

# INVESTIGATION 23

## Polygenic Inheritance: Fingerprint Ridge Count

Polygenic traits tend to be neglected in the classroom and laboratory despite the fact that in most organisms many significant traits are inherited in this manner. Human examples of polygenic traits often cited in textbooks include skin color in black and white matings, stature, and intelligence as measured by IQ tests. Although these traits do exhibit some of the characteristics associated with polygenic inheritance, they are not illustrated easily with concrete examples in the typical classroom laboratory.

In this investigation, you will explore how the trait of total fingerprint ridge count illustrates the polygenic model of inheritance. Student fingerprint data will be collected and a graphic profile of the class prepared. Experience suggests that most of you are interested in your own fingerprints and those of your peers, so you can expect to find this an interesting investigation to pursue.

### I. BACKGROUND

In 1890, Francis Galton suggested fingerprints as a useful tool in personal identification (Galton, 1892; Penrose, 1969). Over the years, the patterns of epidermal ridges and flexion creases on the fingers, toes, palms of the hands, and soles of the feet have become of interest to a variety of specialists. **Dermatoglyphics**, a term coined in 1926 by Harold Cummins, is the study of the epidermal ridges but in practice includes other aspects of hand, finger, and footprints (Penrose, 1969). Fingerprints and other dermatoglyphic data can be obtained from newborns to support clinical diagnoses of chromosome abnormalities such as Down syndrome (see Table 23.1). Although certain dermatoglyphic patterns may be associated with specific chromosome aberrations, be assured that no single fingerprint pattern or ridge count is in itself abnormal.

Although the formation of the epidermal ridge pattern and the total ridge count are polygenic, they are also influenced by environmental factors and thus are more accurately said to be **multifactorial** (Penrose, 1969). The embryology of the epidermal ridges offers clues to the prenatal environmental influence on their pattern of development. Fetal fingertip pads are observable around the sixth week of gestation and reach their maximal size by week 12 or 13, after which they regress, giving rise to elevated dermal ridges (Moore, 1987). The ridges, once formed, are very resistant to later prenatal or postnatal influences, making them an ideal trait for genetic studies as well as for identification of individuals.

### II. CLASSIFICATION OF FINGERPRINTS

Fingerprint patterns of dermal ridges can be classified into three major groups: arches, loops, and whorls (see Figure 23.1). The **arch** is the simplest and least frequent pattern. It may be subclassified as "plain" when the ridges rise slightly over the middle of the finger or "tented" when the ridges rise to a point.

The **loop** pattern has a triradius and a core. A **triradius** is a point at which three groups of ridges, coming from three directions, meet at angles of about 120 degrees. The core is essentially a ridge that

**TABLE 23.1.** Fingerprint Data That May Be Strongly Suggestive of a Diagnosis for Chromosome Anomalies (Reed, 1981; Penrose, 1969)

**Trisomy 21:**

Fingers primarily ulnar loops; radial loops on fingers 4 and 5

**Trisomy 18:**

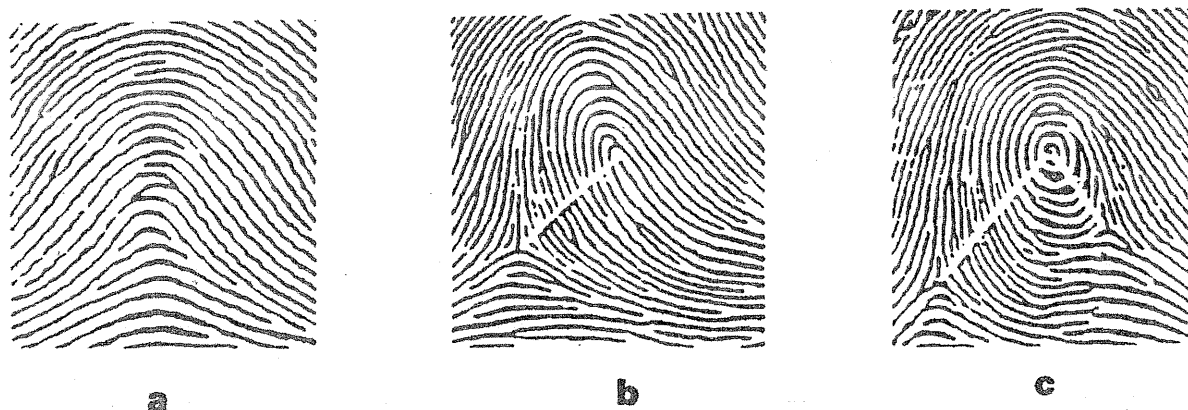
Underdeveloped epidermal ridges; high frequency of arches (average 7–8; without at least one arch, the diagnosis is suspect); thumbs lacking arches have radial loops; low TRC

