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Stimulating with the Socratic Method in Lab Notebooks

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Extended Abstract

Students in BIOL 2101:Genetics learn to do problem based learning largely through end-of-chapter questions or worksheets which are text-based problems. This, along with modeling of problem-based exercises in the classroom is standard for genetics instruction. Over time, students learn to pick out key pieces of information and develop a system for determining methods of inheritance. There are several skills involved in these kinds of problems. Eliminating "distractors" (information which is not relevant to the problem at hand), evaluating the hypothesis of one or more possible genetic models, formulating good gene symbols, and several other skills are required for proper resolution.

As instructors, we want to get students to engage with the material rather than just go through a set series of steps without thinking about them. We want to be able to see what they are thinking at each stage in order to analyze how they are creating models as well as evaluate the logic students use to solve the problem. In order to do this, we have developed an exercise which presents data to students and tracks their logic and reasoning as they request and then process new data. We follow their intellectual journey through entries the students create in a laboratory notebook.

Anatomy of a Genetics Problem

An example of a typical genetics text-based problem would be: "You cross a soft-haired, short-tailed male mouse with a wiry-haired, long-tailed female. Both parents are true-breeding. The offspring are all wiry-haired and have long tails." Students would be expected to recognize that mice are diploid, and because they are true-breeding they are homozygous for both traits but have different alleles for the trait. They might conclude that wiry hair and long tail are dominant alleles. Questions they might come up with are whether the traits are independently assorting or X-linked. If you add: "When you do the reciprocal cross, all the male progeny have soft hair and long tails but all the females have wiry hair and long tails" you have introduced X-linkage and therefore another consideration. This typical type of problem in its very structure suggests the strategy for solving, and students drilling with these problems, produce responses which become automatic. Students learn to create gene symbols and manipulate them to test their hypotheses. In our experience, students quickly learn how to solve these problems correctly.

However, a context specific phenomenon occurs when students are simply presented data and asked to analyze it. Although the parameters and resulting queries are pretty much identical to the text-based question, if students have to think about the next logical step they tend to be uncertain about how to design the strategy. For example, in our genetics class we tell students that we are interested in the genetics of a hypothetical organism – let's call it a grue. Some preliminary genetics of the grue are explained. For our system, we invoke XY sex determination and two autosomes, thus a genome of 2n=6. A genetic notation system (adapted from Drosophila genetics, **http://flybase.org/static_pages/docs/nomenclature/nomenclature3.html**) is provided and warm-up exercises are assigned to allow students to become familiar with the notation system. Each student is given an identical sample of a wild-type male and female plus a different mutant stock. Students are told that both the wild-type stock and the mutant are true-breeding and are told to do science with them. An example of the first set of data is shown in Figure 1.

There are a few things students can do with this information, but no further suggestions are provided. Eventually students will realize they must do a cross. In fact, more enlightened students will suggest reciprocal crosses. Instead of a textual response, we would give whatever cross(es) they asked for. If they ask for results from a cross between a wild-type female and a mutant male, they receive the data shown in Figure 2a. If they ask for data from a cross between a wild-type male and a mutant female, they receive data shown in Figure 2b. They might, on their own, ask for both crosses, and both sets of data are provided.

Figure 1. Sample data given to students. Wild-type and mutant represent individuals in two separate true-breeding stocks.

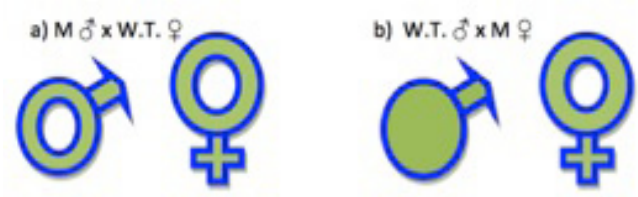

Figure 2 a and b. F1 data provided based on what students request. Students should eventually be able to recognize that there is a recessive X-linked mutation for no hole and that the color green is a dominant autosomal mutation.

