

GENETICS BIO2133 - VERSION A, B, C, and D

Each exams had the same questions. Hence only one copy of the correction key is provided.

The correction key provides answers and reasons for answers. In most cases I have written much more than was required on the exam. I have indicated where the points would be awarded.

This correction key is the exact copy that the T.A.s are using for marking. They have received specific instructions on how the corrections should proceed. They are very aware that the information provided in this key is to help you understand why the answers are as such.

The key also provides, in some cases, for alternative answers that may be correct. This is done to give the TAs the opportunity to understand that, in some cases, different types of answers may be provided by the students.

AGAIN THIS KEY PROVIDES EXPLANATIONS FOR EACH ANSWERS. IN MOST CASES, YOU DID NOT HAVE TO WRITE EVERYTHING THAT I HAVE WRITTEN.

SECTION I – CONCEPTS OF GENETIC ANALYSIS (12 points)

1. On an Arprior farm, a mutation arose that gave a platinum coat colour to dogs. The platinum coat colour is popular among buyers and breeders. Every time two platinums are crossed, some normal dogs appeared in the progeny. For example, the repeated matings of the same pair of platinums produced 82 platinums, 43 blacks, and 41 brown progeny. Based on this information, state a concise genetic hypothesis that accounts for these results. **Explain. (3 points)**

This is a case of incomplete dominance. It cannot be epistasis (two genes) because we would not be able to produce this phenotypic ratio in the progeny in a dihybrid cross. This is a case of one gene with two alleles exhibiting incomplete dominance.

The platinum dogs must be heterozygous for us to obtain black and brown dogs with a 2 platinum :1 black :1 brown dog ratio in their cross based on our finding of incomplete dominance.

2. Explain what is complementation and how is it detected. **(3 points)**

Complementation refers to multiple genes that must exhibit a dominant allele for a given phenotype to be expressed. In the case of two genes, if either one of the genes is homozygous recessive, the phenotype will not be expressed.

This can be detected in a dihybrid cross and obtaining a 9:7 phenotypic ratio.

3. Briefly explain how one may determine the order of dominance in a case where multiple alleles exist for a given gene. **(3 points)**

Perform crosses using pure lines for each allele. Self the F1 and measure the phenotypic ratio. The one that gives the highest number in the phenotype is the dominant allele (as this would give a 3:1 ratio – 2 homozygous and 1 heterozygous = 3 dominant phenotype individuals and 1 homozygous recessive).

Repeat procedure with every possible combination of pure lines. Using the 3:1 benchmark, then one can determine order of dominance.

4. What is meant by penetrance and expressivity? **(3 points)**

Often the phenotype is attributed to a gene is recognized as dependant to unknown factors.

Penetrance : the % of individuals of a given genotype that manifests the phenotype usually associated to the genotype.

Expressivity: the degree of expression of a given genotype in a given individual

SECTION II – (38 points)

1. (8 points) “Lord of the Rings (Chapter 95 – The Hobbit Geneticist)”

Hobbits, who live in the Shire, are short people who have long feet and hairy backs; Orcs (really ugly ogres) are tall, have small feet and have hairless backs. Following many mating experiments, Sauron (the Lord of the Rings) determined that the Orc alleles are recessive to the Hobbit alleles, and that these genes are on a single autosomal chromosome and that they are linked in the following order:

height 24 cM. feet 8 cM hair on back

In attempt to create an army of orcs, Sauron has captured many hobbits to use in mating experiments with Orcs. He therefore initially crossed Orcs and Hobbits

- a) If the F1 (results of the initial cross) are crossed with Orcs, what proportion of the progeny will have Orc height (tall), long feet, and hairless back? (2 pts)

Calculate the proportion of double crossovers: $(0.24 \times 0.08) = 1.92\%$ (this is the number of recombinants involved in double crossovers). Therefore 0.96% of the gametes will have orc height (tall), long feet, and hairless back alleles. Since Sauron is crossing the F1 with orcs (pure breeding; in this case a tester), **then 0.96% of the F2 will have orc height (tall), long feet, and hairless back.**

