

## POPULATION GENETICS

SPRING 1999

PROJECT #2

Due: Friday, 23 April 1999

You (or more likely, your graduate students and post-docs) crossed two inbred lines of *Arabidopsis thaliana*, intercrossed the  $F_1$ 's, measured the height of 750 randomly chosen progeny in the  $F_2$ , and genotyped each of those individuals at each of 59 polymorphic molecular markers. The reason you undertook this study, of course, was to learn something about the genetic basis of height variation in *A. thaliana*. Specifically, your grant proposal said you were going to answer the following questions:

1. How many loci contribute to the expression of height variation in *A. thaliana*?
2. What is the map position of each locus?
3. What are the allelic effects at each locus, i.e., what is the mean genotype, the additive effect, and the dominance effect?
4. How much of the variation in phenotype does each locus account for individually?
5. How much of the variation in phenotype do all identified loci account for together?
6. What is the narrow sense heritability of height in this population?<sup>1</sup>

Now you've collected the data,<sup>2</sup> and the program officer wants a report answering each of the questions you posed.<sup>3</sup>

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<sup>1</sup> Your answer to the last question gives you the broad sense heritability, but you told the review panel that you could calculate the narrow sense heritability simply by adding up the additive genetic variance across loci—and they bought it.

<sup>2</sup> One of your senior graduate students has put it on the web so that you can download it.

<sup>3</sup> I'm not going to tell you how many linkage groups there are or which loci are on which ones. I will tell you, that the loci are numbered sequentially in the order of their map position, so you don't have to fiddle around with that part of constructing the map.