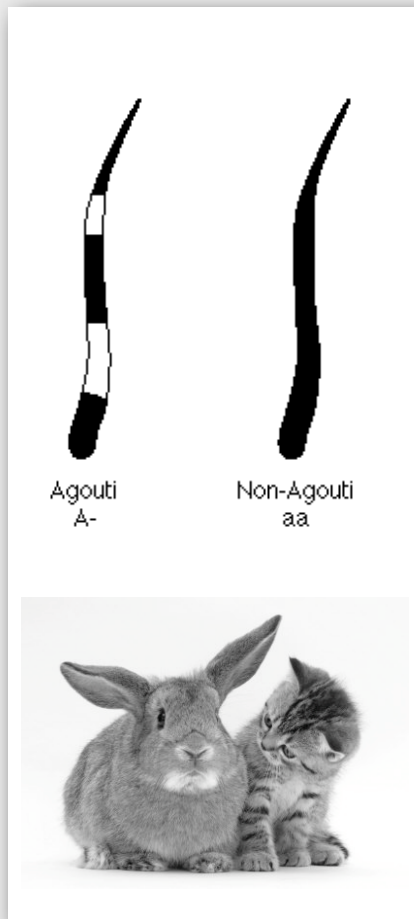


Genetic Variation - Agouti gene working example

The **agouti gene** is responsible for determining whether a mammal coat color is banded agouti coat color or a solid non-agouti coat color. The dominant, wild-type A causes the agouti shift phenomenon which causes hairs to be black pigmented at the tips and red pigmented at the roots (revealing the underlying tabby pattern), while the recessive non-agouti or "hypermelanistic" allele prevents this shift in the pigmentation pathway. In its homozygous form (aa) this results in black pigment production throughout the growth cycle of the hair.



We have 60 agouti and 51 non-agouti individuals in a local rabbit population. How many % of the individuals are homozygote for the agouti gene?

Genotype of agouti rabbits : AA or Aa

Genotype of non-agouti rabbits : aa

$$f(aa) = q^2 = \frac{51}{111} = 0.46 \Rightarrow 46\% \text{ are non-agouti rabbits}$$

$$q = \sqrt{0.46} = 0.68 \Rightarrow f(a) = 0.68$$

$$p + q = 1 \Rightarrow p = 1 - 0.68 = 0.32 \Rightarrow f(A) = 0.32$$

$$f(AA) = f(A)^2 = p^2 = 0.10$$

$\Rightarrow 10\%$ of the animals are homozygous agouti rabbits.

Genetic Variation - Exercises : Three Alleles

Example: 1 locus 3 alleles							
Genotypes	AA	AB	AC	BB	BC	CC	Sum
Counts	17	86	5	61	9	0	178
Frequencies	0.096	0.483	0.028	0.343	0.051	0.000	1

Allele frequencies

$$f(A) = 0.096 + 0.5(0.483 + 0.028) = \mathbf{0.351} \Rightarrow 35.1\%$$

$$f(B) = 0.343 + 0.5(0.051 + 0.483) = \mathbf{0.609} \Rightarrow 60.9\%$$

$$f(C) = 0.000 + 0.5(0.051 + 0.028) = \mathbf{0.039} \Rightarrow 3.9\%$$

Assuming H-W to test alternative models of inheritance

4 blood group phenotypes: A, B, AB, and O

Hypothesis: ① two independent loci, both dominant
 ② single loci with A and B co-dominant over O

Blood Type	Genotype		Expected gt frequency		Observed
	①	②	①	②	
O	aa bb	OO	$f_a^2 f_b^2$	f_O^2	148
A	A_ bb	AA, AO	$(1-f_a^2) f_b^2$	$f_A^2 + 2f_A f_O$	212
B	aa B_	BB, BO	$f_a^2 (1-f_b^2)$	$f_B^2 + 2f_B f_O$	103
AB	A_ B_	AB	$(1-f_a^2)(1-f_b^2)$	$2f_A f_B$	39
					502

Assuming H-W to test alternative models of inheritance

	Observed	exp-①	$\frac{(\text{obs}-\text{exp})^2}{\text{exp}}$	exp-②	$\frac{(\text{obs}-\text{exp})^2}{\text{exp}}$
O	148	180	5.7	154	0.24
A	212	180	5.7	206	0.17
B	103	71	14.4	97	0.39
AB	39	71	14.4	45	0.80

Hypothesis: ~~① two independent loci, both dominant~~
② single loci with A and B co-dominant over O