

## Determining the Crossover Frequency in *Sordaria fimicola*

### Abstract

*During meiosis, there is always crossing over of genes between the chromosomes, allowing for genetic variation. In Sordaria fimicola, a fungus, meiosis followed by a mitotic division produces eight ascospores contained within an ascus. Four of these spores are black and four are tan, but their order depends on whether or not there was crossing over – if there was, they are in a 2:2:2:2 or 2:4:2 pattern, and if not, they are in a 4:4 pattern. The frequency of crossing over can be used to determine the distance between the locus of the gene in question and the centromere, and by using established knowledge, it was hypothesized that this distance would be 26 map units. This was tested by observing and recording the number of asci showing crossover and the number not showing crossover within a sample of two strains – one black and one tan – of Sordaria grown and fused together in a petri dish. It was found that there were 1194 asci showing no crossover and 1446 showing crossover, so the gene and the centromere are 27 map units apart. A  $\chi^2$  analysis was conducted to determine whether or not this data supported the null hypothesis, and the  $\chi^2$ -value found was 8.09, which is higher than the critical value of 3.841, so the null hypothesis cannot be accepted. However, because it is known that the distance between the gene and the centromere is 26 map units, errors must have been made in conducting the lab, such as observing inconsistent samples of the Sordaria. Still, crossing over is an important part of meiosis that contributes towards genetic variation and the survival of organisms.*

## Introduction

Many organisms reproduce sexually, which happens when two gametes come together and form a zygote. Each gamete is produced through meiosis, which produces four daughter cells that may not be identical. This allows for genetic variation in populations, and this can be caused by genes crossing over from one chromosome to another, which occurs during meiosis. In meiosis I, chromosomes duplicate and form tetrads. Along the tetrad, there may be an exchange of genetic material between nonsister chromatids – crossing over. Although the process of crossing over cannot be observed, the effects of crossing over can (Feingold, 427).

Chromosomes that have experienced crossing over are split into separate chromatids in meiosis II, with a single chromatid in each daughter cell. If there is crossing over, these chromatids do not resemble the chromatids of the parents, thus causing genetic variation. Genetic variation is what drives evolution, and it also allows for a population to have a higher chance of having members who are capable of surviving.

Offspring exhibiting different phenotypes from their parents are known as recombinant types, and the percentage of recombinant types in a population of offspring can be used to determine the distance between the locus of the gene that crossed over and the centromere – the distance, in map units, is that percentage divided by two.

*Sordaria fimicola* is an ascomycete fungus that becomes diploid only when the mycelia of two different strains are fused together, which fuses two different types of haploid nuclei to form a diploid nucleus. This nucleus then undergoes meiosis, which, followed by mitosis, forms eight haploid ascospores within an ascus. These asci are contained within a perithecium, a fruiting body, and they rupture and release the ascospores when the ascospores are mature.

Crossing over in *Sordaria* occurs when hybrids are formed between wild type (black) and mutant (in this case, tan) strains of *Sordaria*. When this hybridization occurs, the asci that form contain four black and four tan ascospores. The arrangement of these spores indicates whether or not there was crossing over. If there was no crossing over, the spores would be in a 4:4 pattern, but if there was crossing over, the spores would be in a 2:2:2:2 or 2:4:2 pattern.

To determine the distance between the gene for ascospore color and the centromere of the chromosome, this experiment was conducted. It was hypothesized that that distance is 26 map units, since that is the accepted value from past studies, and the null hypothesis states that there is no difference between the data acquired from the experiment and the established values. This was tested by recording the number of *Sordaria* asci exhibiting crossing over by observing with a microscope.

## **Methods**

Two strains of *Sordaria fimicola* were grown in a petri dish filled with agar. A toothpick was used to collect a sample of *Sordaria* from where the two strains fused, and this sample was placed on an observation slide along with a drop of water. An eraser of a pencil was used to gently push the cover slip down upon the sample, popping the perithecia and releasing the asci. A microscope at 10x magnification was then used to observe the sample of *Sordaria*, and the number of asci showing crossover (2:2:2:2 or 2:4:2) was recorded, as well as the number of 4:4 (no crossover) asci.

