Nic Tapon proposed that we elect people to cross-serve on boards. This was raised as many issues require coordination across countries (shipping and outreach).

- There was discussion regarding whether it was appropriate for one member of the North American Fly board to be chosen using different rules/procedures.
- It was agreed that it would be the duty of the past-president to be the representative on the European Board.

- It was suggested that a European Board Member be *ex officio* on the North American Fly Board.

6) Looking on 2022-2023
a) *Ballot Measures*: The results of ballot measures were presented by President Tin Tin Su. The flyboard voted to conduct a survey to generate a database of the fly community. This will be implemented by GSA, with input from the Fly Board. The board voted to elect a new board member to represent HBCU and community college institutions. The board voted to implement a clear way to transfer information to board members across years. This will be implemented by the new president. The board voted to provide a set of recommendations to the ADRC committee.
b) *White Paper*: The new white paper was announced by Tin Tin Su. She provided a link for colleagues to comment on the Draft through April 30, 2022.

Attachments:
1) 2022 Board Meeting Agenda
2) Reports_2022
3) Service Award Policy
4) Ballot measures that were approved
5) Flybase White Paper (??? Include?)
6) Drosophila Board White Paper(??? Include?)

2021 Drosophila White Paper

The first Drosophila White Paper was written in 1999. Revisions to this document were made in 2001, 2003, 2005, 2007, 2009, 2012 and 2016; these versions are available through the Drosophila Board website. Here, the Drosophila Board of Directors presents an updated White Paper identifying and prioritizing current and future needs of the Drosophila research community, based on input from community leaders and comments received from community members. This document is a resource and reference for the Drosophila research community, for national funding agencies (NIH, NSF), and for leaders in other fields of research, scientific communication, and education. This White Paper was approved by the Drosophila Board on MONTH DAY, 2022.

Part I: Drosophila as an experimental system for research – past, present, and future

Drosophila is a leading animal model for biomedical research and for understanding the basic biology of animal systems. Data and discoveries acquired from studies in Drosophila directly impact our understanding of evolutionarily distant metazoans, including humans and other vertebrates, as well as invertebrates such as insects that are of medical or of agricultural importance.

Our understanding of the basic principles of genetics, including the nature of the gene, genetic linkage, meiotic chromosome segregation, recombination, and the appreciation that genetic information can be permanently altered by external insults such as X-rays all arose from studies in Drosophila, particularly *D. melanogaster*. Pioneering cloning studies with *D. melanogaster* that linked molecular lesions in the genome with mutant phenotypes led to the identification of many genes and their products that play essential and conserved roles in development and physiology of all animals including humans. Drosophila research has led to deeper understanding of fundamental biological processes, including the innate immune response, stem cell determination and maintenance, cell and tissue polarity, cell proliferation and growth control, pattern formation, organ morphogenesis and physiology, circadian rhythms, sensory biology, animal behavior, learning and memory, sex determination, fertility, neuronal pathfinding, meiosis and mitosis, interphase chromosome structure through the study of polytene chromosomes, synaptic transmission and evolution. Additional areas where Drosophila research has provided critical, fundamental insights include investigations of organ development and physiology, neural function across scales from genes and molecules to neural networks to behaviors, transcriptional regulation including cis-regulation, nuclear architecture, gene regulatory networks, epigenetics, and the genetic basis of complex traits. Drosophila studies also provide insight into the importance of gene-gene interactions and powerful tools to identify genes and pathways relevant to homologous traits in humans, gene-environment interactions including interaction between the microbiome and animal physiology, metabolomics and pharmacogenetics, and the characterization of human disease genes. Studies that differentiate cell-autonomous versus non-cell autonomous effects, especially those addressing systemic inputs into cell behavior, are routine in Drosophila, whereas they remain challenging in other animal models, organoids and other ex vivo models. For example, many of the components of signaling pathways that cells use to communicate with each other, including Notch, Wnt, Hedgehog, Dpp, receptor tyrosine kinases, Hippo, and Toll, were first discovered and characterized in Drosophila. Mutations in genes in these pathways are now recognized as central contributing factors to major human diseases including cancer, cardiovascular disease, developmental disorders and neurological disorders. Drugs targeting these pathways are in use or in clinical trials today, with current Drosophila research helping to identify new drug targets. Drosophila research has led to unexpected discoveries about human disease and animal biology, such as insights about human basal cell carcinoma based on knowledge

gained from studying Drosophila embryonic patterning genes. Therefore, Drosophila research provides an essential pipeline for discovery of drug targets and, in some cases, direct identification of drug candidates and drugs. More recently, Drosophila screens have been used for personalized human medicine, where the most efficacious drug regimen can be identified for a patient based on tests in Drosophila of the effects of disease-specific mutations from the patient. Drosophila thus serves as an outstanding model organism for understanding animal biology and modeling human disease, including identifying molecular mechanisms and new therapeutic strategies.