- b) If the males and females of the F1 (results of the initial cross) are crossed with each other, which proportion of the progeny will have Orc height, long feet, and and hairless back? (2 pts)

We already know that these hobbits/orc hybrids produce 0.96% of gametes with the orc height (tall), long feet, and hairless back alleles. Since Sauron is crossing F1 hobbit/orc hybrids, then the proportion will be:

The following genotypes are the possibilities to have an individual with the following characteristics described above: (One has to calculate the possibility of each gamete fusing together at fertilization. Therefore:

$$hFb/hFb \rightarrow (0.96\% \times 0.96\%) = 0.009216\%$$

and

$$hFb/hfb \rightarrow (0.96\%) \times ((76\% \times 92\%)/2) \times 2 = 0.67\%$$

(to calculate hfb, one has the calculate the proportion of gametes that do not undergo crossovers between each gene....as such the probability of no crossovers to occur is 76% between the first two genes and 92% between the last two genes. We have to divide by 2 because two chromatids are

affected but we are only interested in one of them. Multiply by 2 because there are two ways to obtain this genotypes – both parents have equal chances of providing each of these gametes)

Therefore the total chances of individual with this phenotype is:

$$0.67 + 0.009216 = 0.68\%$$

- c) If the males and females of the F1 (results of the initial cross) are crossed with each other, which proportion will have Hobbit height and long feet but with hairless backs? (2 pts)

Once again, we have to calculate the probability of the following genotypes taking into account crossovers in each parents: (same logic as above):

$$\text{HFb}/\text{HFb} \rightarrow ((0.76 \times 0.08)/2) \times ((0.76 \times 0.08)/2) = 0.092\%$$

$$\text{HFb}/\text{hFb} \text{ (can be produced two ways)} \rightarrow ((0.76 \times 0.08)/2) \times (0.0096) \times 2 = 0.06\%$$

$$\text{HFb} / \text{Hfb} \text{ (can be produced two ways)} \rightarrow ((0.76 \times 0.08)/2) \times ((0.24 \times 0.92)/2) \times 2 = 0.67\%$$

$$\text{HFb}/\text{hfb} \text{ (can be produced two ways)} \rightarrow ((0.76 \times 0.08)/2) \times ((0.76 \times 0.92)/2) \times 2 = 2.13\%$$

$$\text{Hfb}/\text{hFb} \text{ (can be produced two ways)} \rightarrow ((0.24 \times 0.92)/2) \times (0.0096) \times 2 = 0.211$$

$$0.092\% + 0.06\% + 0.67\% + 2.13\% + 0.211\% = 3.163\%$$

- d) If the males and females of the F1 (results of the initial cross) are crossed with each other, which proportion will have Hobbit height and hairy back, with Orc feet? (2 pts)

Same logic as above:

$$\text{HfB} / \text{HfB} \rightarrow ((0.0096) \times (0.096)) = 0.009216\%$$

$$\text{HfB} / \text{hfb} \text{ (can be produced two ways)} \rightarrow (0.0096) \times ((0.76 \times 0.92)/2) \times 2 = 0.67\%$$

$$\text{HfB} / \text{Hfb} \text{ (can be produced two ways)} \rightarrow (0.0096) \times ((0.24 \times 0.92)/2) \times 2 = 0.211\%$$

$$\text{HfB} / \text{hfB} \text{ (can be produced two ways)} \rightarrow (0.0096) \times ((0.76 \times 0.08)/2) \times 2 = 0.06\%$$

$$\text{hfB} / \text{Hfb} \text{ (can be produced two ways)} \rightarrow ((0.76 \times 0.08)/2) \times ((0.24 \times 0.92)/2) \times 2 = 0.67\%$$

$$0.009216\% + 0.67\% + 0.211\% + 0.06\% + 0.67\% = 1.62\%$$

The easiest way to do this question is to calculate all gamete proportions produced during meiosis. Then it's simply a case of applying the product and sum rules!

2. (10 points) As an undergraduate student in the genetic lab, you are given the task to “confirm” the role of gene C and gene B in the expression of coat color in cats. Only the following information is provided: Gene C displays dominant epistasis to gene B and produces gray coat.

