

Biol 213L: Genetics Lab (Fall 2000)

Comments on Lab 3 Progress Report: *Genetic Analysis of Mutant Flies*

Again, I've set down several comments that I would otherwise write over and over on many of your reports. Some of them apply to yours, others don't. For the first time, you are asked to REVISE and IMPROVE what you've written. Actually, I hope this is standard procedure. Any manuscript can be improved just by reading it over slowly and with an open mind.

I may have suggested that you make a figure or a table. Don't feel limited by what may be inexperience in using Word or whatever are your favorite programs or by anything except your imagination (and struggle to expand those limitations). If you find yourself able to conceive of a figure or table but don't know how to make it a reality, see me or give me a call. Almost always it's a lot easier than you might think.

G30. Write to the point

Every year students complain that there is too much writing in Genetics Lab – so many pages of so many lab reports. Add it up over the semester and it's almost a book! Now think about me. I have to read all those books, fifteen of them, and write something helpful about each part of each one. Don't think about Paula, who has to read. . . no, don't think about Paula.

WHY DO WE DO THIS TO EACH OTHER?

You may well point the finger in my direction. After all, I instigated the assignment, not you. But take a look at the assignment. Didn't we give you the knife to slice pages off your reports? The lab manual stresses: Write to the scientific question. Let that and your data dictate what you write.

How about the other direction? Isn't it better to say too much than too little? Wrong. Every extra word makes the sense more difficult to find. Defensive writing is bad writing. You may presume that the purpose of a report is to showcase what you know, but as soon as you accept this premise, you lose the best organizational tool you have -- devotion to your reader.

Holding an estimated 36,000 words in my hand plus about 30 tables of varying complexity, I offer the following comments.

Introduction

I.30. No need for extras

Never mind the biographies of Mendel, Morgan, and Benzer. Skip the treatise on molecular recombination or even the essay on how you did the experiment (leave that -- shortened -- to **Materials and Methods**). If you feel the need to extol the benefits of the lab exercise to your intellectual development, then send your comments to the department chairperson. No need to put them in the report.

I.31. Focus on the scientific questions

What *should* be there are specific questions. For example, you probably wanted to know whether any of the three traits were X-linked. Listing the specific questions you asked at the outset will help you organize the rest of the report.

Materials and Methods

M.30. Focus on the scientific questions.

Explain the strategy of how you answered that question. For example, what kind of experiment can distinguish between autosomal and X-linked transmission of a trait? What kind of results would you expect in each case? A figure might help us appreciate the possible answers to the scientific question. Don't bother rehashing what's in the manual.

Results

R.30. Focus on the scientific story

Read over your **Results** section. Chances are it is as difficult for you to read now after a couple of weeks as it is for me to read now. What's missing in [almost] every report is the engagement of the reader in the story. There needs to be a story, one with expectations and fulfillment of those expectations or if not, then surprise. Let us know what to expect (refer to your discussion in the **Materials and Methods** section). Only then can we appreciate the numbers you throw at us. Why did you examine the progeny of the F1 cross? What did you hope to learn? It may well be that you had no idea what you were doing at the time, but you do now, and you should use that insight to craft a logical story.

R.31. Don't rely on numbers to identify your strains

Don't expect the reader to remember strain numbers. Use more memorable phenotypes.

R.32. Explain how the χ^2 test values were obtained

The χ^2 test doesn't mean anything unless you clearly explain the model on which it is based. At minimum, we need to know the ratio of phenotypes your model predicted, but often that isn't enough. Where progeny of different gender combined or kept separate? How many degrees of freedom? The clearest way is to provide the expected values used to calculate χ^2 , preferably next to the observed values. Doing this has the added benefit of laying out clearly where the biggest discrepancies are. This may inspire you to figure out what may have gone wrong.

R.33. Take care in declaring autosomal transmission

Just because the F1 progeny are all wild type, that doesn't mean that the both traits are autosomal. Work it out. Suppose that the maternal trait were X-linked – what would you expect in the F1 progeny? Suppose that the paternal trait were X-linked – what then?

R.34. Don't overinterpret the results of χ^2 tests

Make sure you understand what χ^2 tests tell you and what they don't tell you. Review Lab 3-10 through 3-12.

R.35. If you don't have data (or much data) for a cross, say why

Did one strain grow poorly, making it difficult to get females? Was there an accident of some sort? All of this is data too, and often provides valuable clues to explain later results.

R.36. Don't expect the reader to absorb numbers in the text

It's just too difficult. Numbers are more easily comprehended in tables, where they can be readily compared one with another.

R.37. Give credit where credit is due

If you didn't perform a cross yourself, then identify the source of the data (e.g. in footnote, "Data graciously provided by. . .")

R.38. Don't try to apply χ^2 tests to models where there is no predicted variation

See the lab manual, Lab 3-11, point 3 near the bottom of the page.

Discussion

D.30. Organize the Discussion around conclusions

This section differs from the **Results** primarily in its *organization*. The **Results** section is organized around *experiments*. You give us a guided tour through what you did. The **Discussion** is organized around *conclusions*. You marshal results from various sources to prop up or undermine possible conclusions. There is no sense running through the same experiments in both sections!

Interpretation is necessary in both the **Results** and **Discussion** section. In the former, interpretations come directly from an experiment and are provided to move the story along. In the latter, interpretations are integrated, often more subtle. Many have been trained to believe that all interpretation should be relegated to the **Discussion** section. At its best, this philosophy helps the reader distinguish between what was observed and what was inferred -- certainly to the good. At its worst, however, the approach leads to Objects of Art that are beautiful in form but totally incomprehensible. Your highest goal is to serve your reader, and it is yours to judge when it's best to offer some interpretation in the **Results** for sake of the story or instead to hold the interpretation in reserve until the **Discussion**.

Checklist for Final Report

- Did you include all of your group's data?
 - F1 progeny?
 - F2 progeny?
 - Virtual crosses?
- Did you list somewhere (preferably in a table) how many flies you counted?
- Did you explain how you determined:
 - Whether a trait was dominant/recessive?
 - Whether a trait was autosomal/X-linked?
 - Whether any two of your traits are linked to one another?
 - The chromosome and map position of each trait?
 - Did you use the formula for correcting map distances (see lab web page)?
- Did you make clear HOW you computed χ^2 values?
- Did you note any peculiarities in your data, propose possible explanations, and test these explanations quantitatively, using your data?
- Did you look for ways to use figures to reduce the need to explain complex ideas with words?
- Did you read and reread your report, looking for opportunities to make your arguments more concise and compelling?

