



Introduction

[OrthoDB](#) provides evolutionary and functional annotations of orthologs amongst a broad range of species. For several years, FlyBase has incorporated OrthoDB orthology calls between the genes of *D. melanogaster* and ~40 other species, including additional *Drosophila* species and other arthropods. These OrthoDB data are displayed within FlyBase gene reports (see the [dpp report](#) for an example) and are searchable using the Homologs tab of our QuickSearch tool on the [homepage](#), as well as being available via JBrowse, bulk downloads and our GFF files. Before committing to a major update of OrthoDB data within FlyBase, we wish to understand if and how researchers access these data. (Note that orthology data in FlyBase between *D. melanogaster*, other model organisms and humans are derived from [DIOPT](#) - these data will not be affected by the changes being considered here.)



Questions

*** 1. Do you use OrthoDB data within FlyBase?**

- Yes
- No, but I will now I know about it!
- No (selecting this will end the survey)

*** 2. Approximately how often do (or would) you use OrthoDB data in FlyBase?**

- weekly or more often
- once a month
- once a year
- less than once a year

*** 3. How do (or would) you access OrthoDB data in FlyBase? (Tick as many as apply)**

- viewing data directly in the 'Orthologs' section on gene reports (e.g. [dpp](#))
- searching OrthoDB using the Homologs tab of QuickSearch on the [homepage](#)
- viewing OrthoDB orthologs in JBrowse (e.g. [dpp](#))
- downloading the '*D. melanogaster* orthologs in other *Drosophila* species' bulk file from our [Downloads](#) page or [ftp site](#)
- accessing OrthoDB feature lines present in our [GFF files](#)

*** 4. What would be the effect on your research if we only displayed OrthoDB data on gene reports? That is, OrthoDB data within QuickSearch, JBrowse, downloadable files and GFF files would be removed. (Note that current orthology data display between *D. melanogaster*, other model organisms and humans will not be affected by the changes being considered here.)**

- This would present major problems for me
- This would present minor problems for me
- No effect
- This would be better than the current implementation!

Explain your answer.

*** 5. What would be the effect on your research if we entirely removed OrthoDB data from FlyBase, and instead only displayed a link from FlyBase gene reports to the relevant OrthoDB page(s)? (Note that orthology data between *D. melanogaster*, other model organisms and humans will not be affected by the changes being considered here.)**

- This would present major problems for me
- This would present minor problems for me
- No effect
- This would be better than the current implementation!

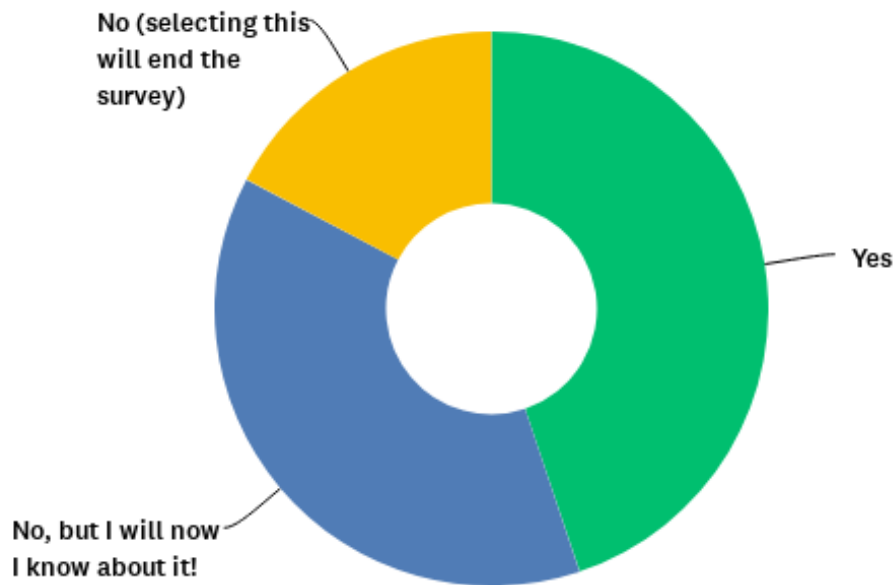
Explain your answer.

6. Do you have any other comments about if/how FlyBase should incorporate or link to *D. melanogaster* orthologs in non-model organisms, especially those in additional *Drosophila* species and other arthropods?

Answers

Q1: Do you use OrthoDB data within FlyBase?

