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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

Df(3L)ED215 flies. Approximately half of the offspring flies presented eyes drastically reduced, indicating that most probably *su* was an *eyg* gene mutation:

e su × Df(3L)ED215

↓

≈1/2 normal eyes + ≈1/2 reduced eyes

Furthermore, to confirm that the *su* mutation maps to the *eyg* gene, the students performed a complementation test crossing *e su* with *eyg* flies. All offspring individuals showed drastic eye reduction, and thus confirmed our hypothesis:

e su × *eyg*

↓

100% reduced eyes

We complemented the study with a couple of computer sessions using the *Drosophila* database Flybase (http://flybase.org/). In the first one, the students analyzed possible candidate genes presenting mutations that produced a similar phenotype to *su*. We selected *lz* (*lozenge*), *eya* (*eyes absent*), *eyg* (*eyegone*), and *ey* (*eyeless*) located in chromosomes I, II, III, and IV, respectively. The second computer session was programmed at the end of the laboratory course to present and comment the Df(3L)ED215 deletion and the balancer chromosome used to maintain it (TM6C).

The answer to question 3 implied a lot of work for our students and we had logistical problems to implement the whole experimental design (a restricted number of laboratory sessions, too many vials needed, *etc*.). For these reasons, we decided to simplify the crosses to be carried out by the students. They all worked in teams of four members: two of them carried out the initial reciprocal crosses, the third member performed the pseudodominance cross, and the fourth the complementation test. Particular details on the organization of the work can be found in Mestres *et al.* (2016b).

We introduced this new pattern of laboratory classes during the 2015-2016 academic year to 320 undergraduate students divided in 16 laboratory groups. The result of the experience was excellent. Students understood much better the genetic concepts of pseudodominance and complementation, obtaining better qualifications in the corresponding questions of the final exam. Additionally, they were satisfied to carry out a complete genetic study being able to properly answer the three proposed questions on *su* mutation. We also obtained an additional indirect benefit, which is the active study of a balancer chromosome is needed to maintain the Df(3L)ED215. For all these reasons we encourage other colleagues to use this pattern of laboratory classes in general courses of Genetics. We can send the necessary strains (*e su*, *vg*, Df(3L)ED215, and *eyg*) upon request to those interested in this experimental design.

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