Pick the Risk: The Polygenic Pedigree Challenge

Abstract

Students are challenged to track and record the passage of colored pom poms (representing genes) through generations of a family using a pedigree. Students learn that common chronic diseases (such as heart disease) run in families and are caused by the combined action of multiple genes.

Learning Objectives

- An inherited trait can be determined by one or by many genes.
- All humans have the same genes, but each inherits slightly different forms or "flavors" of each gene.
- Many common diseases (such as heart disease) run in families and have a genetic component.
- Most common diseases are caused by the combined action of multiple genes and environmental factors.
- An individual's risk of developing a common disease is estimated by looking at siblings, parents and grandparents in a family medical history.

Estimated time

- Class time 30-45 minutes
- Prep time 30 minutes

Materials

Per group of 2

- 1 copy of student pages
- colored pencils or crayons
- 2-3 disposable cups
- Colored pom poms (5 different colors: at least 10 red, 2 yellow, 1 each of orange, green, blue)

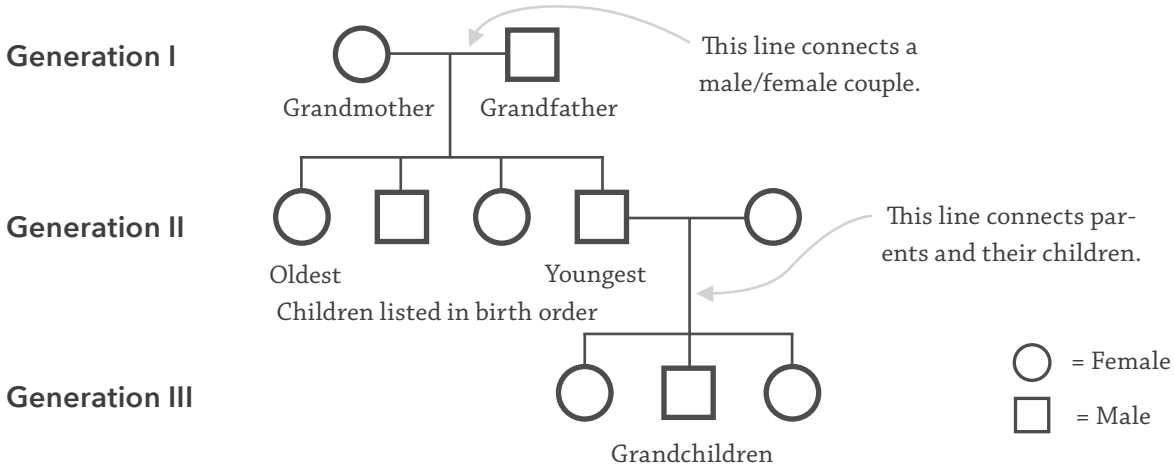
To engage students in this topic:

- Compare the prevalence of rare genetic disorders caused by a single gene such as cystic fibrosis (1 in 10,000) with the prevalence of more common diseases such as heart disease (1 in 3).
- Ask the students: Do common diseases like heart disease, diabetes, or colon cancer have a genetic component?
- Explain that most common diseases do have a genetic component and tend to run in families. However, common diseases differ from rare genetic disorders in that they are usually not caused by defects in a single gene. Rather, they result from the combined effects of multiple genes and environmental factors. Thus, they are called multifactorial diseases.
- Explain that because more than one gene is involved in most common diseases, the inheritance of a common disease is not predictable.

- Information found in a family health history and recorded on a pedigree is used to estimate an individual's genetic risk (low, medium, or high) of developing a common disease.

Instructions

- Explain that the following activity will explore how common "polygenic" diseases (in this case, heart disease) are inherited.
- Invite students to find a partner with whom they will work to complete the activity; pass out the student pages and other materials.
- Review the symbols and structure used for a pedigree:



- Invite students to begin by following the instructions found on the student pages; each pair of students should complete the pedigree analysis and answer the questions that follow.

Discuss

- Point out that this activity differs from reality in the following ways:
  - The number of genes contributing to a polygenic disease is usually not known.
  - The number of genes carried by parents or offspring that can increase heart disease risk is not known.
  - Environmental factors can also vary an individual's risk of developing multifactorial diseases.
- Emphasize that these are a few of the reasons why heart disease and other common diseases are so complex, and why the inheritance patterns for such diseases are difficult to predict.
- Therefore, individuals are placed in general categories (high, medium, or low risk groups) based on features from their family health history that correlate with a certain probability of developing a disease.
  - For example, it is said that an individual who has a parent (or possibly a grandparent) with heart disease may be "at risk" and should take steps to protect themselves.
- Describe the important features to identify in a family health history (see chart at http://learn.genetics.utah.edu/units/health), including what is meant by a "close" relative.

    - Siblings, parents, and possibly grandparents, are informative when assessing an individual's risk of developing a common disease and need be included in a family health history. It is unlikely that all of the same risk factors (genes) will be present in less closely related family members.
- Discuss why each feature in the chart indicates an individual may be at increased risk for developing heart disease.
    - Each feature indicates that the family has accumulated more risk factors (genetic or environmental). Therefore, an individual in this family is more likely to develop disease.
- Discuss behaviors and choices that can reduce an individual's risk of developing heart disease.
- Conclude the class discussion by reminding students that genetic susceptibility does not mean an individual will inevitably inherit a disease. Positive lifestyle changes and healthy living can reduce genetic risk dramatically. That is why it is so important to know your family health history. If you know you are "at risk" you can take steps to protect yourself.

Common Misconception

Students may think that all heritable traits (and genetic disorders) are caused by a single gene and exhibit dominant or recessive patterns of inheritance. But more commonly, traits result from the combined action of many genes and environmental factors. Such multifactorial traits can exhibit varied and complex patterns of inheritance that are not easy to predict.

Extension

Illustrate that multifactorial traits vary within a population along a continuum:

- Combine class results from Grandma and Grandpa's children (not grandchildren) to generate a population of people who inherited a low, medium, or high risk of developing heart disease.
- Calculate the total number of individuals in the population (4 X # of student pairs).
- Calculate the number of individuals that inherited a low, medium or high risk of developing heart disease.
- Graph the results with the low, medium and high risk categories along the x axis, and the number of individuals along the y axis.
- Draw a curved line over the histogram to show that this trait follows a bell-shaped distribution in the population, with most people at medium (or average) risk of developing heart disease.
- Emphasize that in reality heart disease risk varies within a population along a continuum, and an individual's location along this risk continuum is determined by his or her genes and environment.

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