**Turner syndrome 45,X:**

Increased TRC with no increase in whorls

**Relationship between Average TRC and the Number of X and Y Chromosomes:**

45, X - 165	47, XYY - 103
46, XY - 145	48, XXYY - 88
46, XX - 126	48, XYYY - 83
47, XXY - 114	49, XXXXX - 17 (only 2 individuals examined)



**FIGURE 23.1.** Three principal types of fingerprint patterns: (a) arch with no triradius and a ridge count of 0, (b) loop with one triradius and a ridge count of 12, and (c) whorl with two triradii and a ridge count of 15 (the higher of the two possible counts). (Reproduced with permission of the Biological Sciences Curriculum Study from *Basic genetics: a human approach*. Dubuque, IA: Kendall/Hunt Publishing Company, 1983.)

is surrounded by fields of ridges, which turn back on themselves at 180 degrees. Loops can be either radial or ulnar. A finger possesses a **radial loop** if its triradius is on the side of the little finger for the hand in question, and the loop opens toward the thumb. A finger has an **ulnar loop** if its triradius is on the side of the thumb for that hand and the loop opens toward the little finger. The **whorl** pattern has two triradii, with the ridges forming various patterns inside. The frequencies of these fingerprint pattern types in the general population are as follows (Holt, 1968): arch, 5.0%; radial loop, 5.4%; ulnar loop, 63.5%; and whorl, 26.1%.

### III. RIDGE COUNT

The focus of this investigation is the polygenic or quantitative trait called the **total ridge count** (TRC), the sum of the ridge counts for all 10 fingers. Holt (1968) found that the average TRC for males is 145 and that for females is 126.

For an arch, the ridge count is 0. The ridge count on a finger with a loop is determined by counting the number of ridges between the triradius and the center or core of the pattern. For a whorl, a ridge count is made from each triradius to the center of the fingerprint, but only the higher of the two possible counts is used (Figure 23.1).

Once all students in the class have prepared their own fingerprints (see Section V) and determined their own TRCs and individual fingerprint patterns, the class can examine how the TRC data support a polygenic model of inheritance.

#### IV. THE POLYGENIC INHERITANCE MODEL

The inheritance of many significant human behavioral, anatomical, and physiological characteristics is best explained by a polygenic model of transmission. The inheritance of polygenic traits cannot be analyzed by the pedigree method used for single-gene traits, nor by chromosome studies as might be done in the case of suspected chromosomal anomalies. Polygenic traits, in contrast to single-gene traits and chromosome abnormalities, exhibit a wide and continuous range of expression that is measurable. Expression of polygenic traits is often markedly affected by the environment, causing them to be referred to as **multifactorial traits**.

The assumptions underlying the polygenic model of inheritance include the following (Nagle, 1984; Russell, 1998):

- The trait is controlled by many independently assorting gene loci.
- Each gene locus is represented by an active allele that contributes an increment or by an inactive allele that contributes no increment to the phenotype.
- The alleles at each gene locus lack dominance, and each active allele has an effect on phenotype that is small and equal to that of each of the other active alleles affecting the trait.
- Phenotype is determined by the sum of all the active alleles present in the individual.
- Finally, polygenes are not qualitatively different from other genes, they regulate the production of polypeptides and they segregate and independently assort according to Mendelian principles.