## **Data & Results**

Data was collected from this class of researchers and from all classes combined. This data is recorded in Table 1. It has been established that the distance, in map units, between the

gene that is crossing over and the centromere is equal to the percentage of asci showing crossover divided by two.

Table 1: Class and composite data concerning the number of asci showing or not showing crossover and resulting calculations

	Number of 4:4 (No crossover)	Number of 2:2:2:2 or 2:4:2 (Crossover)	Total Asci	% Asci Showing Crossover Divided by 2	Gene to Centromere Distance (map units)
Class Data	382	443	825	28	28
Composite Data	1194	1446	2640	27	27

A chi-square analysis test was conducted in order to determine the accuracy of this experiment in whether or not the observed data agrees with the null hypothesis. Because the expected distance between the gene for ascospore color and the centromere was 26, that value is also half the expected percentage of asci showing crossing over, which would then be 52%. 2640 asci were observed by the entire group of researchers, so the expected number of crossover asci was 52% of 2640, or approximately 1373. The rest of the data was calculated accordingly, and a  $\chi^2$  value of 8.09 was found (Table 2).

Table 2:  $\chi^2$  analysis for composite data

Phenotype	# observed (o)	# expected (e)	(o-e)	(o-e) <sup>2</sup>	(o-e) <sup>2</sup> /e
Crossover Asci	1446	1373	73	5329	3.88
Non-crossover Asci	1194	1267	-73	5329	4.21

$$\chi^2 = \sum (o-e)^2/e = 8.09$$

This value was then used to determine whether or not the null hypothesis can be accepted by comparing it to critical values of the chi-square distribution.

Table 3: Critical Values of the Chi-square Distribution

Degrees of Freedom	Probability	(Level	of	Significance)
	0.1	<b>0.05</b>	0.01	0.001
1	2.706	<b>3.841</b>	6.635	7.879

### Discussion & Analysis

The distance from the gene controlling ascospore color to the centromere of the chromosome is equal to the half the percentage of asci showing crossover. In the composite data, there were 1446 asci showing crossover out of 2640 asci total, so 54.7% showed crossover, and thus the distance between the gene and the centromere was found to be 27 map units, which only slightly deviates from the accepted value of 26 map units (Table 1)

There are two possible types of asci accounted for in this experiment (crossover and non-crossover), so  $n = 2$ . The degrees of freedom (df) equals  $n-1$ , so it is 1 in this case. A probability level (p) of 0.05 is usually used (that is, there is a 5% chance of being wrong if the null hypothesis is rejected) to find a critical value to compare the  $\chi^2$  value to. The critical value when  $p = 0.05$  and  $df = 1$  is 3.841 (Table 3), and the calculated  $\chi^2$  value is 8.09 (Table 2). 8.09 is much greater than 3.841, so the null hypothesis cannot be accepted.

The data thus disagrees with accepted knowledge and with the hypothesis that 52% of the asci would show crossover. This discrepancy could be due to inconsistencies in conducting the experiment. Various samples of *Sordaria* were used, and though the average percentage of asci showing crossover should have been 52%, in some samples it may have varied. Some researchers also had difficulties bursting the asci and finding ascospores to observe, and there may have been errors in reporting the data.

Nonetheless, it can be concluded that there was crossing over, contributing to the genetic diversity of *Sordaria*. Likewise, in humans (as well as all other organisms), crossing over during meiosis causes genetic variations, granting the human race a higher chance of survival.

### **Works Cited**

Yu, Kai, and Eleanor Feingold. "Estimating the Frequency Distribution of Crossovers during Meiosis from Recombination Data." *Biometrics* 57.2 (2001): 427-434. *JStor*. Web. 13 Jan. 2011.