

Carefully read each question to determine what it wants you to do.

We are studying genetic traits in the tin-hatted, red-cloaked hunchback (let us call them hunchbacks for short)(→). One of these traits is the presence or absence of a pointy, hat-like structure that appears to be under the control of a single genetic locus.



Q1: In your studies you have isolated hat-less and pointy-hat strains.

- 1) **Describe** how you would prove that a strain (whether dominant or recessive) was true breeding and what does it imply about its genotype?
&
- 2) How would you go about determining whether the allele responsible for the pointy hat phenotype (hat⁺) is dominant or recessive compared to hat-less (hat⁻) allele?

When backcrossed to itself (as in peas), it produces only organisms with the trait. If backcrossing not possible, repeated inbreeding with other individuals with the trait produces organisms that always display the trait.

Cross pure breeding hat⁺ and hat⁻ individuals; the phenotype of their offspring represents the dominant allele.

Q2: In your collection of hunchbacks, you find a second genetically-determined phenotypic variant: long-beak versus short beak. When you mate pure breeding long-beak hunchbacks with pure-breeding short-beak hunchback all of the offspring have long beaks.

long-beak is dominant

You discover a wild long beak hunchback. To determine its genotype, you mate it to a short beak hunchback. Many offspring are produced of whom ~50% are long beaked and ~50% are short beaked. What are the genotypes of the two hunchback parents used in the mating?

To get any short beak offspring, the long beak parent must be heterozygous.

Q3: Using your true breeding lines, how would you determine whether the genes encoding the hat and the beak phenotypes were linked? Outline and explain your approach.

First breed the two parents together (all will express the dominant phenotype), then these offspring. If the genes are unlinked, the offspring should occur in the ratio 9: dominant/dominant ; 3 dominant / recessive : 3 recessive / dominant : 1 recessive / recessive.

If we assume that the parents are dominant / dominant and recessive / recessive in their phenotypes, if the genes are linked, we would expect to find fewer of the dominant / dominant and more of the recessive/recessive offspring in the F2 generation.

Q4A: You characterize a new phenotype, a large versus a small back. The allele leading to the large back phenotype (B) is dominant to the allele responsible for the small back phenotype (b). You cross pure breeding tin-hat, large back animals with hat-less, small back animals: what are the expected percentages of phenotypes in these F1 offspring?

All tin-hat, large back

Q4B: You now cross a number of F1 animals and generate ~3600 offspring. You find their phenotypes are

tin-hat, large back	1450
tin-hat, small back	420
no hat, large back	410
no hat, small back	1390

Are the tin-hat and hunchback genes linked or not (explain your reasoning)

As described in the answer to question 3. the genes are linked (non-mendelian ratios)

Q5: Assume that in the previous study, you had 100 times fewer organisms (30 versus 3600), explain how would this effect the certainty in your conclusions.

You would likely be less sure of your conclusion.

Q6A: You have another trait to examine, long ear (LE) versus short ear (se). You find that the long ear allele is dominant to the short ear allele. You have true breeding large back / long ear and small back/short ear strains. What is the phenotype of the offspring (F1) animals?

All long-ear, large back

Q6B: You now cross a number of F1 animals, and generate ~3200 offspring. You find their phenotypes are

large back, long ear	1840
large back, short ear	610
small back, long ear	595
small back, short ear	0

How you would explain these numbers, what does it say about the alleles of these two genes.

The result suggest an interaction between the small back and short ear gene, leading to an embryonic (no offspring) phenotype.

Q7: Now let us consider one last trait - white or black ears. When you cross a pure breeding white ear parent to a pure breeding black ear parent, all of the F1 offspring have grey ears.

Which type of morph do you think the white allele is likely to be and how might you test your hypothesis - there is not a single right answer, your answer just needs to make sense.

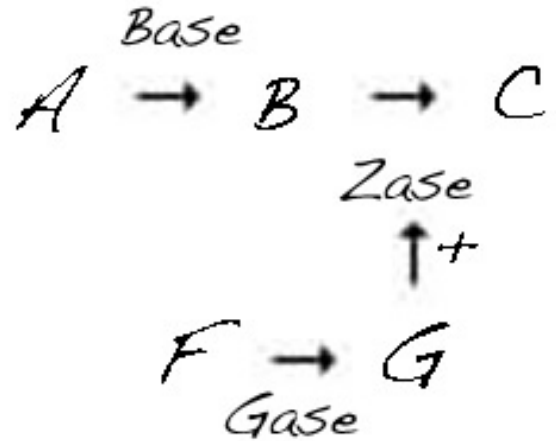
The could be that the white allele is hypo- or amorphic, the black allele normal activity. Ear color could determined by how much gene product is produced.

So black/black is high, white/white is low, and black/white is intermediate. That is, I think the simplest model.

Q8: Why would you expect the effects of a CRISPR CAS9 based mutagenesis to be more or less specific than (for example) exposing an organism to X-rays. Be sure to explain what you mean by specific.

It would be more specific - X-rays would produce mutations everywhere (randomly). CRISPR leads to targeted mutagenesis (determined by the guide RNA sequence) - Even if there are some "off-target" effects, CRISPR is expected to be very much more specific

Q9: You are looking at the following metabolic pathway (→); compound C is essential for the survival of the organism. C is generated from B in a reaction catalyzed by the enzyme Zase (the product of the Zsyn gene). G is synthesized from F in a reaction catalyzed by Gase, the product of the Gsyn gene.



The compound G binds to Zase, in the absence of G, Zase is completely inactive.

You discover two mutant alleles. The first is in the Zsyn gene (Zsyn^{AC}); it renders Zase active in the absence of G. The other is in the Gsyn gene (Gsyn⁻); it completely inactivates the Gase enzyme. The normal (wild type) alleles of these genes are Zsyn⁺ and Gsyn⁺.

Predict the phenotypes (dead or alive) of these organisms and briefly explain your reasoning):

- 1) Zsyn⁺/Zsyn⁺ Gsyn⁺/Gsyn⁺
Alive - this is the wild type genotype leading to synthesis of both G and C
- 2) Zsyn⁺/Zsyn⁺ Gsyn⁻/Gsyn⁻
Dead - since in the absence of G, Zase is inactive, no C synthesized
- 3) Zsyn^{AC}/Zsyn^{AC} Gsyn⁻/Gsyn⁻
Alive - even though G is not made, Zase is active, C synthesized
- 4) Zsyn^{AC}/Zsyn^{AC} Gsyn⁺/Gsyn⁺
Alive - G and C are made

Q10A: How might an amorphic allele behave in a dominant manner.
Not enough (50% of the gene product leads to a phenotype (there is necessary threshold))

Q10B: How might an amorphic allele behave in a recessive manner.
50% of the "normal" gene product is enough for the wild type (normal) phenotype.

Q10C: How might a neomorphic allele behave in a dominant manner.
Its new function produces a phenotype. "normal" gene product is enough for the wild type (normal) phenotype.