The students make their request in the form of an entry in their laboratory notebook in which they detail their observations and structure their logic. The notebook is graded by the instructor using a rubric. Students are directed to structure their entries in a way similar to how a practicing scientist would track his or her own research. The entries should be in an iterative sequence in which they: 1) record observations, 2) plan experiments, 3) record an experimental plan, 4) record predictions, 5) and record results.

Tracking Logic and Reasoning

The laboratory notebook entries provide a window into what students are thinking and how they are processing their data. They often lack confidence in their choices of what to put into the lab book, and when they ask for what we specifically want them to put down, we respond by having them envision what Mendel would have written. What kinds of observations would he make? What conclusions would he draw from data he received from his experiments? The notation system helps students focus their thoughts and provide formal hypotheses about their mutant stock. In the above example, students would be expected to apply the provided notation system to formalize their hypothesis about their mutant. Two traits are observed: *no hole* and *Green*, where the former is X-linked recessive, and the latter is autosomal dominant. In the notation system, the hypothetical genotype of an unknown mutant male appear as:

$$X^{nho}/\,Y;\;\; Grn/Grn$$

where X^{nho} is the gene symbol for the X-linked recessive trait *no hole* and *Grn* is the gene symbol for the autosomal dominant trait Green. The corresponding wild-type grue would be annotated with wild-type alleles in all relevant loci with a superscript + symbol:

$$X^{nho^+}/X^{nho^+};\;\; Grn^+/Grn^+$$

Students often communicate to us that they want sample entries. We learned from experience that providing complete "perfect" entries is unhelpful: we typically received plagiarized entries with the assigned phenotypes substituted for our sample entries. To rectify this, we created a *C grade entry with some terminology misused and small logical flaws introduced. This was clearly communicated to students* to put them on their guard and foster them to modify the entries to make them more correct. The students are also assigned to groups who jointly submit a single notebook. This increases the opportunities for the students to communicate with each other about what the data show.

As mentioned above, this process is reiterative. Students are provided with data from which they must again record their observations, make interpretations which lead to subsequent experiments and so on. In our course, we ensure that each *stock* displays sex-linked loci, linkage between loci, and gene interactions between at least 2 loci (such as epistasis). Such a complex mixture of genetic possibilities provides a rich environment for students to test hypotheses that often are falsified when tested with experiments they have designed. Thus, students are naturally

directed to the re-iterative process of science and recording their progress through a problem. Typically, students are able to develop a genetic model (i.e. genotype) that fully explains their observations within 3-4 *rounds* of experiments. Such rounds would begin with a first cross (and hopefully a reciprocal cross) between the *wildtype* and their unknown, followed by an F_2 or cross of their own design. When students have reached a point where they have determined a model consistent with the data, we provide them the data from a hypothetical testcross which they interpret using the genetic model they constructed.

Guidelines for the notebook were constructed from a document obtained from MIT (**http://ocw.mit.edu/courses/biology/7-16-experimental-molecular-biology-biotechnology-ii-spring-2005/labs/lab_notebook.pdf**). We stress clarity of thought and the fact that the laboratory notebook constitutes a legal document and in a professional laboratory is actually the property of the company or primary investigator in charge of the lab. Students are told to affix all data (i.e., the printouts of the Grue data), write their ideas legibly in pen, and to cross out mistakes with a single line (no whiteout or CIA-style redacted bars).

Outcomes

Although students find the lack of step-by-step instruction frustrating at first, they do adjust and learn to articulate their thinking more clearly. In addition, students come to subsequent courses which require laboratory notebook entries with more confidence and professionalism.

When I query the students on whether the exercise seemed relevant to them, the answers were overwhelmingly positive. They also recognized that although the textual genetics problems were challenging the same kinds of skills as the picture entries, they felt more challenging. By pushing the students to articulate their observations and strategies in writing, they learned better problem solving skills. It is the intentionality of this kind of exercise that was most helpful to the students: they had to find out what they knew, what they needed to find out, and construct a logical path that connected the two.

Rubrics, the adapted genetic nomenclature system, and the modified laboratory notebook guidelines are available upon request from the authors.

Keywords: genetic problems, lab notebook, teaching method

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