Predict $F_3$ generation

• How can we predict the distribution of traits in the $F_3$ generation?
Focus question

• How can we predict the distribution of traits in a future generation?
1. If one larkey parent is homozygous dominant for eye color, what do we know about the offspring?

2. How do we know this?
Punnett squares predict the probability for one offspring to inherit a trait, and they predict the distribution of a trait in a generation if all the parents are the same genotype.
Use Punnett squares

Notebook sheet 10, *Punnett Squares A*
Use Punnett squares

Procedure

a. Refer to your Larkey Breeding Record.

b. Swap males with another pair of students. Record the genotype of the new immigrant male in the $F_2$ generation of your Larkey Breeding Record.
Use Punnett squares

c. Record the genotypes of the two \( F_2 \) parents on notebook sheet 10.

d. Complete the four Punnett squares (one for each feature) on the notebook sheet to determine the probability of each trait for the individuals. Complete question 1 on the notebook sheet.
Breed $F_2$ larkeys

• Are there any features that you can predict for certain what the phenotype of the offspring will be?
Breed $F_2$ larkeys

“A Model for Predicting Genetic Variation”

Click Breed $F_2$ Generation to start.
Breed $F_2$ larkeys

Notebook sheet 11, *Punnett Squares B*
Think about results

1. Are the percentages of possible genotypes for your individual larkey offspring the same as the percentages of possible genotypes for the next generation of larkeys (the class percentages)?

2. Are there traits that were absent from earlier generations that reappeared? What makes that possible?
Homework

“Larkey Punnett Squares”
Homework

Read “Mapping the Human Genome” in FOSS Science Resources on page 36.

Mapping the Human Genome

The first eukaryotic organism to have its entire set of genes mapped was baker's yeast, a single-celled fungus. The DNA sequence was released in 1996.

As the close of the 20th century the scientific community proposed a bold project to map the entire human genome. This huge international project would identify the entire sequence of human DNA. Millions of base pairs. It was less than 100 years earlier that Mendel published his laws of heredity. Now the Human Genome Project began.

Every organism has a unique genome. A genome is a catalog of the complete sequence of DNA in all of an organism's chromosomes. Remember, it is these sequences that code for the proteins that organize and build the rest of the body. If you could unravel all these chromosomes to look in the base pairs to the DNA molecule, you would be looking at your genome.

An organism has exactly the same genome as all other members of its species. For example, more than 99% of the genome of your genome is exactly the same as your mother's, your brother's, your best friend's, and everyone else's too. This common genetic code is called the human genome.

Heredity and Adaptation Course, 2.4: Punnett Squares
Step 14
Read “Mendel and Punnett Squares” on page 28.
Review vocabulary

Spend a few minutes reviewing the vocabulary for this part. Update the vocabulary index and table of contents in your notebook.
Answer the focus question

• How can we predict the distribution of traits in a future generation?
Wrap-Up: Big ideas

• Review your notebook entries.
• Generate a list of key points (including drawings or illustrations) on a piece of chart paper.
• Be prepared to explain what you have added to your list.
Go through your notebook and think about everything you have learned about heredity. Then respond to this question:

- How have genetics and heredity contributed to biodiversity on Earth?