The observed $h^2$ values of 0.05 using female progeny and 0.04 using male progeny for sternopleural bristle numbers are at the low end of those reported in the literature (Falconer and Mackay, 1996; van Heerwaarden *et al*., 2008). Woodruff and Thompson (2005), however, reported $h^2$ values of 0.01 for females and males based on a selection response experiment in lines that were inbred by brother-sister matings for 41 generations and possessed low levels of genetic variation, whereas flies with greater levels of genetic variation had $h^2$ values of 0.11 for males and 0.15 for female. Since the OBL1&2 wild-type stock used in this study had been maintained in the laboratory for six years before this study (Carr *et al*., 2014), it may contain a reduced amount of genetic variation due to partial inbreeding, resulting in the observed low $h^2$ values.

A class discussion of the results of this study could include: 1) Ask students to estimate the number of quantitative trait genes controlling bristle number in *D. melanogaster*. It is about eight (Gurganus *et al*., 1999). 2) Ask students to estimate the narrow sense heritability for height in humans by determining the slope of the regression line for their heights *vs*. their mid-parent heights. The height of female parents and students should be multiplied by 1.08, because of the difference in height of men and women.

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## Description of a double mutant strain of *Drosophila melanogaster* useful for genetic laboratory courses.

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Many years ago, individuals showing drastically reduced eyes arose in our laboratory *e* (*ebony*) strain (Bridges and Morgan, 1923). We selected those flies presenting both traits and constituted a new double mutant strain *e su* (*e*, ebony; *su*, '*sense ulls*', eyes drastically reduced). Both mutations were linked and located in the chromosome III. We used this strain in linkage analyses with our undergraduate students. We then proceeded to assess which described gene was allelic to our *su* mutation. With a recombination experiment we deduced that *su* was located at 36.7 m.u. from the *e* gene. Consulting the genetic map of chromosome III we hypothesized that *su* could be the *eyg* (*eyegone*) gene (Ives 1940), whose phenotype is also eye reduction. We carried out a pseudodominance study using a deletion that covered the *eyg* region (ED2015, http://flybase.org/), and we observed that the individuals not showing the dominant marker (*Sb*, *Stubble*, Dobzhansky 1930) of the balancer chromosome (TM6C, Chyb and Gompel 2013) presented drastically reduced eyes. Finally, we wanted to confirm that *su* was actually *eyg* carrying out a complementation test crossing both strains. We obtained *eyg* strain from a stock center and the result of complementation test confirmed that *su* was a mutation of *eyg* gene.

This double mutant strain *e su* can be used for different genetic laboratory courses and we can send it upon request.

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## A hands-on genetics teaching approach at university level.

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Teaching general Genetics is a cornerstone of a large number of university degrees. Being a scientific topic, laboratory classes are an essential element in student-centered learning. Here, we present our experience in implementing new material for teaching hands-on genetics, a subject of interest for other academic professionals in the field of Genetics. Our students carry out a genetic analysis of the *su* (*sense ulls*) mutation of *Drosophila melanogaster*, which produces a drastic eye reduction. The complete strain description can be found in Mestres *et al.* (2016a). The aim of the course is to give students the appropriate genetics tools to answer the three following questions: 1) Is the *su* mutation dominant or recessive? 2) In which chromosome is *su* located? 3) Can we identify in which gene the *su* mutation is?

To answer the first two questions we designed a pattern of genetic crosses taking advantage of a double mutant strain *e su*, being *ebony* a recessive mutant producing black body color (Lindsley and Zimm, 1992; Chyb and Gomple, 2013). *Drosophila melanogaster* presents a karyotype composed by two large metacentric autosomes (II and III), a punctual autosome (IV), and the sexual chromosomes (I = X and Y). For chromosome location we first inform our students that the *su* mutation could be either inherited as a sex-linked or autosomal trait and discard other genetic patterns such as partial sex-linked inheritance, uniparental inheritance, maternal effect, and others. The genetics crosses proposed to the students are:

*e su* females (virgin) × *vg* males

and the reciprocal cross:

*vg* females (virgin) × *e su* males

The recessive mutation *vg* (*vestigial*, wings extremely reduced and held at right angles to the body) is located in chromosome II (Lindsley and Zimm, 1992; Chyb and Gomple, 2013), whereas *e* is in chromosome III. In both reciprocal crosses, all $F_1$ individuals show wild type phenotype, and thus students should conclude that *su* mutation is autosomal recessive. Later, analyzing the $F_2$ offspring it is possible to observe that *su* presents an independent inheritance with regard to *vg*, but is linked to *e*. Therefore, it is logical to deduce that *su* is located in chromosome III.

In past years, we finished the laboratory experiments at this level (solving only questions 1 and 2), but last year we decided to go further and try to answer question 3. To do so, we estimated the recombination between *su* and *e*. The value obtained was 36.65 m.u. from the location of *e* gene (70.7). We searched in the genetic map of the species (Lindsley and Zimm, 1992) which genes were located to the right (70.7 + 36.65 = 107.34) and left (70.7 – 36.65 = 34.05) of *e*. At 37.5 is *eyg* (*eyegone*), whose phenotypic description fits well with that of *su*. To confirm whether *su* mutation belongs to the *eyg* gene, we designed a pseudodominance experiment choosing the deletion Df(3L)ED215 from the DrosDel deletion collection (Ryder *et al.*, 2007) that spans the *eyg* gene. To study the pseudodominance the students carried out the cross between *e su* and