D. melanogaster's was the second animal genome ever fully sequenced and the first animal genome completed by whole genome shotgun sequencing, which was the approach later used for the human genome. The experimental and computational approaches used in that effort helped guide the trajectory of other genome projects that consequently moved forward rapidly. There are now hundreds of different *D. melanogaster* strains with fully sequenced genomes, providing resources for research on natural variation, population- and quantitative-genetics, areas that have greatly expanded in scope with the reduced cost of genome sequencing. In addition, the genus Drosophila – with a known phylogeny, including several species that have been characterized for different biological traits, 108 species with sequenced genomes, and increasing amenability to genetic manipulation – has been a key model for understanding variation and conservation. Comparative genomics studies across Drosophila species have elucidated molecular contributors of speciation and evolution, which helped to identify important genomic elements that are highly conserved. Studies across *D. melanogaster* strains performed using the Drosophila Genetics Reference Panel have elucidated the extent and consequences of natural sequence variation within species. This, in turn, has guided the best approaches for human genome-wide-association-studies (GWAS) that seek to understand individual human differences, including disease susceptibility and drug-sensitivity/effectiveness. Drosophila also serves as the closest genetic model for the major insect vectors of disease, including *Anopheles gambiae* (malaria), *Aedes aegypti* (zika, dengue fever, yellow fever), and *Culex pipiens* (West Nile fever). Understanding medically and agriculturally important insects has been facilitated by Drosophila research, including pollinators such as honeybees and pests that include many species of Diptera (for example, Tephritids and *Drosophila suzukii*), beetles and aphids. The enormous contributions of Drosophila research have been acknowledged in part through recognition of many Drosophila researchers with major scientific prizes, including six Nobel prizes awarded to ten researchers.

Drosophila offers a unique and overwhelming combination of strengths as an experimental model. Drosophila research is facilitated by a vigorous and collaborative community of researchers, relatively low fly-maintenance costs, short generation time, and a relatively simple genome that can be readily engineered for molecular-genetic studies. The Drosophila research community has built an extensive and accessible research toolkit that provides diverse strategies for manipulation and visualization of gene/protein functions; cells, stock-centers and curated online resources; and detailed databases of gene and protein-expression at the tissue, stage, and single-cell level. Recently, a complete map of the adult brain connectome at electron microscopy resolution and a single-nucleus transcriptomic atlas of the adult fruit fly were completed. The entrenched tradition in the community that cutting-edge resources are made readily available to all researchers has greatly facilitated progress for all biomedical and animal research. The unique position of Drosophila as a biologically complex, yet easily manipulated and analyzed, animal model makes it especially well-suited for a broad range of studies.

D. melanogaster has also been widely used for educational outreach and training. In pre-college classrooms, *D. melanogaster* is an accessible, simple and safe model system to introduce children to experimental science, which is critical for sparking scientific interest. In college classrooms, *D. melanogaster* has long been an important mainstay for introducing a broad range of genetic and developmental biology concepts. Importantly, classroom laboratory exercises that teach sophisticated biological concepts can be performed without the use of vertebrate animals. Drosophila community members have shared laboratory exercises that use readily obtainable Drosophila strains. Scholars earning their PhD or conducting post-doctoral research using Drosophila as a model are trained in a broad range of experimental, computational and theoretical biology areas. The expertise gained by these trainees enables them to contribute in diverse and important professional settings.

Part II: Maximizing resources for Drosophila research

The ability of Drosophila research to continue to pioneer our understanding of general principles underlying the biology of animals, including humans, depends both on the availability of funding and on continual reassessment of and investment in the resources necessary to support Drosophila research. We strongly emphasize the need for continued funding of investigator-initiated research into both basic and applied problems in biological sciences, for instance through the NIH R01 or R35 mechanisms. Such research, in turn, requires continued and robust support of community resources (databases, stock centers, etc.). We also encourage better integration of Drosophila researchers during the planning stages of larger projects, much like our community's participation in the Drosophila Genome Sequencing Project led by the Berkeley Drosophila Genome Project, NIH/ NHGRI ENCODE, NIH/ NHGRI modENCODE and NIH/ NHGRI ModERN projects. We strongly emphasize the need for continued and increased support of these shared resources that serve as the foundation of the Drosophila research community as outlined in this document. Here, we outline current resource priorities of the Drosophila research community.

