



Study of linkage between *miniature* and *singed* genes in *Drosophila melanogaster*.

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We have developed a practical exercise for undergraduate students whose main aim is to identify, using genetic crosses, a pair of *D. melanogaster* mutations (*miniature* and *singed*). Each student receives a vial with the problem strain containing two unknown mutations. The first step is to observe and describe both mutations. Then, the students carry out genetic crosses between mutant and normal strains:

(P) ♀ mutant strain × ♂ normal strain

(P) ♀ normal strain × ♂ mutant strain

A different offspring is expected in these crosses: in the first one we will obtain normal females and *m sn* males, whereas in the second all individuals will present normal phenotype. It is possible to deduce that both are sex linked mutations. With this information and to simplify the amount of work, only F₁ individuals from the first cross will be used ($m^+sn^+ / m sn \times m sn / Y chrom.$) to obtain the F₂ generation. The results expected for this F₂ generation would be:

Parental type	m^+sn^+	$m sn$ $m^+sn^+ / m sn$	$Y chrom.$ $m^+sn^+ / Y chrom.$
Parental type	$m sn$	$m sn / m sn$	$m sn / Y chrom.$
Recombinant type	m^+sn	$m^+sn / m sn$	$m^+sn / Y chrom.$
Recombinant type	$m sn^+$	$m sn^+ / m sn$	$m sn^+ / Y chrom.$

By counting the number of *miniature* (recombinant type), *singed* (recombinant type), *miniature-singed* (parental type) and *normal* (parental type) flies it is possible to estimate the recombination frequency between both genes. Knowing the phenotype, their chromosomal location (X chromosome) and the genetic distance between both mutations, it is possible to identify them by finding all this information in a *Drosophila melanogaster* genetic map (Gardner *et al.*, 1991; Russell, 1992; Griffiths *et al.*, 1996; Klug and Cummings, 1997; Pierce, 2009).

Additionally, a statistical analysis can be carried out to compare the number of expected F₂ individuals with those observed in the experiment. As the distance between both genes is 15.1 m.u., then the expected percentages for each phenotype would be: *normal* (42.45%), *miniature-singed* (42.45%), *miniature* (7.55%) and *singed* (7.55%). Multiplying the frequency of each class by the total number of individuals obtained in the F₂ it is possible to estimate the expected number of flies for each class. Finally, a χ^2 test can be computed to ascertain whether there are significant differences between expected and observed number of individuals.

References: Gardner, E.J., M.J. Simmons, and D.P. Snustad 1991, *Principles of Genetics*. John Wiley and sons, Inc., N.Y.; Griffiths, A.J.F., J.H. Miller, D.T. Suzuki, R.C. Lewontin, and W.M. Gelbart 1996, *An Introduction to Genetic Analysis*. W.H. Freeman and Co, N.Y. 6th ed.; Klug, W.S., and M.R. Cummings 1997, *Concepts of Genetics*. Prentice Hall International, Inc., Upper Saddle River, N.J.; Pierce, B.A., 2009, *Genetics: a Conceptual Approach*. W.H. Freeman and Co, N.Y. 3rd ed.; Russell, P.J., 1992, *Genetics*. Harper Collins Pub., N.Y. 3rd ed.

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