

# Mendel's Laws In Corn

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## Data

**Table 1:** Corn A (Monohybrid Cross)

Purple Kernels ( $P_A$ )	White Kernels ( $W_A$ )
320	74
374	83
353	120
424	130
328	112
375	114
373	145
377	120
199	221
415	159
303	84

It is obvious that this corn is a monohybrid cross, as there are only two different versions of one trait (colour). The dominant trait is purple, due to it occurring more often than white.

The the average number of each can be caclulated using the following:

$$\mu_{P_A} = \frac{\sum P_A}{|P_A|} = \frac{3841}{11} \approx 349.19$$

$$\mu_{W_A} = \frac{\sum W_A}{|W_A|} = \frac{1362}{11} \approx 123.81$$

Using these averages, approximate a phenotype ratio.

$$\begin{aligned} \mu_{P_A} : \mu_{W_A} \\ &\approx 349.19 : 123.81 \\ &\approx 350 : 120 \\ &\approx 36 : 12 \\ &\approx 3 : 1 \end{aligned}$$

**Table 2:** Corn B (Monohybrid Cross)

Purple Kernels ( $P_B$ )	White Kernels ( $W_B$ )
290	261
212	239
265	245
248	270
227	151
247	269
225	249
279	272

Similarly to part A, this corn is a monohybrid cross, as there are only two different versions of one trait (colour). The dominant trait is still purple, as the dominance does not change from one corn to another (as they are still the same species).

Using the same method, the average of each genotype for Corn B can be calculated, along with the phenotype ratios:

$$\mu_{P_B} = \frac{\sum P_B}{|P_B|} = \frac{1993}{8} \approx 249.125$$

$$\mu_{W_B} = \frac{\sum W_B}{|W_B|} = \frac{1956}{8} = 244.5$$

$$\begin{aligned} \mu_{P_B} : \mu_{W_B} \\ \approx 249.125 : 244.5 \\ \approx 245 : 245 \\ \approx 1 : 1 \end{aligned}$$

**Table 3:** Corn C (Dihybrid Cross)

Purple Smooth ( $P_S$ )	Purple Wrinkled ( $P_W$ )	White Smooth ( $W_S$ )	White Wrinkled ( $W_W$ )
265	78	88	46
243	71	80	25
250	75	154	17
252	75	100	28
182	98	93	42
419	110	95	17
238	112	77	32
274	59	175	42
346	95	115	41
295	93	112	94
223	89	34	23

This is a dihybrid cross due to two traits varying, the colour and texture. As this is still the same corn species as the other two, the colour purple is still dominant over the white. As for the texture, it can be seen that smooth kernels are more common than wrinkled for the same colour ( $P_{S_i} > P_{W_i}$  and  $W_{S_i} > W_{W_i}$  for most  $\{i \in \mathbb{N} \mid i \leq |P_S|\}$ ).

By extending the method for 4 traits, the averages and phenotype ratios for

Corn C can be determined as well.

$$\begin{aligned}\mu_{P_S} &= \frac{\sum P_S}{|P_S|} = \frac{2987}{11} \approx 271.55 \\ \mu_{P_W} &= \frac{\sum P_W}{|P_W|} = \frac{955}{11} \approx 86.82 \\ \mu_{W_S} &= \frac{\sum W_S}{|W_S|} = \frac{1123}{11} \approx 102.09 \\ \mu_{W_W} &= \frac{\sum W_W}{|W_W|} = \frac{320}{11} \approx 29.09\end{aligned}$$

$$\begin{aligned}\mu_{P_S} : \mu_{P_W} : \mu_{W_S} : \mu_{W_W} \\ \approx 271.55 : 86.82 : 102.09 : 29.09 \\ \approx 270 : 90 : 90 : 30 \\ \approx 9 : 3 : 3 : 1\end{aligned}$$

## Analysis

### Monohybrid Crosses

In figures 1-3, the alleles for the colour will be represented with P (purple, dominant), and p (white, recessive).

**Figure 1:** Homozygous Dominant ( $PP$ )  $\times$  Homozygous Recessive ( $pp$ )

	$P$	$P$
$p$	$Pp$	$Pp$
$p$	$Pp$	$Pp$

From the Punnett square in Fig. 1, it can be seen that a cross between a homozygous dominant and a homozygous recessive organism, the expected genotype ratios of the F1 generation are as follows:

**Table 4:** Genotype Ratios and Percentages of Fig. 1

Genotype	Percentage	Ratio
$Pp$	100%	1:1

In terms of phenotypes, this means that the all of the F1 generation will be purple in colour.