1) Database and informatics resources for Drosophila research

To ensure that Drosophila research continues to effectively play a leading role in biomedical and animal research, it is crucial to have a central database resource that captures, organizes and presents core information on Drosophila. The primary resource for such information is Flybase, which is invaluable to the Drosophila community, as well as non-Drosophila researchers, and educators. High quality literature curation is one of the features that makes FlyBase a unique and highly valued resource. Such expert literature curation cannot be automated. There is universal agreement within the Drosophila community that continued support for the Flybase curated database is essential to all Drosophila research. The Flybase portal provides search tools and links that allow one to access information at different levels. One of the most widely used tools is for acquiring information about a specific gene of interest. Flybase provides a range of critical information on each Drosophila gene page that helps research move forward efficiently. This information includes a summary of the function of the gene, up- to-date gene annotations, characterization of mutant phenotypes in different tissues/organs, RNA and protein expression profiles, Drosophila stocks/mutant alleles and molecular reagents, links to orthologs/homologs in other species, as well as many other types of information that are annotated in detail on the gene page. The page greatly simplifies the process of identifying the reagents that are available to study that gene and the sources from which they can be obtained. There are also key bioinformatics resources that are linked to each gene page, including genomic-scale resources such as genome and transcriptome sequence information, protein sequence

information, and protein structure prediction including AlphaFold. Additionally, gene expression information is provided from different developmental stages and tissues, including the results of RNA-sequence analysis and single-cell RNA-sequencing. Flybase offers several additional query tools to provide efficient access to the available data and to facilitate the discovery of significant relationships between genes, proteins, and phenotypes. For example, a Parkinson's Disease "Human Disease Query" yields the names of Drosophila homologs of genes implicated in Parkinson's Disease along with the information from Drosophila research on Parkinson's Disease. Another example is the ability to search for all Drosophila Transcription Factors or sub-classes of Transcription Factors, by performing a "Gene Groups Query". The ability to access Drosophila data at such different levels is critical for making connections across disparate bodies of information and accelerating scientific discovery. The Flybase portal provides access to large-scale datasets including whole genome sequences, full RNA-seq data sets, and focused BLAST searches. The Flybase homepage also serves as a community page for announcements, educational outreach, and links for multi-species mining, among many resources. Whereas capture of some classes of information from the literature may be automated, organizing and presenting most classes of information requires manual curation. Furthermore, all data classes require community input, direction and oversight. Non-specific or all-purpose genetics and genomics databases are not a viable substitute for Flybase.

To enhance the accessibility and utility of Drosophila database resources for Drosophila researchers and for those working with other systems, it is essential to link resources dedicated to Drosophila with those dedicated to other organisms. Linking FlyBase and external databases provides opportunities for further exploration to gain insights about connections to human disease, and additional resources of biological and molecular information to understand animal biology. Altogether, it is essential that the unique classes of information fundamental to Drosophila research be preserved and enhanced so that these databases will continue to benefit future research. Over the years, FlyBase has matured from a database to a knowledgebase (for example see Larkin et al., 2021). We strongly support FlyBase's current efforts to continue to curate the Drosophila literature and reagents. It is also essential to improve the utility of Flybase for colleagues in the human genetics/population-genetics and other model organism communities to maximize discovery. In the future it is important that Flybase continues to curate and integrate relevant and emerging data sets, and to develop tools that enable better access to this wealth of data. Flybase should facilitate more integrative analyses and bioinformatic approaches, specifically for the exploration of transcriptomic, proteomic and other large data sets. We support FlyBase's future plans to more rapidly and effectively curate and disseminate genetic and genomic data to benefit the rapidly changing scientific data landscape. We also support the continued contribution of Flybase to the Alliance of Genome Resources (the "Alliance") in harmonizing and integrating model organism databases (MODs), so long as these efforts do not interfere with or distract from the unique features of Flybase that are so critical to the Drosophila community. Flybase should also continue to improve two-way interactions with the community through outreach and feedback, which has already led to improvements in Flybase utilities. We also applaud FlyBase's effort to support the use of Drosophila as a classroom and outreach teaching tool. Given the importance of Flybase to all Drosophila researchers, a separate White Paper has been generated that provides more detail specific to Flybase.

We are seriously concerned about the absence of coordination of NIH policies on database support and the lack of national and international efforts to support FlyBase. In the past, most funding for FlyBase has come from a large grant from the National Human Genome Research Institute

(NHGRI) and a smaller grant from the UK Medical Research Council. This situation changed in 2016 when NHGRI decided to reduce FlyBase support, in an effort to promote the Alliance. The projected budget for FlyBase's final year of the current 5-year grant cycle and for its next renewal in 2023 will be 50% of what it was in 2016. Additional funds for FlyBase are presently provided by an NHGRI supplement for the Alliance and an NSF grant, which altogether will bring FlyBase's funding closer to 60-65% of its 2016 funding. It is expected that funding needs will be greater in the future given the increased curation necessary with the expanding number of genomic, proteomic and metabolomic data sets, for example. In addition, development of new query tools will be important so the rich dataset resources can be fully explored. Efforts to explore mechanisms that would bring in more international funding have so far been unsuccessful. The Drosophila community has responded well to the request by FlyBase for annual usage fee contributions, but these amount to approximately 5% of the current FlyBase needs. Community contributions will not solve the funding deficit. A 2021 letter from Fly Board presidents (past, current and future) to solicit help from the NIH Director and Directors of five Institutes (NICHD, NHGRI, NINDS, NIGMS and NIDDK) did not lead to additional funding opportunities. We support the plan by FlyBase organizers to seek face-to-face meetings with the NIH Institute Directors to discuss Flybase's critical support needs and how to meet them.