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#### OBJECTIVES OF THE INVESTIGATION

*Upon completion of this investigation, the student should be able to*

1. **construct** a chart of his or her own fingerprints,
  2. **classify** fingerprints into arches, radial and ulnar loops, and whorls,
  3. **determine** the total ridge count for a full set of fingerprints,
  4. **construct** a histogram using the class data of total ridge counts,
  5. **discuss** the characteristics of the polygenic inheritance model and why polygenic traits are more difficult to study than single-gene traits, and
  6. **solve** problems concerning TRC by using a four-gene model to explain the inheritance of human fingerprint total ridge counts.
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Materials needed for each student for this investigation:

- number 2 lead pencil
- sheet of plain white paper
- roll of 3/4-inch Scotch brand Magic Tape
- hand lens, magnifying glass, or dissecting microscope

## V. PROCEDURE

The following instructions will provide you with information sufficient to prepare your fingerprints, determine your individual total ridge count, collect class data on TRC, and prepare a histogram of the class data.

1. With a number 2 lead pencil, on a piece of paper shade in a square having sides 3 cm long.
2. Rub one of your fingers in a circular motion on the graphite square, making certain you have covered all of the triradii on the fingerprint. It is important that the sides of your finger be covered with graphite. Now carefully place a piece of Scotch Tape onto your blackened finger so that the tape comes in contact with the entire print. Make certain that you include any triradii on the outer edges of the finger by rolling the finger over the tape in one continuous motion. Peel away the tape and affix it to the appropriate place on your record sheet (Table 23.2).
3. Repeat this process, preparing a print of each of your 10 fingers.
4. Examine each print carefully; if a print is incomplete, prepare a new one. Use a hand lens, magnifying glass, or dissecting microscope to classify the pattern (arch, loop, or whorl) and to determine the ridge count for each print.
5. Record your fingerprint pattern data, total ridge count, and sex in the table on the chalkboard, as directed by the class instructor. Transfer class records from the chalkboard to Table 23.3 and make the calculations indicated in the table.
6. Use the class data to answer the following questions and to construct a histogram (see example in Figure 23.2) in which frequencies are plotted against total ridge count.

**Questions.** Use the class data recorded on the chalkboard to answer the following questions.

1. What is the average TRC for the class? \_\_\_\_\_

2. What is the average TRC for the males in the class? \_\_\_\_\_

For the females? \_\_\_\_\_

3. How does your TRC compare to the average for the class? \_\_\_\_\_

The average for your sex? \_\_\_\_\_

4. Is there a difference between male and female average TRCs? \_\_\_\_\_

What might account for this difference? \_\_\_\_\_

How do the class data compare to the averages published by Holt (1968): 145 for males and 126

for females? \_\_\_\_\_

5. In your own words, summarize and describe the histogram you produced from the class data.

How do the data collected by your class compare to Figure 23.2? \_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

### TABLE 23.2 Data Sheet for Fingerprints

Right Hand					
	Thumb	Second	Third	Fourth	Fifth
Pattern					
Ridge count					
					Total = <span style="border-bottom: 1px solid black; display: inline-block; width: 100px;"></span>
Place prints in this space:					

Left Hand					
	Thumb	Second	Third	Fourth	Fifth
Pattern					
Ridge count					
					Total = <span style="border-bottom: 1px solid black; display: inline-block; width: 100px;"></span>
Place prints in this space:					

TRC =

6. If you had collected TRC data from more people, do you think the histogram for this larger sample of data would look different from the one you prepared? Explain. \_\_\_\_\_

