Teacher Tune-up

Quick Content Refresher for Busy Professionals

What is a Punnett Square and how does it relate to dominant and recessive traits?

One of Mendel's most important findings was that each parent passes on just one of the two genes that they carry for a trait, and that by using mathematical patterns, we can predict the ratios of traits found in offspring.

Part of deciphering Mendel's findings requires thinking about combinations of genes. As we think about all the different ways that genes might combine, one useful representation is the Punnett Square. Created long after Mendel's death, the Punnett Square is a simple visual guide to help us think about combinations. By listing the possible genes that one parent can give along the top of a table, and the possible genes that the other parent provides along the side, the user can quickly check the intersections of rows and columns to determine possible outcomes.

For example, the following table illustrates possible genetic combinations from mating two hybrid plants. The letters "Aa" represent a pair of genes for a trait—let's say pea color—with capital "A" representing the **dominant** version of the gene for pea color (yellow), and lowercase "a" represents the **recessive** version of the gene (green). These variant forms of a gene are called its "alleles" (short for allelomorph, meaning "other form"). The table shows that, in general, one out of four offspring will have the genetic makeup AA (yellow peas), two out of four will have Aa (yellow peas), and one out of four will have aa (green peas).

Parent has genes Aa
Two possible genes it can give:

	A	a
A	AA	Aa
a	Aa	aa

Parent has genes Aa
Two possible genes it can give:

(Possible genetic combinations for offspring)

Punnett Squares can also be used for tracking the results of more challenging crosses, such as looking at two traits at the same time, as Mendel did when he created his Law of Independent Assortment. This law describes his finding that traits are passed along independently of one another, allowing all sorts of unique combinations of traits to arise from just a few genes. In the table below, let's say that the letters A and a once again stand for alleles of the pea-color gene, and that B and b stand for, respectively, the dominant and recessive alleles for stem length (B is

long, b is short). Here we are tabulating the possible offspring of parent plants with the **genotype** (combination of genes) AaBb:

Parent has genes Aa and Bb.

Four possible ways to pass on genes:

	A & B	A & b	a & B	a & b
A & B	AABB	AABb	AaBB	AaBb
A & b	AABb	AAbb	AaBb	Aabb
a & B	AaBB	AaBb	aaBB	aaBb
a & b	AaBb	Aabb	aaBb	aabb

Parent has genes Aa and Bb. Four possible ways to pass on genes: (left row labels)

As in the simpler case of tracking just one trait, dominant traits will appear in the organism wherever at least one dominant allele for a trait is present; recessive traits will appear only if two recessive alleles for the trait are present. Given those genetic facts, what are we to make of the blizzard of letters in the table above? A careful examination of the 16 combinations reveals some redundancies; we can see that mating parents who both have genotype AaBb yields nine unique genotypes, and four possible **phenotypes** (manifestations of visible traits):

Results from the above Punnett Square crossing AaBb x AaBb

Genotype (What alleles a plant has)	Relative number of occurrences	Phenotype (What a plant looks like)
AABB	1	yellow-long —
AABb	2	yellow-long —
AaBB	2	yellow-long —
AaBb	4	yellow-long —
AAbb	1	yellow-short -
Aabb	2	yellow-short -
aaBB	1	green-long —
aaBb	2	green-long —
aabb	1	green-short -

So on average, for every 16 offspring of this cross, there are 9 yellow-long plants; 3 yellow-short plants; 3 green-long plants; and 1 green-short plant. And sure enough, Mendel found that this 9:3:3:1 ratio (of dominant-dominant, dominant-recessive, recessive-dominant, and recessive-recessive phenotypes) showed up in all comparable pea plant crosses (i.e., ones where both parents shared the same two dominant traits, but carried a recessive allele for both of those traits: AaBb).

Punnett Squares have proven handy for scientists and genetic counselors for over a century, though they are not the only way to represent combinations.

Look out! Student Misconceptions about Punnett Squares

Symbolic modeling is an important tool in science, but can lead to confusion for students when they fail to connect the symbols to the microscopic and macroscopic concepts that the symbols are supposed to represent. Many students can easily go through the rote mechanism of completing a Punnett Square correctly, memorizing the procedure, but then may have difficulty explaining what that "Aa" meant, or why they "bring one down from the top and one over from the side." To incorporate Punnett Squares into the curriculum meaningfully, it's critical for students to be able to explain *why* the procedure works, connecting to the language of genes and traits. Some teachers have students develop their own visual methods of finding combinations before introducing the Punnett Square, and others encourage students to explain their thinking through writing or oral explanations.

One additional area that may confuse students is the use of color (as in the example used above) to distinguish between genes that come from one parent versus the other. While this approach can be a handy tool in explaining the procedure of completing a Punnett Square, it can easily lead to the misconception that an "A" allele from the mother is inherently different from the "A" allele that comes from the father. Students may wonder which allele should be written first or second, imagining that the order matters. The order doesn't matter conceptually, although conventionally scientists list the dominant allele before the recessive allele. Helping students see this pattern as a convenient convention of academic language rather than a representation with profound genetic meaning may prevent further misconceptions.