2) Resources for analysis of genes and phenotypes

Resources that facilitate functional analysis of genes and elucidation of mutant phenotypes are a high priority for Drosophila researchers. Gene expression databases such as BDGP in situ homepage, FlyFISH and FlyLight provide initial insights into gene function. A powerful advantage of Drosophila as a model system lies in the wide repertoire of genetic manipulations that are possible with this organism. In North America, efforts to generate large strain collections have recently been accomplished by consortia including: the Gene Disruption Project at Baylor (led by Hugo Bellen), the DRSC/TRiP Functional Genomics Resources at Harvard (led by Norbert Perrimon), and the FlyLight Project (Janelia). The continued enhancement of this genetic toolkit should include expanding the set of genes with loss-of-function mutations, including null alleles created by gene deletion or disruption, and resources that facilitate replacement of genomic loci with allelic variants. CRISPR/Cas9 technology makes it possible to target any gene. An expanded collection of mutations that covers most or all genes, including genes without large ORFs (encoding peptides or small RNAs) and hence underrepresented in existing gene disruption collections, will be a valuable resource. Development of genetic resources should advance strategies for manipulating the activity and expression of genes with tight spatial and temporal control, including expression of wild-type or variant alleles, optogenetic methods, and strategies that enable targeted knock-out or knock-down of gene expression through transgenic RNAi, CRISPR/Cas9 and its derivatives, or protein degradation. The continued development of systems for spatial and temporal manipulation of expression (e.g. GAL4, LexA, QF, MIMIC/CRIMIC, MARCM, regulatable GAL4s such as tet-on, split-Gal4, etc.) will also be critical. Together, these will allow for conditional and reversible removal of genes, mRNA or proteins with exquisite precision. Insertional alleles created by targeting GAL4/LexA/QF to recapitulate gene expression, and/or knock down gene function, combined with expression of cDNAs under GAL4/LexA/QF control, will enable proper spatial and temporal expression for rescue experiments, including expressing altered genes for structure-function studies and following developmental histories using lineage tracers such as G-Trace and FlyBow. These tools can also be used for expressing tagged proteins for analysis of protein localization, expressing reagents for cell-type specific genomic studies, expressing genes to manipulate physiology, and expressing homologous genes from humans or other species, among many approaches.

We support continued development of tools to study human genes and their disease variants using Drosophila, facilitating emerging strategies in precision medicine, and accelerating characterization of rare diseases, or diseases for which little is known about the biological mechanisms. Creation of a library of human cDNAs in fly-ready vectors allows all researchers to quickly obtain, modify and study human genes. In addition, we advocate for creation of a collection of transgenic fly stocks that carry tagged UAS-human cDNAs. This will permit rapidly testing the function of human genes in Drosophila and provide a basis for the functional testing of different human disease alleles/variants, an increasingly common need in medical genomics. We support the efforts by the Bloomington Stock Center to provide curated collections of mutants for genes that have homology to human disease genes.

We advocate support of community facilities and resources for high-throughput screening, including RNAi or CRISPR/Cas9-based screening, and pharmacological screening, both in cell lines and in whole animals. Efforts such as these have already been initiated at DRSC/TRiP Functional Genomics Resources at Harvard. While the ability to analyze genes and phenotypes in vivo, in an intact animal, is a particular strength of Drosophila, some classes of experiments can be more easily performed on cultured cells. Expanding the collection of Drosophila cell lines available at the DGRC to include more diverse cell and tissue types and improving on methods to culture cells and tissues in vitro will facilitate live imaging studies and biochemical and pharmacological characterization and screening of cells and tissues.

We advocate for resources that enable, enhance, and expand physiological and phenotypic characterization of Drosophila. These will provide a deeper understanding of responses to environmental perturbations, gene-environment interactions, and polygenic traits. This should include determination and annotation of the Drosophila metabolome, and the establishment of standardized protocols and resources to permit comparisons of the metabolome across tissues, genotypes, and species. It should also include analysis of the Drosophila microbiome and its contribution to physiology, including resources to characterize microbiomes in diverse Drosophila genetic backgrounds and environments. It is clear that translational control adds another layer to gene expression regulation. Therefore, we support the expansion of proteomic studies and generation of proteome datasets across cell types, tissues and developmental stages (for example, Casas-Vila et al., 2017 and Fabre et al., 2019). We support the efforts to profile the translational landscape under different conditions, for example with ribosome profiling studies using tagged ribosomal subunits.