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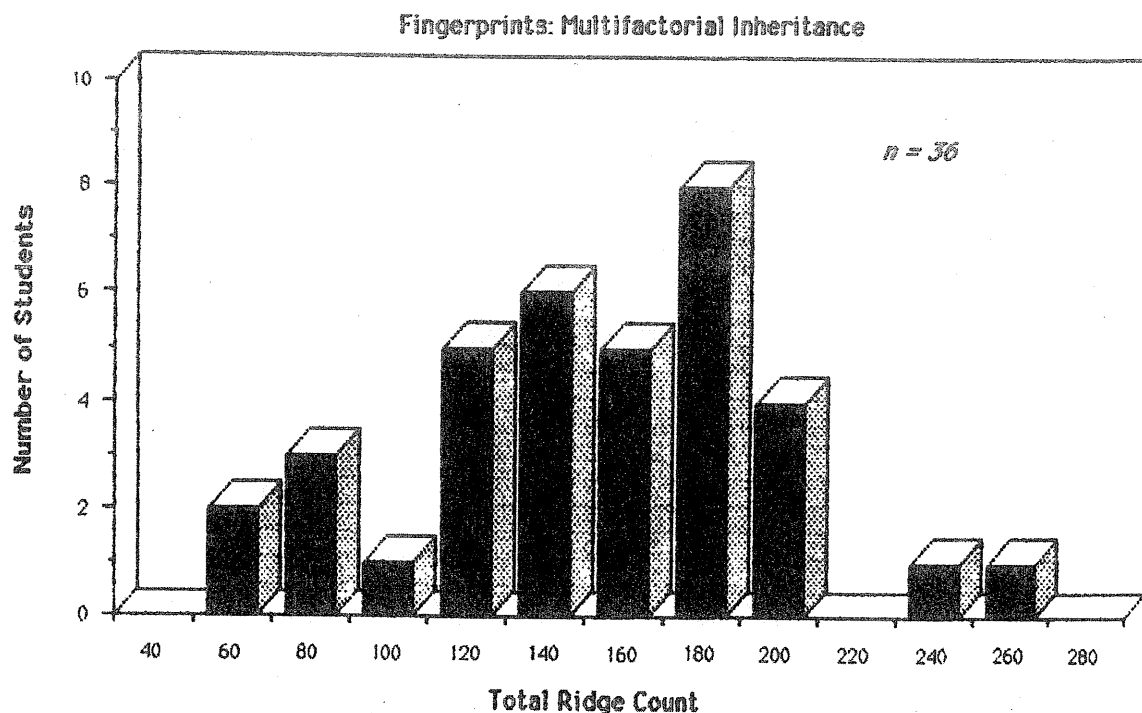
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**TABLE 23.3.** Record of Class Data for Fingerprint Patterns, Total Ridge Count, and Sex of Students \*

Student	Number of Fingers Having			TRC	Sex
	Loop	Whorl	Arch		
1	_____	_____	_____	_____	_____
2	_____	_____	_____	_____	_____
3	_____	_____	_____	_____	_____
4	_____	_____	_____	_____	_____
5	_____	_____	_____	_____	_____
6	_____	_____	_____	_____	_____
7	_____	_____	_____	_____	_____
8	_____	_____	_____	_____	_____
9	_____	_____	_____	_____	_____
10	_____	_____	_____	_____	_____
11	_____	_____	_____	_____	_____
12	_____	_____	_____	_____	_____
13	_____	_____	_____	_____	_____
14	_____	_____	_____	_____	_____
15	_____	_____	_____	_____	_____
16	_____	_____	_____	_____	_____
17	_____	_____	_____	_____	_____
18	_____	_____	_____	_____	_____
19	_____	_____	_____	_____	_____
20	_____	_____	_____	_____	_____
21	_____	_____	_____	_____	_____
22	_____	_____	_____	_____	_____
23	_____	_____	_____	_____	_____
24	_____	_____	_____	_____	_____
25	_____	_____	_____	_____	_____
Totals	_____	_____	_____	_____	_____
Percentages of totals	_____	_____	_____	_____	_____
Mean TRC				_____	
Mean TRC, females				_____	
Mean TRC, males				_____	

\* A table similar to this can be placed on the chalkboard to collect class data.