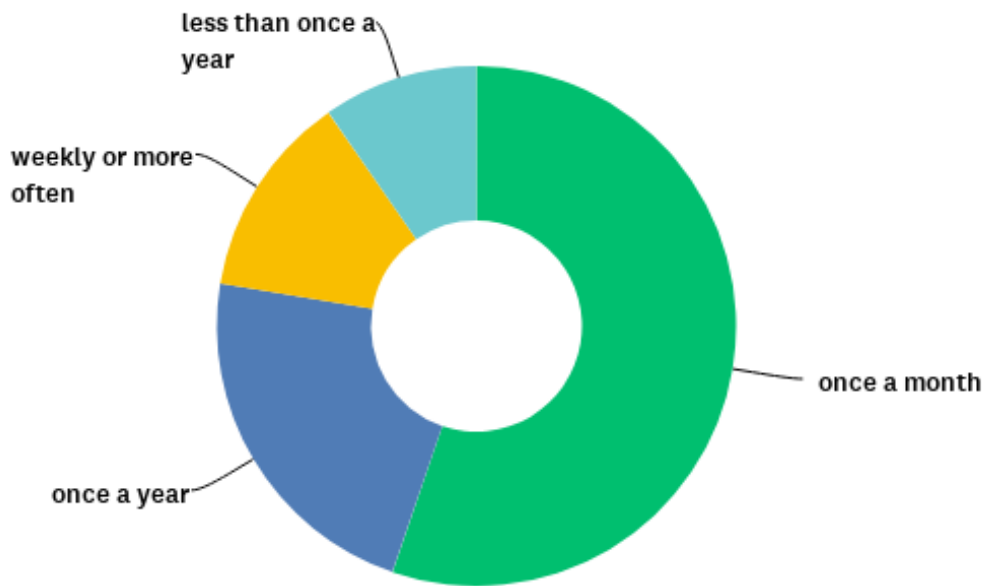
Answered: 272 Skipped: 0



ANSWER CHOICES	RESPONSES	
Yes	44.85%	122
No, but I will now I know about it!	37.87%	103
No (selecting this will end the survey)	17.28%	47
TOTAL		272

Q2: Approximately how often do (or would) you use OrthoDB data in FlyBase?

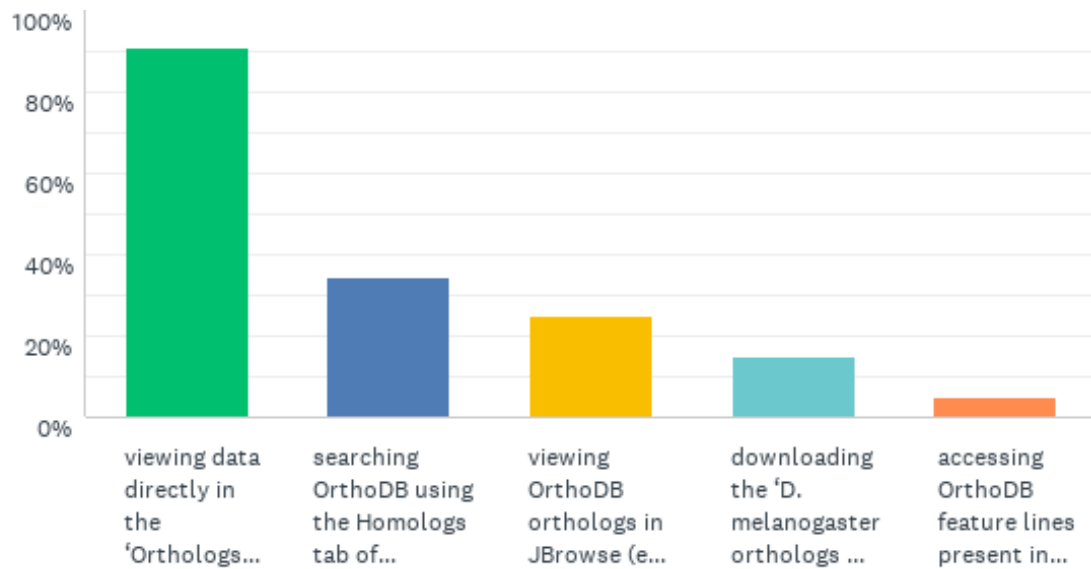
Answered: 228 Skipped: 44



ANSWER CHOICES	RESPONSES	
once a month	55.26%	126
once a year	22.37%	51
weekly or more often	12.72%	29
less than once a year	9.65%	22
TOTAL		228

Q3: How do (or would) you access OrthoDB data in FlyBase? (Tick as many as apply)