**Figure 2:** Homozygous Recessive ( $pp$ )  $\times$  Heterozygous ( $Pp$ )

	$p$	$p$
$P$	$Pp$	$Pp$
$p$	$pp$	$pp$

As shown in Fig. 2, a cross between a homozygous recessive and a heterozygous organism will produce the following genotype ratios for the F1 generation:

**Table 5:** Genotype Ratios and Percentages of Fig. 2

Genotype	Percentage	Ratio
$Pp$	50%	1:2
$pp$	50%	1:2

Overall the genotype ratios in the same order are 1:1. Using these genotypes, phenotype ratios can be found:

**Table 6:** Phenotype Ratios and Percentages of Fig. 2

Phenotype	Percentage	Ratio
Purple	50%	1:2
White	50%	1:2

The overall phenotype ratio in the same order is 1:1.

**Figure 3:** Heterozygous ( $Pp$ )  $\times$  Heterozygous ( $Pp$ )

	$P$	$p$
$P$	$PP$	$Pp$
$p$	$Pp$	$pp$

From Fig. 3, it can be concluded that for a cross between two heterozygous organisms, the expected genotype ratios of the F1 generation will be:

**Table 7:** Genotype Ratios and Percentages of Fig. 3

Genotype	Percentage	Ratio
$PP$	25%	1:4
$Pp$	50%	1:2
$pp$	25%	1:4

Overall the genotype ratios in the same order are 1:2:1. Just as with Fig. 2, the phenotype ratios and percentages can be found.

**Table 8:** Phenotype Ratios and Percentages of Fig. 3

Phenotype	Percentage	Ratio
Purple	75%	3:4
White	25%	1:4

The overall phenotype ratio in the same order is 3:1.

## Dihybrid Crosses

In figures 4 and 5, the alleles for the colour will be represented with  $P$  (purple, dominant), and  $p$  (white, recessive), while the alleles for texture will be  $W$  (smooth, dominant), and  $w$  (wrinkled, recessive).

**Figure 4:** Heterozygous ( $PpWw$ )  $\times$  Heterozygous ( $PpWw$ ) on both traits

	<i>PW</i>	<i>Pw</i>	<i>pW</i>	<i>pw</i>
<i>PW</i>	<i>PPWW</i>	<i>PPWw</i>	<i>PpWW</i>	<i>PpWw</i>
<i>Pw</i>	<i>PPWw</i>	<i>PPww</i>	<i>PpWw</i>	<i>Ppww</i>
<i>pW</i>	<i>PpWW</i>	<i>PpWw</i>	<i>ppWW</i>	<i>ppWw</i>
<i>pw</i>	<i>PpWw</i>	<i>Ppww</i>	<i>ppWw</i>	<i>ppww</i>

**Table 9:** Genotype Ratios and Percentages of Fig. 4

Genotype	Percentage	Ratio
<i>PPWW</i>	6.25%	1:16
<i>PPWw</i>	12.5%	1:8
<i>PPww</i>	6.25%	1:16
<i>PpWW</i>	12.5%	1:8
<i>PpWw</i>	25.0%	1:4
<i>Ppww</i>	12.5%	1:8
<i>ppWW</i>	6.25%	1:16
<i>ppWw</i>	12.5%	1:8
<i>ppww</i>	6.25%	1:16

Expressed as an overall ratio in the same order, this is 9:3:3:1.

By looking at each genotype in Table 7, determining its phenotype, the phenotype ratios can then be determined.

**Table 10:** Phenotype Ratios and Percentages of Fig. 4

Phenotype	Percentage	Ratio
Purple and Smooth	56.25%	9:16
Purple and Wrinkled	18.75%	3:16
White and Smooth	18.75%	3:16
White and Wrinkled	6.25%	1:16

**Figure 5:** Heterozygous (*PpWw*) × Homozygous Recessive (*ppww*) on both traits

	<i>PW</i>	<i>Pw</i>	<i>pW</i>	<i>pw</i>
<i>pw</i>	<i>PpWw</i>	<i>Ppww</i>	<i>ppWw</i>	<i>ppww</i>

**Table 11:** Genotype Ratios and Percentages of Fig. 5

Genotype	Percentage	Ratio
<i>PpWw</i>	25.0%	1:4
<i>Ppww</i>	25.0%	1:4
<i>ppWw</i>	25.0%	1:4
<i>ppww</i>	25.0%	1:4

Expressed as an overall ratio in the same order, this is 1:1:1:1. By looking at each genotype in Table 9, determining its phenotype, the ratio of each phenotype can then be determined.

**Table 12:** Phenotype Ratios and Percentages of Fig. 5

Phenotype	Percentage	Ratio
Purple and Smooth	25.0%	1:4
Purple and Wrinkled	25.0%	1:4
White and Smooth	25.0%	1:4
White and Wrinkled	25.0%	1:4

## Conclusion

### 1. Comparison with Data

#### Corn A

Corn A is a monohybrid cross, as it only had two varying characteristics of one trait. Its approximate phenotype ratio for purple to white was 3:1. Comparing this ratio to that of the monohybrid crosses, the only cross with a ratio of 3:1 was the Heterozygous  $\times$  Heterozygous one (Table 8). Due to this being the only match, it can be concluded that Corn A was a cross between two heterozygous corn, which both were purple kernels, but was a carrier of white kernels.

