

The colour and number of wings in drosophila

Introduction

In this study, we will determine how many and where are the genes responsible for the color and the number of the wings. The understanding of the links between genes and phenotypes in drosophila is usually very interesting because this animal is a very good model for human in medicine. Actually there is similarity between the two species, just like in human the sexual determinism is : (Y/X) for male and (X/X) for female. We will make crosses between populations having different phenotypes and by the Mendel law of inheritance, we will be able to answer the question.

Material and methods

Drosophila are small flies. They are easy to manipulate and make grow : in couple of weeks, in small boxes, we can reach a zillion of individuals.

Different hypotheses have been verified : genetic purity of the parental population, dominance and recessivity of the phenotypes, genes on a sexual chromosome, the number of genes and the linkage between the genes. In total, four crosses have been made and the results were compared with the hypotheses. The Chi2 test have been used for the number of genes and linkage hypotheses with a precision of 5%.

Results

First of all, we set down the phenotypes. The number of wings can be [1], [3], [5] and the colour Purple [P] or yellow [y].

In order to understand what phenotypes is dominant, recessive or co-dominant, we make a first cross, F_1 : [5P]X [1y]. The result is a purple population with three wings [3P]. Indeed, we can say that the phenotype purple [P] is dominant over the yellow one [y] and that five wings [5] and one wing [1] are co-dominant.

All the populations of drosophila are necessary homozygous except for the purple with one or five wings because the heterozygous version of the others have three wings. So, we make a second cross [5P] X[5P] in order to make sure that we had homozygous population (five wings and purple).

We suppose that each trait is controlled by one genes. To verify this hypothesis we make a third cross using the first one. Now we can write the first cross with the genotype notation :

F1: T1(P5//P5) X T2(Y1/Y1)

So we have F1(P5//Y1) and the phenotype with the precedents hypotheses is [P3]. Now, we make the third cross : F2: T2(Y1//Y1) X F1(P5//Y1)

T2/F1	(y1)	(P5)
(y1)	(y1//y1)	(y1//P5)
Phenotype	[y1]	[P3]

Results : we consider the two traits independantly.

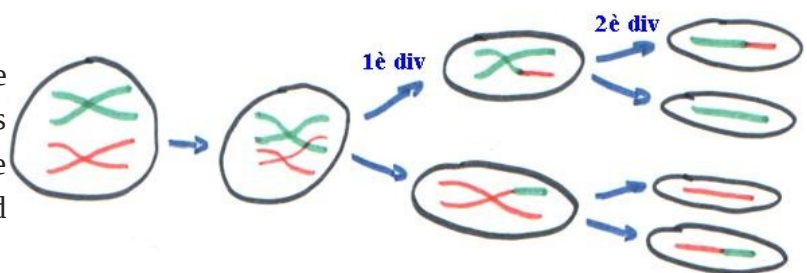
	[P]	[Y]	[1]	[3]
Observed	97	103	113	87
Expected	100	100	100	100

The value of the Chi2 is : $Q_c = (97-100)^2/100 + (103-100)^2/100 = 3,38 < 3.84$ for the color of the wings and $Q_n = 0,18 < 3.84$ of the number of wings.

So we obtain 50% of each phenotypes for each traits, except for the number of the wings but this is logical because of the co-dominant phenotype. Indeed, we can say that each trait is controlled by one gene.

Any of the genes studied can be on the Y chromosome because in this case : the females wouldn't have the traits. The gene controlling the number of wings cannot be on the X chromosome either because the male couldn't be heterozygous for this gene and a male with three wings [3] shouldn't exist. In order to know if the gene controlling we make the fourth cross : F1': $\varphi T'_1(X^{y5}/X^{y5}) \times \sigma T'_2(Y//X^{y5})$. In theory we should only obtain φ [P5] and σ [y5], but with the cross there is also φ [y5] and σ [P5]. So any of the genes studied are neither in the Y or X chromosome.

We suppose that the genes are independent, so if the hypothesis is correct because of the interchromosomal mixing we would have :



T2/F1	(y1)	(y5)	(P1)	(P5)
(y1)	(y1//y1)	(y5//y1)	(P1//y1)	(P5//y1)
Phenotype	[y1] 25 %	[y3] 25 %	[P1] 25 %	[P3] 25 %

And the results of the cross are :

	[y1]	[y3]	[P1]	[P3]
Observed	58	45	55	42
Expected	50	50	50	50

The value of Chi2 is : $Q = [(58-50)^2 + (45-50)^2 + (55-50)^2 + (42-50)^2] / 50 = 3.56 < 7.82$; with 7.82 the limit value 3 freedom degrees. So the hypothesis is confirmed : the genes aren't on the same chromosome.

Discussions

As a conclusion, the number of wings is controlled by one gene having two alleles codominant ; and the colour by one gene also with two alleles : one dominant purple over the other.

The results on animals such as drosophila are usually not usable directly. For example when we use it as a model for human, the next step is to look for the equivalent genes in the human genome. Off course it won't be the number of wings in human, but maybe the number of fingers...

We were very lucky to have directly homozygous population for the first cross. In order to deal with this question without this luck, we could have started by determining what population were homozygous and heterozygous but wouldn't have been able to use the arguments we used.