Tools and resources to determine the expression patterns of Drosophila RNAs and proteins at high temporal and spatial resolution, together with sub-cellular localization profiles, provide essential insights into function and valuable markers for phenotypic characterization. To extend the expression analysis toolkit, we advocate two complementary approaches: the creation of collections of tagged genes and the production of antibodies/nanobodies against Drosophila proteins. Antibodies are a foundational resource in molecular biology, as they enable the study of protein localization, modifications, and interactions, in situ, with genes under endogenous regulatory controls, without any potential for impairment of gene function by tags. A repository of highly specific, high affinity, and sustainable antibodies will be a valuable resource. And in addition to immunization, synthetic techniques including recombinant antibodies, nucleic acid aptamers and non-immunoglobulin protein scaffolds and genetically encoded nanobodies should be expanded. Through the use of

CRISPR/Cas9 strategies it is now also possible to create strain collections that express epitope-tagged proteins, which facilitate rapidly understanding protein localization and protein functions. Tags are needed as an efficient, reliable, and inexpensive way to study protein localization, characterize protein function and to perform immunoprecipitation analyses to understand protein-protein interactions, given current limitations of antibody resources. Limited sets of tagged genes are currently available, but broader gene sets need to be generated, along with stable fly lines expressing them. The activity of tagged proteins needs to be confirmed by genetic experiments. These collections should include tagging endogenous genes with markers (e.g., GFP, Flag, V5, and split-GFP for intersectional strategies) at their genomic loci, without disrupting gene function, to assess expression patterns of genes and subcellular localization of proteins in wild-type and mutant backgrounds, and provide reagents for approaches like tag-based knock-down or immunoprecipitation experiments. Collections of transgenes that express tagged cDNAs (e.g., UAS-cDNA-tag) can also be used for localization and interaction studies, and are valuable for structure-function studies and comparisons to human UAS-cDNA collections. Many genes produce multiple transcript isoforms via alternative promoter use or alternative RNA processing, including regulated alternative splicing; future analysis of expression patterns should include the spatial and temporal distribution of alternative transcripts and protein isoforms.

Support for functional analysis of the Drosophila genes and phenotypes must be coupled to Flybase curation efforts that will establish atlases and databases of the resulting data sets, and make them accessible to all researchers, as described above in the Database and Informatics Resources for Drosophila Research section. It must also be coupled to mechanisms for making tools and resources widely available, as described below in parts 3 and 4.

3) Drosophila stock centers

Stock centers that provide universal access to genetically defined stocks are essential for all Drosophila research and teaching efforts, and they remain a high priority for infrastructure funding. These are complex operations that are heavily used by the national and international fly communities. For example, the Bloomington Drosophila Stock Center (BDSC), the NIH-funded repository for *Drosophila melanogaster* strains, maintains more than 78,000 genetically distinct stocks and distributes approximately 215,000 samples to 2,000 laboratories every year. Distributed stocks include classical mutants (covering approximately X% of all genes), GAL4, split-GAL4 and other driver lines, lines for RNAi of particular genes, marked and balancer chromosomes, species reference-lines, etc. In another example, the National Drosophila Species Stock Center (NDSSC), houses over 250 Drosophila species, maintaining approximately 1600 stocks. These stock centers, whether general or specialized in scope, distribute the “core” stocks necessary for genetic experimentation in Drosophila. The North American Drosophila Board also supports the efforts of our colleagues in other countries that maintain additional centers that distribute other Drosophila stocks.

Stock centers must have the physical ability to maintain the large number and variety of stocks needed for contemporary genetics research in a safe and reliable manner. To retain relevance and impact, they also need the management capacity to assure that the collection contents adjust to changing research needs. Stock centers must keep valuable existing stocks while acquiring new stocks from researchers and integrating with or leading large-scale resource development projects. To maximize the benefit of maintaining the strains, stock centers must provide information that will promote their experimental use by integrating stock information into online model organism databases

such as FlyBase, emphasizing website development and maintenance, and having staff available for consultation. These efforts to provide information on stock applications are particularly important to investigators new to Drosophila research, such as those wishing to pursue discoveries made in vertebrates using the sophisticated genetic approaches available in flies. Stock centers must also have the capacity to deal with regulatory challenges associated with the distribution of live animals and with the administrative challenges of acquiring large proportions of operating budgets from user fees.

We strongly believe that healthy partnerships between stock centers and funding agencies will continue to be a key factor for the continued success of Drosophila as a leading research organism. We urge funding agencies to recognize that the viability and vitality of stock centers depend on both healthy grant support and user-generated income. Cost-recovery programs have enabled stock centers to expand beyond the limits of grant funding and they have contributed enormously to the financial stability and security of these facilities. Nevertheless, both stock centers and funding agencies are constrained in meeting the needs of the Drosophila research community by policies that mandate that ever-increasing proportions of operating costs come from user fees. Given the increasing relevance of Drosophila research to biomedicine, we argue that increased federal investment in Drosophila stock resources is not only appropriate and necessary but also advantageous for the broader biomedical research endeavor.

