

INTRODUCTION

This worksheet complements the “Frequency Primer” section in Case One of the [CSI Wildlife](#) Click & Learn. In this section, you will use allele frequencies to determine the chances of two elephants sharing the same genetic profile.

PROCEDURE

Open the Click & Learn and select Case One at the top. Click on the last section of Case One, Frequency Primer. As you go through each part of the Frequency Primer, follow the instructions below and answer the questions in the spaces provided.

Read through the **Background** section.

1. Explain what is meant by an allele’s relative frequency.

2. The gel on the screen shows a genetic profile of the elephant identified in Case One. Which allele has the *lowest* relative frequency, and which has the *highest*? (Remember that an individual can have one or two alleles for any marker.)

Read through the **Technique** section.

3. Imagine an STR marker that has four known alleles in a population: A, B, C, and D. Below are the alleles’ relative frequencies in one population of elephants. Fill in the missing frequency for allele D.

Allele	Relative frequency
A	0.25
B	0.15
C	0.45
D	

4. Let's take a closer look at how the relative frequencies in Question 3 were calculated. Imagine that the population has 10 elephants. Each elephant's alleles for this STR are shown in the table to the right.

Elephant	Allele 1	Allele 2
1	A	A
2	C	C
3	B	C
4	B	D
5	A	A
6	C	C
7	B	C
8	A	D
9	C	C
10	C	D

Using the information above, complete the table below. The first row has been filled in for you.

Allele	Number of the allele in the population	Total number of alleles in the population	Relative frequency of the allele (Number of that allele/Total)
A	5	20	$5/20 = 0.25$
B		20	
C		20	
D		20	

Do the last columns of the tables in Question 3 and Question 4 match up? If not, check your work.

Read through the **Application** section.

- In the probability formulas shown, what do p and q represent?
- In terms of p and q , what is the formula for the probability of having a *homozygous* genotype?
- In terms of p and q , what is the formula for the probability of having a *heterozygous* genotype?
- Using the table of allele frequencies in Question 3, calculate the probability that an elephant born in this population will:
 - have a copy of allele B
 - have the homozygous genotype BB (Hint: Use the formula from Question 6.)
 - have the heterozygous genotype BD (Hint: Use the formula from Question 7.)

Let's now apply these formulas to some real data. Look at the gel shown on the screen. It represents a four-marker genetic profile for an elephant in a different population. The relative frequencies for the alleles shown are summarized in the table to the right.

Marker	Relative frequency of allele(s) shown
FH19	0.06
FH127	0.08, 0.05
FH67	0.10, 0.24
FH71	0.09

9. Why is there only one frequency for the alleles for the FH19 and FH71 STR markers, but *two* frequencies for the alleles for the FH127 and FH67 markers?

10. The elephant profiled here is homozygous for an allele of the **FH71** marker. As shown in the table, this allele has a relative frequency of **0.09**. Based on the formula in Question 6, the probability of an elephant from this population having the profiled elephant's genotype for the FH71 marker (in other words, for being homozygous for the same FH71 allele) is $(0.09)^2 = 0.008$.

This elephant is also homozygous for an allele of the FH19 marker. What is the probability of an elephant from this population being homozygous for the same **FH19** allele? Show your work.

11. The elephant profiled here is heterozygous for the **FH67** marker; it has two different alleles for this marker with relative frequencies of **0.1** and **0.24**. Based on the formula in Question 7, the probability of an elephant from this population having the profiled elephant's genotype for the FH67 marker is $2(0.1)(0.24) = 0.048$.

What is the probability of an elephant from this population having the profiled elephant's genotype for the **F127** marker? Show your work.

12. Using the probabilities from Questions 10 and 11, calculate the probability of an individual from this population having this exact four-marker genetic profile. Show your work. (Note that the answer in the Click & Learn was calculated without rounding the probabilities from Questions 10 and 11. You may get a slightly different answer if you round these probabilities.)

Go to the **Review** section. The gel shown on the screen represents a more detailed, 16-marker genetic profile for the same elephant. Follow the instructions below to help answer the review question.

13. The relative frequencies for the alleles shown in the gel are summarized in the table below. Fill in the last column, showing your work for each row. Some of the rows have been filled in for you.

Marker	Relative frequency of allele(s) shown	Probability of an individual from this population having this genotype
FH39	0.16, 0.26	$2(0.16)(0.26) = 0.0832$
FH153	0.05, 0.06	$2(0.05)(0.06) = 0.006$
FH40	0.49	$(0.49)^2 = 0.2401$
FH94	0.20, 0.44	$2(0.20)(0.44) = 0.176$
FH102	0.13, 0.12	$2(0.13)(0.12) = 0.0312$
FH19	0.06	<i>Hint: This is the answer to Question 10.</i>
FH48	0.19, 0.14	
FH127	0.08, 0.05	<i>Hint: This is the answer to Question 11.</i>
FH129	0.16, 0.08	
FH60	0.26, 0.06	
LAFMS04	0.78	
FH103	0.15	
LAFMS03	0.10	$(0.10)^2 = 0.0100$
FH126	0.14	$(0.14)^2 = 0.0196$
FH67	0.10, 0.24	$2(0.1)(0.24) = 0.048$
FH71	0.09	$(0.09)^2 = 0.0081$

14. Using the probabilities from Question 13, calculate the probability of an individual from this population having this exact 16-marker genetic profile. (Note that the answer in the Click & Learn was calculated without rounding the probabilities from Question 13. You may get a slightly different answer if you round these probabilities.)

15. Using the probability you calculated in Question 14, fill in the following blank:

The chance that another elephant from this population would have the same 16-marker genetic profile is 1 in _____.

16. There are many more than 16 STRs in an elephant's genome. Why do you think that Sam Wasser and his colleagues reasoned they did not need to use more than 16 markers for their genetic profiles?