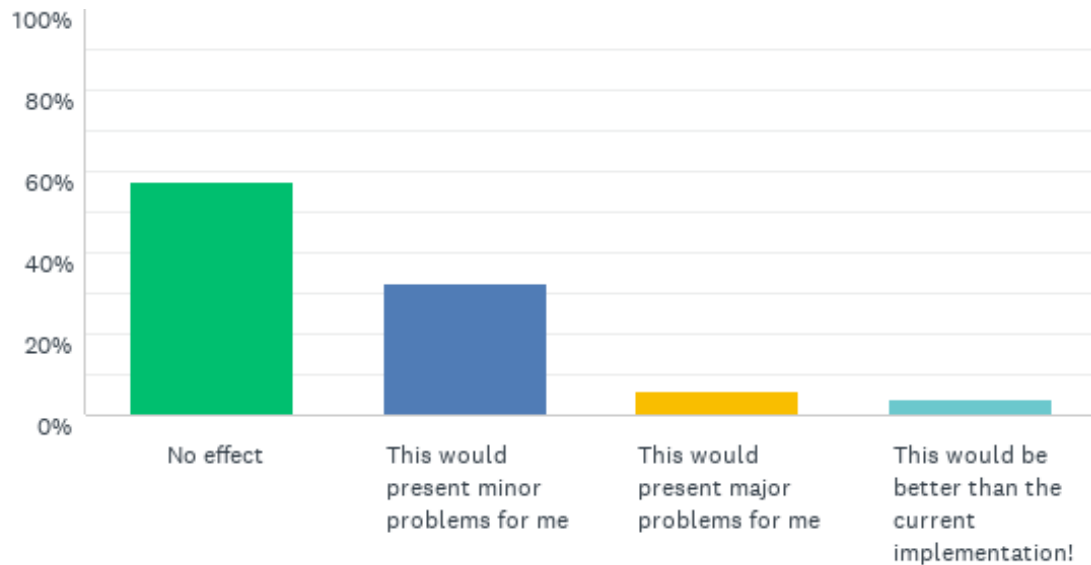
Answered: 222 Skipped: 50



ANSWER CHOICES	RESPONSES
viewing data directly in the 'Orthologs' section on gene reports (e.g. dpp)	90.99% 202
searching OrthoDB using the Homologs tab of QuickSearch on the homepage	34.68% 77
viewing OrthoDB orthologs in JBrowse (e.g. dpp)	24.77% 55
downloading the 'D. melanogaster orthologs in other Drosophila species' bulk file from our Downloads page or ftp site	14.86% 33
accessing OrthoDB feature lines present in our GFF files	4.95% 11
Total Respondents: 222	

Q4: What would be the effect on your research if we only displayed OrthoDB data on gene reports? That is, OrthoDB data within QuickSearch, JBrowse, downloadable files and GFF files would be removed. (Note that current orthology data display between D. melanogaster, other model organisms and humans will not be affected by the changes being considered here.)

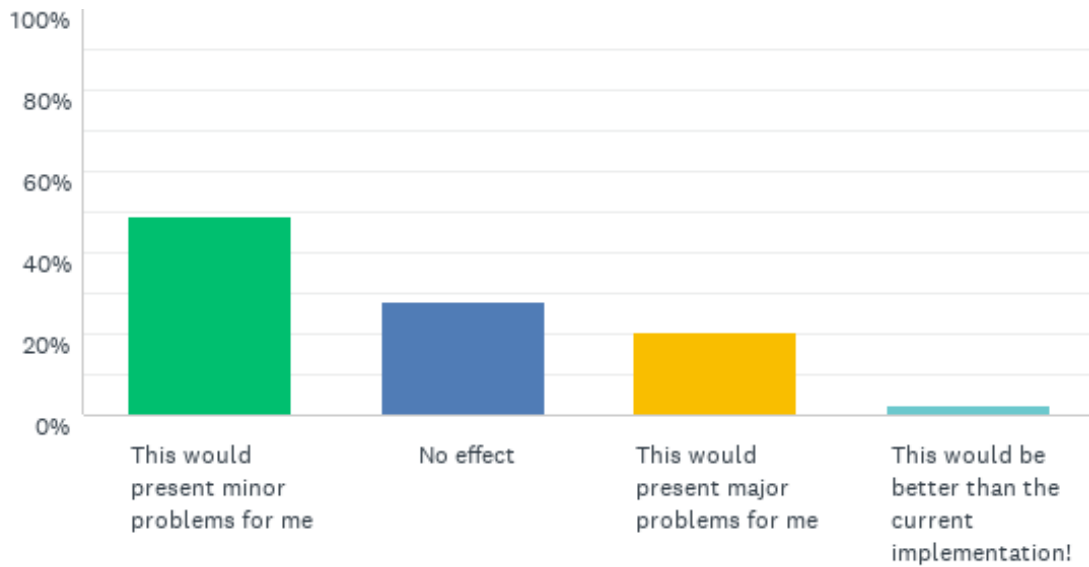
Answered: 222 Skipped: 50



ANSWER CHOICES	RESPONSES	
No effect	57.66%	128
This would present minor problems for me	32.43%	72
This would present major problems for me	5.86%	13
This would be better than the current implementation!	4.05%	9
TOTAL		222

Q5: What would be the effect on your research if we entirely removed OrthoDB data from FlyBase, and instead only displayed a link from FlyBase gene reports to the relevant OrthoDB page(s)? (Note that orthology data between *D. melanogaster*, other model organisms and humans will not be affected by the changes being considered here.)

Answered: 219 Skipped: 53



ANSWER CHOICES	RESPONSES	
This would present minor problems for me	48.86%	107
No effect	27.85%	61
This would present major problems for me	20.55%	45
This would be better than the current implementation!	2.74%	6
TOTAL		219