4) Genomics resources

In addition to a repository for live Drosophila stocks, it is important to maintain reliable, central repositories and centers that generate and distribute key reagents to the scientific community expeditiously, as this can relieve individual labs of this responsibility and afford the end user a dependable timeline for receiving materials. Central repositories also ensures that all community members have access to standardized resources, that these valuable resources are not degraded or lost, for instance when labs close down, and provides technical guidance and ready access to reliable, relevant protocols. The importance of molecular stock centers is magnified by NIH and journal guidelines that emphasize reproducibility and require investigators to make materials widely available.

We continue to support the efforts of the Berkeley Drosophila Genome Project (BDGP), including their efforts in genome sequencing, cDNA library preparations, and genome annotation. We continue to support the efforts of the Drosophila RNAi Screening Center (DRSC) to generate and distribute resources for gene manipulation such as TRiP RNAi and CRISPR stocks, as well as to continue to develop new technologies, modified cell lines and reagents for RNAi and CRISPR cell screening, and to continue to disseminate technological know-how and provide practical training on new technologies through a variety of mechanisms. Currently, we can knock down % of Drosophila genes with RNAi and % with CRISPR, representing remarkable resources. We applaud efforts by individual labs that have produced valuable community resources such as FlyCRISPR, Drosophila Genetic Reference Panel, and Drosophila Synthetic Population Resource. We acknowledge similar efforts by centers and groups outside of North America.

We continue to support the Drosophila community-run genomics/molecular stock center called the Drosophila Genomics Resource Center (DGRC). First and foremost, a molecular stock center needs to be able to accept both resources generated by large-scale projects, as well as donations from

individual labs. The DGRC is the NIH central repository that provides the community with access to an expanding set of key molecular and cell-line resources at affordable costs. As such, this central repository enhances research capabilities, enables efficient use of resources, and facilitates exchange of materials.

New critical resources are being created continually. Currently, key resources being maintained and distributed include germline transformation vectors, as well as collections of full-length cDNA and genomic clones in appropriate vectors for expression in flies, in cell lines, and in yeast or bacteria. Molecular reagents for manipulation of gene expression (e.g. by RNAi or CRISPR/Cas9) as well as the numerous Drosophila cell lines also need to be maintained and distributed. Support for antibody repositories is also invaluable. Some Drosophila monoclonal antibodies are available from the NIH-supported Developmental Studies Hybridoma Bank (DSHB), but in the future, support for storage and distribution of polyclonal antisera, and antibody reagents created by other techniques such as phage display, would also be advantageous.

5) Long-term preservation of Drosophila strains

Unlike the strains of most other genetic model organisms, Drosophila strains presently cannot be maintained practically in any form other than living cultures. The development of robust methods for the long-term preservation of Drosophila strains would benefit biomedical research by providing more options for maintaining and distributing strains, allowing the preservation of important, but rarely used strains, preventing the accumulation of mutations associated with long-term culture, and helping to secure genetic resources from disaster. Recent advances in cryogenics and dehydration technologies, and nutritional and environmental manipulations suggest that new methods for long-term preservation could be developed for Drosophila embryos, larvae or sperm. We welcome the 2021 publication reporting success in cryopreservation of Drosophila embryos and encourage funding agencies to dedicate funds for scaling up cryopreservation from proof-of-principle to high-throughput. In general, we strongly support investing in the development and application of methods that hold promise.

In summary, Drosophila research has made tremendous contributions to biomedicine and will continue to do so with continued support and funding. We hope that information communicated in this document will help the Drosophila research community, funding agencies and external decisions makers in making sure this happens.

FlyBase: History, Present, Future and Funding

A report from FlyBase 6/28/2021

Note: Part of the text below is from Wikipedia as well as from the 2021 FlyBase report to the FlyBoard.

FlyBase: History

Drosophila melanogaster has been an experimental organism since the early 1900s, and has since been placed at the forefront of many areas of research. As this field of research spread and became global, researchers working on the same problems needed a way to communicate and monitor progress in the field. This niche was initially filled by community newsletters such as the Drosophila Information Service (DIS), which dates back to 1934 when the field was starting to spread from Thomas Hunt Morgan's lab. Material in these pages presented regular 'catalogs' of mutations, and bibliographies of the Drosophila literature. These lists of genes, mutant phenotypes and bibliographies were further compiled into more formal publications, notably Herskowitz's* Bibliographies of *Drosophila* and the "Red Books" of Lindsley and Grell and Lindsley and Zim**.