To this end, you are provided with many cats of which the female cats are all gray and the males all brown. Following the mating (and a few months later) you obtain the following results:

Phenotype	number of individuals
Gray cats	54
Black cats	22
Brown cats	24
	Total 100

- a) Based on these findings, what hypothesis can you state about the genotypes of the female and male cats of the parental line? (2 points)

Based on these results (2:1:1 ratio) and the information provided in the description, one would have to predict the following genotypes of the cats: (remember that C displays dominant epistasis to B and produces gray coat).

Gray cats – $Cc Bb$ and Brown cat – $cc bb$

- b) Determine whether the results are compatible with your hypothesis in (a) and that gene C is epistatic (dominant) to gene B (8 points). **Show your work!**

We know C is epistatic to B. What we wanted to do was to test the hypothesis that our cats have the genotypes predicted in (a) knowing there was epistasis.

Therefore: expected ratio based on the genotypes of my two cats will be 2 grays ($CcBB$ and $Ccbb$): 1 Black ($ccBb$): and 1 brown ($ccbb$) therefore the expected numbers will be 50 grays, 25 blacks, and 25 browns.

$$\begin{aligned} \text{Grays : } (O-E)^2/E &= (54 - 50)^2/50 = 0.32 \\ \text{Blacks} &= (22-25)^2/25 = 0.36 \\ \text{Browns} &= (24-25)^2/25 = 0.04 \end{aligned}$$

$$\begin{aligned} \text{Chi}^2 &= 0.32 + 0.36 + 0.04 = 0.72 \\ \text{Degrees of freedom} &= 3-1 = 2 \end{aligned}$$

Probability (p) is between 0.9 and 0.5 which is higher than the fiducial limit of 0.05. We therefore accept the hypothesis.

Table 2-2 Critical Values of the χ^2 Distribution

df	P								df	
	0.995	0.975	0.9	0.5	0.1	0.05	0.025	0.01		0.005
1	.000	.000	0.016	0.455	2.706	3.841	5.024	6.635	7.879	1
2	0.010	0.051	0.211	1.386	4.605	5.991	7.378	9.210	10.597	2
3	0.072	0.216	0.584	2.366	6.251	7.815	9.348	11.345	12.838	3
4	0.207	0.484	1.064	3.357	7.779	9.488	11.143	13.277	14.860	4
5	0.412	0.831	1.610	4.351	9.236	11.070	12.832	15.086	16.750	5
6	0.676	1.237	2.204	5.348	10.645	12.592	14.449	16.812	18.548	6
7	0.989	1.690	2.833	6.346	12.017	14.067	16.013	18.475	20.278	7
8	1.344	2.180	3.490	7.344	13.362	15.507	17.535	20.090	21.955	8
9	1.735	2.700	4.168	8.343	14.684	16.919	19.023	21.666	23.589	9
10	2.156	3.247	4.865	9.342	15.987	18.307	20.483	23.209	25.188	10
11	2.603	3.816	5.578	10.341	17.275	19.675	21.920	24.725	26.757	11
12	3.074	4.404	6.304	11.340	18.549	21.026	23.337	26.217	28.300	12
13	3.565	5.009	7.042	12.340	19.812	22.362	24.736	27.688	29.819	13
14	4.075	5.629	7.790	13.339	21.064	23.685	26.119	29.141	31.319	14
15	4.601	6.262	8.547	14.339	22.307	24.996	27.488	30.578	32.801	15

3. (10 points) The Smurfs!

In smurfs, the color of bodies, caps and pants are coded by three different genes. The color of the body is determined by the blue allele (B) or the black allele (b); the color of their caps is determined by the white allele (W) or the red allele (w); and the color of their pants is determined by the white allele (Y) or the yellow allele (y). While you are interested in determining if these genes are linked, you are not interested in finding out their order if all three genes are linked. Therefore, on a field trip, you collected pure breeding lines of smurfs from the forest to determine linkage of these genes.