**FIGURE 23.2.** Total ridge counts for 36 participants in a workshop at Ball State University. (Graph prepared by Richard Menger.)

## VI. A SAMPLE OF DATA

The following fingerprint data were collected from 36 individuals participating in a workshop at Ball State University (Figure 23.2). The average TRC for the 19 males in the sample population was 149.2 and that for the females was 129.6. These results compare favorably with those reported by Holt (1968): 145 for males and 126 for females.

The frequencies for the different fingerprint patterns for the 36 participants in the workshop also compared favorably with Holt's (1968) data from the general population:

	Workshop participants	General population
Loop	62.2%	68.9%
Whorl	29.7%	26.1%
Arch	8.1%	5.0%
Totals	100.0%	100.0%

## VII. EXTEND YOUR UNDERSTANDING WITH ADDITIONAL TRC PROBLEMS

Total fingerprint ridge count exemplifies a polygenic inheritance pattern. Penrose (1969) and others have suggested that a minimum of seven gene loci contribute to TRC, but a four-locus model is hypothesized in the problems that follow. Thus, *AABBCCDD* represents the genotype for maximum ridge count and *aabbccdd* symbolizes the genotype for the minimum ridge count. Assume that each

active allele adds 10 ridges to the TRC of the male and 8 to the TRC of the female and that having the genotype *aabbccdd* produces a baseline TRC of 70 for males and 60 for females.

1. Predict the TRC for each of the following individuals:

Genotype	Male	Female
<i>AABBCCDD</i>	_____	_____
<i>AabbccDd</i>	_____	_____
<i>AaBBCcDD</i>	_____	_____
<i>aaBbCCDd</i>	_____	_____

2. Write the genotypes of parents who are heterozygous for all four genes.

Write the genotype of their child who has the maximum number of active alleles possible.

- a. What are the TRCs for the parents and their child (assume that the child is a male)?

Parents: \_\_\_\_\_

Child: \_\_\_\_\_

- b. Calculate the probability that these parents would produce a child with the minimum number of active alleles. Show your calculations.

3. If an *AaBbCcdd* male mates with an *AaBbCCDD* female,

- a. What is the minimum number of ridge-producing genes possible in one of their children?

- b. What would be the TRC for this child if it is a male? \_\_\_\_\_

A female? \_\_\_\_\_

- c. If this child is a male, will he have a higher or lower TRC than the parent with the lower ridge count? \_\_\_\_\_

- d. What is the maximum number of ridge-producing genes possible in a child of this couple?

- e. If this child is a female, will she have a higher or lower TRC than the parent with the higher ridge count? \_\_\_\_\_

Explain. \_\_\_\_\_

4. If an *AaBBCcdd* male mates with an *AABbCcDd* female,

- a. What is the minimum number of active alleles possible in a child this couple could produce?



- b. What would be the probability of producing a child with the minimum number of active alleles? Show your calculations. \_\_\_\_\_  
\_\_\_\_\_
- c. What would be the TRC for this child if it were male? \_\_\_\_\_  
Female? \_\_\_\_\_
5. How would you expect your TRC to compare with that of your parents? \_\_\_\_\_  
\_\_\_\_\_ Your siblings? \_\_\_\_\_  
Your grandparents? \_\_\_\_\_
6. In solving problems 1–4, you made some predictions of TRCs based on the genotypes of the individuals involved. Suppose we could measure the TRCs for some people with those genotypes and found the actual values to be different from those predicted by your calculations. How would you explain these discrepancies? \_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_
7. Write a paragraph in which you discuss the genetic and environmental components of multifactorial inheritance. \_\_\_\_\_  
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\_\_\_\_\_  
\_\_\_\_\_  
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