As the compilations of Drosophila data became more and more extensive it became clear that this method of summarization of the aggregate knowledge of the field was no longer scalable. It was therefore proposed in 1991 to utilize the growing computing infrastructure to shift the newsletters and books into an online database. In October 1992, the National Center for Human Genome Research (NHGRI) of the NIH funded the FlyBase project with the objective of designing, building and releasing a database of genetic and molecular information concerning *Drosophila melanogaster*. Through this funding and support from the UK Medical Research Council a variety of data were made available over the Internet through the nascent FlyBase website, including: the gene and chromosomal aberration lists of the RedBook; an accumulated bibliography; lists of stocks; and lists of clones. As the sequencing of the *Drosophila melanogaster* genome progressed FlyBase collaborated with the informatics groups of the Berkeley Drosophila Genome Project (BDGP) and European Drosophila Genome Project (EDGP) to unify the genome sequence and associated gene predictions with genetic data.

Following the transfer of existing data into FlyBase, mechanisms for biocuration of the wealth of new data being steadily produced by the community were developed. This included: regular updating of the FlyBase bibiliography; curation of new alleles, transgenic constructs and phenotypes from the majority of the primary research literature; using new data sources (such as large scale RNA sequencing) to update gene models; annotating gene expression using controlled vocabularies (ontologies) to ensure searches return comprehensive results; and annotation of Drosophila models of human disease. FlyBase members were amongst the founders of the Gene Ontology Consortium, which utilizes a shared ontology to annotate gene function in many organisms.

FlyBase is a mature project with an experienced staff of long-term employees and many of our activities are continuous. Currently, the FlyBase project is carried out by a consortium of Drosophila researchers and computer scientists at Harvard University, University of Cambridge (UK), Indiana University, and the University of New Mexico. For a list of current FlyBase team members see: https://wiki.flybase.org/wiki/FlyBase:About#FlyBase_Consortium.

FlyBase: Present

Information in FlyBase originates from a variety of sources ranging from the primary research literature to large-scale genome projects. FlyBase staff currently curate a wealth of data types including: molecular descriptions of new mutant alleles and other abberations; details of transgenic constructs and transposon insertions; stock information on these new genetic tools; sequence-level gene models; mutant phenotypes and inferred gene function with the Gene Ontology; Genetic and Protein-Protein interactions; and high-throughput and manually curated expression data on genes and Gal4 drivers. FlyBase query tools allow navigation through DNA or protein sequence, by gene or mutant name, or through terms from the several ontologies used to capture functional, phenotypic, and anatomical data. The database offers several different query tools in order to provide efficient access to the data available and facilitate the discovery of significant relationships within the database. Links between FlyBase and external databases provide opportunity for further exploration into other model organism databases and other resources of biological and molecular information. Altogether, FlyBase over the years has matured from database to knowledgebase. See for example a recent publication (Larkin et al., 2021).

FlyBase has three main goals:

1. To continue curation of literature and reagents relevant to Drosophila research. This is an essential goal that ensures that Drosophila researchers can continue to rely on FlyBase to find the latest innovations in the field and the reagents for experimental design. FlyBase prioritizes curation of data on previously uncharacterized genes, as well as those revealing new information on gene function, signaling pathways, and human diseases. Over the years, FlyBase curation has continuously evolved to integrate machine learning tools with human expert curation to generate high quality information. This goal standard data is an essential training set for the development of new AI tools to assist essential human curation. Flybase continuously develops new ways to display this 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 of Genome Resources (the “Alliance”), FlyBase works closely with other Model Organism Databases (MODs) to integrate data sets and develop tools to enable cross-species analyses. This effort has a major impact on the fly community, accelerating the development of models of human diseases.

3. To facilitate more integrative analyses and approaches, FlyBase integrates and

displays large-scale studies, transcriptomic and proteomic data sets. In addition, FlyBase provides access and displays tools available within the community, and incorporates the most useful data sets and tools for retrieving and displaying complex data sets to enable more researchers to take a global approach to their genetic research.

Overall, FlyBase has become an invaluable tool used to conduct research with *Drosophila*. One measure of success is that the average number of sessions and page views in 2020 were 137k and 662k, respectively. It is also worth reflecting how much researcher time and money is saved by having an up-to-date compendium of research findings on each Drosophila gene; assembling this information on just one gene through searching the literature is a very lengthy process.

FlyBase Future

As noted, FlyBase has become an invaluable tool used to conduct research with Drosophila. In the next five years, FlyBase efforts will focus on three main areas:

1. ***FlyBase contribution to the specific needs of the Drosophila community.*** FlyBase provides a crucial openly-accessible centralized resource for Drosophila genetic and genomic data to enable researchers and educators worldwide, both in the Drosophila community and broader biomedical sciences community, to further their research. In addition to the curation activities already mentioned, more recent innovations include: rapid appearance of relevant papers on each gene report thanks to author curation; Gene Group and Signalling Pathway curation; import of graphical abstracts in FlyBase references; identification of new lncRNAs, anti-sense lncRNAs and smORFs; incorporation of available transcription start site data into FlyBase; addition of new anatomy terms, especially new neuron types; review and improvement of phenotypic class ontologies; annotation of all Drosophila cell types and curation of scRNAseq data sets; updating genomic sequences of Drosophila Genetic Reference Panel (DGRP) strains.
2. ***FlyBase contribution to the Alliance.*** FlyBase is involved in direct data-sharing collaborations with a number of external data resources and is a member of the Alliance. The Alliance consortium is organized to design a web portal that gathers and integrates the data from several model organism databases (MODs) (*D. melanogaster*, *C. elegans*, *S. cerevisiae*, *D. rerio*, *M. musculus* and *R. norvegicus),* in collaboration with the Gene Ontology Consortium (GOC), so that at one site a researcher can find out what is known about a particular gene's function in all these model organisms. This data integration and harmonization also enables clinical researchers to efficiently access and translate findings in model organisms to new disease diagnoses and treatments. The primary goals of the Alliance are: **a.** To provide unprecedented support for comparative genomics *via* unified user interfaces and APIs for data types shared by the MODs, and **b.** To promote sustainability and operational efficiencies by building a “knowledge commons” based on shared, modular infrastructure. FlyBase helps the Alliance to develop the next generation of model organism knowledgebases capable of adapting to the rapidly changing data science landscape.

3. FlyBase outreach. FlyBase will continue to meet user community needs by: **a.** Enabling accelerated incorporation of published data by identifying new opportunities for direct user data submissions and improving existing tools; **b.** Maintain project-wide help desk *via* email; **c.** Providing in-person training through presentations and demonstrations at Drosophila and other conferences; **d.** Providing on-line training through maintenance and development of documentation and video tutorials; **e.** Publicizing updates and new features through various media, including an email-based Newsletter, our Twitter feed and peer-reviewed publications**; f.** Enhancing community-driven webpages and portals; **g.** Soliciting and responding to feedback from research community *via* the FlyBase Community Advisory Group; **h.** Collaborating with Model Organism Database and biocuration communities to find common solutions to shared goals; and **i.** Illustrating and supporting the exceptional value of FlyBase and *Drosophila* in the classroom as teaching tool for the next generation of wet bench researchers and data scientists.

FlyBase Funding

Most of FlyBase funding in the past has come from a large grant from the National Human Genome Research Institute (NHGRI) and a smaller grant the UK Medical Research Council. This situation changed in 2016 when NHGRI decided to reduce FlyBase support in an effort to promote the Alliance. Our projected budget for our final year of current 5-year grant cycle and for our next renewal in 2023 will be 50% of what it was in 2016. Additional funds for FlyBase are an NHGRI supplement for the Alliance and an NSF grant, which altogether will bring FlyBase's funding closer to 60-65% of 2016. Our efforts to explore mechanisms that would bring in more international funding have so far been unsuccessful. We therefore went to the community to request they contribute to help FlyBase keep up to date. We have been touched by the diversity of these contributions, such as from the hat passed round at the end of an advanced genetics class. However, since contributions to the community correspond to approximately 5% of the current FlyBase needs, these valuable contributions cannot be the sole solution to the funding deficit.

We plan to continue the user-fee collection to supplement FlyBase funding and are grateful for the strong support from our community. Nonetheless, the projected shortfall will severely restrict the ability of FlyBase to keep pace with the developments in the Drosophila field. Not only has the pace of research continued to increase the amount of data per publication, but the increasing diversity of the field, for example into physiology and metabolism, requires substantial new effort to curate, integrate and display these new data types. Overall, the steady decrease in FlyBase support since 2016 is a concern as it negatively impact on biomedical discovery.

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DRAFT

Drosophila Community Service Award

The Drosophila Community Service award will be given once a year to acknowledge outstanding contributions to the Drosophila community. The award was initiated in 2021 in gratitude for the service of colleagues like Dan Lindsley, Kathy Matthews and Bill Gelbart. A major goal of the award is to raise awareness within the fly community about the depth and diversity of efforts supporting its success. The selection committee is encouraged to recognize colleagues who might not be selected for Genetics Society of America service awards.

Any member of the Drosophila research community is eligible including professionals not holding traditional tenure-track positions. A team or small group may be recognized. The awardee(s) will be announced at the Annual Drosophila Research Conference by a member of the selection committee. The conference organizers are encouraged to provide time for awardees to give a presentation at the meeting.

The selection committee will issue a call each year for nominations through appropriate platforms (*e.g*. GSA mailings, FlyBase announcements, social media), allowing enough time for evaluation before the next ADRC. Anyone may make a nomination by submitting a letter describing the contributions of the nominee(s). The selection committee may consider nominations from the previous three years.

Selection committee members will be appointed by the FlyBoard president. The committee will have at least three members, each of whom will be appointed for at least two years. Staggered terms are preferred to provide continuity. The committee Chair will be appointed by the Flyboard president. It is suggested that the longest-serving member chair the committee. At least one committee member should be a research resource professional. The selection committee will coordinate the award presentation with the Annual Drosophila Research Conference Organizing Committee.