#### Corn B

The only monohybrid cross with a phenotype ratio of 1:1 was the cross between homozygous recessive and a heterozygous corn (Punnett Square in Figure 2, Phenotypes in Table 6). As this is the only way to get a phenotype distribution of 50% and 50%, Corn B was a cross between a homozygous recessive and heterozygous corn, one purple, and the other white.

#### Corn C

Corn C is a dihybrid cross, as it had two different versions of two traits. Its phenotype ratio for purple smooth, to purple wrinkled, to white smooth, to white wrinkled, was approximately 9:3:3:1. Out of the dihybrid crosses done, the only one with this specific ratio was the one between two corn which were heterozygous on both traits (Punnett Square in Figure 4, Phenotypes in Table 10). Therefore, Corn C was produced as a result of two corn which were heterozygous on both traits. They were both smooth purple kernels.

## 2. Mendel's 3 Laws

### 2.1. Law of Segregation

Mendel's Law of Segregation states that each organism has two alleles for one trait, which separate during the formation of gametes, only passing one onto their offspring.

This law was used in the creation of each Punnett square, which was confirmed to match correctly. An example of this working is on Corn A, which can be

modeled by the Punnett square in Figure 3. Each gamete had a heterozygous (Pp) set of alleles, which were segregated to give either a dominant allele (P) or a recessive allele (p).

## 2.2. Law of Independent Assortment

The Law of Independent Assortment describes the way that alleles of different genes are sorted into gametes. It states that each allele of different genes are sorted independently of the other, meaning that when the allele one gamete receives does not affect the allele another gene.

This law was applied when doing the dihybrid crosses for the corn. In Figure 4, each parent genotype was independently assorted into 4 possible gametes each. As the theoretical outcome was extremely similar to the experimental outcome for Corn C, it can be concluded that the Law of independent Assortment is applied to corn as well.

## 2.3. Law of Dominance

Mendel's Law of Dominance describes the relationship between two alleles. It states that if a dominant genotype is present, that will be the one displayed.

While generating phenotype ratios from genotypes (in turn, generated from a Punnett square), this law was used. Since the phenotypes ratios of each of the corn could be matched with one generated, it can be concluded that the Law of Dominance apply on corn as well.

## Making Connections

Mendel's laws are applicable in many cases in the real world. Some examples include breeding animals and eugenics.

### Breeding Animals

Many organisms are bred to have desired traits. This selective breeding takes advantage of Mendelian laws to find a mate which will produce the desired trait.

For example, rats have a pattern of pigmentation called Agouti, which is carried on the gene for coat colour. The Agouti allele is the dominant one, while white is recessive. If there was a rat which was known to be heterozygous for Agouti, and someone wanted to make sure its offspring was Agouti as well, Mendelian laws could be used to find a mate which would guarantee Agouti offspring.



In the following Punnett square, the heterozygous rat is crossed with a mate, whose alleles are represented with  $X$  and  $Y$ .

**Figure 6:** Heterozygous Agouti ( $Aa$ ) x Mate ( $XY$ )

	$X$	$Y$
$A$	$AX$	$AY$
$a$	$Xa$	$Ya$

Since each offspring must be Agouti,  $X$  and  $Y$  must both be  $A$ , as shown in the second row (if  $X$  and  $Y$  were not  $A$ ,  $Ya$  would be white, and not Agouti).

In this example, it is clear that the mate must be homozygous dominant ( $AA$ ) to guarantee Agouti offspring. Using this information, one could then obtain a homozygous Agouti rat and mate them to guarantee their desired offspring.

This can be applied to other animals and organisms as well, to produce offspring with the desired characteristics.

## Eugenics

DISCLAIMER: The following does not reflect the real opinion of the writer.

Mendel's laws can be used to predict certain disorders, such as Huntington's disease, sickle-cell anemia, and hereditary breast-ovarian cancer syndrome (HBOC). Although these may not be exactly the same two allele genes that Mendel describes, they are considered Mendelian due to them following the law of dominance.

If these disorders could be eradicated, future generations would not have to deal with these quality-of-life lowering conditions.

To eradicate these disorders, Mendelian laws can be used to predict if a couple will produce a child which is a carrier of the trait which causes the disorder. If the chance is non-zero, they could be forbidden to mate. When this generation dies without the negative trait being passed, the trait will be largely eradicated. By doing this, the entire human population will have an improved genetic quality, with less suffering.

For example, two people who are unaffected, but are carriers for sickle-cell disease (a recessive trait), wish to have a child. As shown in Table 7 (generated from Figure 3), there is a non-zero chance of producing a child with two unaffected carriers to produce a non-carrier for sickle-cell disease. Therefore, they should not be able to reproduce and spread the trait.

The only people able to reproduce would hence only be those who are unaffected and aren't carriers (homozygous dominant).