In a preliminary experiment, you cross pure breeding lines of smurfs (blue bodies, white caps and white pants X black bodies, red caps and yellow pants), and obtained smurfs that only exhibited blue bodies, white caps and pants. Following this experiment, you crossed males and females of the F1. However, in your haste to complete the experiment you only noted results that considered two phenotypes at a time, and not the three. The following is what was noted in your lab book.

Result #1 - Phenotypes considered: body colour and cap colour

Phenotype	Number in progeny
Blue ; white	110
Black; red	115
Blue ; red	39
Black; white	36



Result #2 - Phenotypes considered: body colour and pant colour

Phenotype	Number in progeny
Blue; white	68
Black; yellow	70
Blue; yellow	70
Black; white	69

Result #3 - Phenotypes considered: cap colour and pant colour

Phenotype	Number in progeny
White; white	131
Red; yellow	149
White; yellow	59
Red; white	61

a) Considering all of these results, what can you conclude about the linkage of these genes? (hint: are they linked, if so determine the distance in map units between them. Based on the results are they linked?). **Show your work!**

Although not explicitly stated, to perform a linkage test, one has to cross an individual from the F1 with a tester. In this case the male was the tester and the female was from the F1.

The conclusion that should be drawn in this question is that all three genes are linked. At first glance, one would assume that they are not but.....they are!!!!

2 pts- Body colour and cap colour distance: $39+36/300 = 25 \text{ cM}$ (conclusion - linked)

2 pts - Body colour and pant colour distance: $70+69 /277 = 50 \text{ cM}$ (conclusion - unlinked)

2 pts - Cap colour and pant colour distance: $59+61 /400 = 30 \text{ cM}$ (conclusion - linked)

If body colour and cap colour are linked and that cap colour and pant colour are linked, it must also be concluded that body colour and pant colour are also linked. In this case, the distance between body colour and pant colour are well over 50 cM. In such experiments they will behave as unlinked because some many crossovers occur in between them.

4 pts Conclusion – all three genes are linked. (Must show justification (-2 pts without conclusion))

One only has to look at the gene map of drosophila to realize that while genes may be linked, some may be separated by much more than 50 cM. To map these genes, one has to perform these types of experiments using genes that are closer together. In many instances, linkage has been deduced the same way as in this answer. Again, one has to consider all the results to draw appropriate conclusions

4. (10 points) Crime Scene Investigation (CSI) – The case of the switched babies

In a maternity ward, four babies were taken from their cribs and placed in different cribs by a disgruntled nurse. In your investigation to give the babies to their rightful parents, you determined the blood types of the babies and the parents. The ABO types of the babies and parents are as follows:

Results from the babies

Baby 1 (Tristan) – AB
 Baby 2 (Benoit) – B
 Baby 3 (Nicholas) – A
 Baby 4 (Cristine) – O

Results from the parents

Lucie (A) and Colin (AB)
 Chantal (A) and Harold (O)
 Brenda (O) and Marc (O)
 Josee (O) and Donat (AB)

Indicate to which baby belongs to each set of parents. Justify your answer.

An important thing to catch on to is the fact that each baby can only belong to one set of parents.

Baby 4 must belong to Brenda and Marc. Both parents have O blood, therefore are $I^O I^O$. These parents can only produce babies with O blood.

.....3 babies left

Baby 3 must belong to Harold and Chantal. Chantal's genotype is $I^A I^A$ or $I^A I^O$ and Harold is $I^O I^O$. While they can produce a baby with O blood, the baby with the O blood must belong to Brenda and Marc.

..... 2 babies are left

Lucie and Colin can make babies with A blood ($I^A I^A$) or AB blood ($I^A I^B$). They cannot make babies with B blood ($I^B I^B$ or $I^B I^O$). Only Josee and Donat can produce such a child. In fact Donat and Josee can only make babies that are $I^A I^O$ or $I^B I^O$. **Therefore baby 2 belongs to Donat and Josee.**

Baby 1 belongs to Lucie and Colin by deduction. Nevertheless there is also a biological reason. Colin and Lucie can make babies with AB blood ($I^A I^B$) or A blood ($I^A I^A$).

Luckily for us, the babies had different types of blood. Had any of these babies had similar blood types, we would have had to perform additional tests.

By the way, the names were real – the story is not!!