

Two genetic loci, *A* and *B*, are independently assorting, and alleles *A* and *B* are dominant over alleles *a* and *b*. Indicate the probabilities of producing the following. (20 points)

I have answered each in the form of a sentence that describes the probability outcome and then put in some numbers

a. An *AB* gamete from an *AaBb* individual?

The chance getting an A and a B = $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$

c. An *Aabb* progeny from the cross *AaBb* x *AAbb*?

It is easiest to break this into two monohybrid crosses to determine the probability. The chance of getting Aa and bb = $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$

d. An *A_B_* progeny from the cross *aabb* x *AABB*?

All of the progeny will be *AaBb* so the probability is 1 or 100%

e. An *aaB_* progeny from the cross *AaBb* x *AaBB*?

It is easiest to break this into two monohybrid crosses to determine the probability. The chance of aa and B_ = $\frac{1}{4} \times 1 = \frac{1}{4}$. All of the B locus outcomes are B_, either BB or Bb.

You have identified a new chemical that can produce transversion mutations in DNA sequence. If you were to treat the codon CGG with this chemical could you produce a missense mutation? Could you produce a nonsense mutation? *Explain.* (15 points)

		Second base							
		U	C	A	G				
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC		UCC		UAC		UGC		C
	UUA	Leu	UCA		UAA	Stop	UGA	Stop	A
	UUG		UCG		UAG	Stop	UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	Gln	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	Lys	AGA	Arg	A
	AUG	Met	ACG		AAG		AGG		G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA		GGA		A
	GUG		GCG		GAG	Glu	GGG		G

Transversion mutations change a pyrimidine base to a purine base or vice versa. So with our CGG codon we are looking at C to G or A and G to T or C. There are multiple correct answers.

Missense mutation: CGG to GGG. This contains a C to G change and that is a Arg to Gly change.

Nonsense Mutation: It cannot produce a nonsense mutation. In order to change CGG to a stop codon you must be able to change the first C to a U (or T in DNA). A transversion would change C to G or A, but not a T. So this change is not possible.

In jimsonweed, two alleles of one gene determine the character difference of purple (P) versus white (W) flowers, and two alleles of a *separate, independent* gene determine the character difference of spiny (Sp) versus smooth (Sm) leaves. The results for three different matings of jimsonweed plants are as follows:

Mating	Parental Phenotypes	P, Sp	W, Sp	P, Sm	W, Sm
1	purple, spiny x purple spiny	94	32	28	11
2	purple, spiny x purple, smooth	40	0	38	0
3	purple, spiny x white, spiny	34	30	0	0

Determine the dominant allele and the genotypes of the parents for each of the crosses (25 points).

This is all about looking at the ratios that will reveal the patterns of inheritance. Since they are independently assorting we can look at each phenotype separately. Let's start with Mating 1 and work our way through.

Mating 1: This cross reveals a 9:3:3:1 ratio that occurs when doing a dihybrid cross between two individuals that are heterozygous at both loci. The progeny that fall into the 1 category are the White and Smooth group with 11. These are homozygous for the two recessive alleles—WWSmSm. This means that Purple is dominant to White and Spiny is dominant to Smooth. We just determined the dominance relationships and are half way there. So the parents genotypes for Mating 1 are both PWSpSm.

Mating 2: All the Progeny are purple. This means that at least one of the parents is homozygous for the Purple allele. For simplicity let's say that both parents are homozygous for Purple. If we look at the other phenotype you see that we get a 1:1 ration of Spiny to Smooth. Smooth is recessive so these progeny have to be homozygous for the Smooth allele (Sm). The one parent is spiny and the other is smooth. In order for smooth to appear in the next generation, the spiny parent must carry a Sm allele and thus be heterozygous. So putting this all together the Parent's likely genotypes are PPSpSm and PPSmSm.

Mating 3: In this cross we see the opposite of mating 2. All the progeny are spiny. So for simplicity sake we will say the parents are both homozygous for the dominant Sp allele. The white and purple appear in a 1:1 ratio. In addition, one of the parents is white. This means that they are homozygous for the W allele. In order to get white to appear in the progeny the purple parent must be heterozygous and carry a W allele. So putting this all together the Parent's genotypes are PWSpSp and WWSpSp.

In the *X-linked dominantly inherited* fragile-X syndrome, individuals who have no symptoms but carry long repeats that have not expanded across the threshold are said to carry a “premutation” in the fragile-X gene. When a parent has a premutation of a particular size, there is a certain probability that the repeat will expand past the disease threshold and produce Fragile-X syndrome in their child. The likelihood of this expansion occurring is related to the length of the premutation. Use the following information to answer the question:

- A normal father with a normal repeat allele and a mother who is heterozygous for a premutation of 65 repeats and a normal repeat allele want to have children.
- They have a 50% chance of having a child carrying a premutation and a 50% chance of having a child with only normal repeat alleles of the gene.
- There is a 17% chance that the mother’s allele will expand past the threshold to produce Fragile-X Syndrome in her child.

Read the following carefully: What is the probability that the couple will have two children who both carry the premutation but with **only one** of the two children developing an expansion to the disease producing mutation? (10 points)

All the information is present in the question. The key is to develop a sentence that will describe our probability outcome. Let’s obtain the pieces we need:

- 1. We want both children to carry the permutation. The question tells us that there is 50% probability that a child will get the permutation.**
- 2. One child will develop an expansion and one will not. The question tells us that the probability that an expansion will occur is 17%. This means that there is an 83% chance that the repeat won’t expand. This is an important piece of information.**
- 3. Finally only one is going to expand so how many different ways can this occur. There are two mutually exclusive ways (think addition rule) that it can occur when birth order is taken into account—First child expands, second doesn’t OR First child doesn’t, second expands.**

Let’s put it together:

Child with premutation **and** no expansion **and** Child with premutation **and** expansion

(.50) **x** (.83) **x** (.50) **x** (.17)

Or (+)

Child with premutation **and** expansion **and** Child with premutation **and** no expansion

(.50) **x** (.17) **x** (.50) **x** (.83)

= ~0.07 or a 7% chance