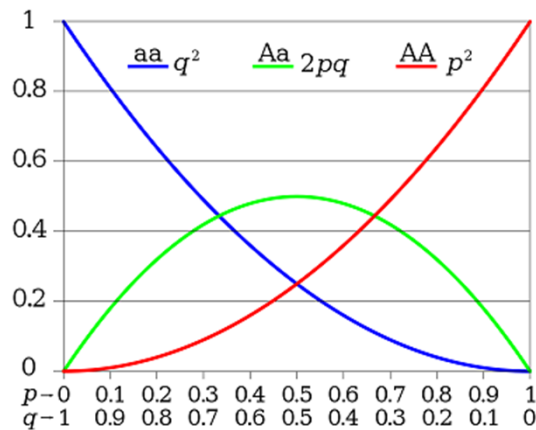




$$(p + q)^2 = \underset{AA}{p^2} + \underset{Aa}{2pq} + \underset{aa}{q^2} = 1.0$$

# The Hardy Weinberg Equilibrium

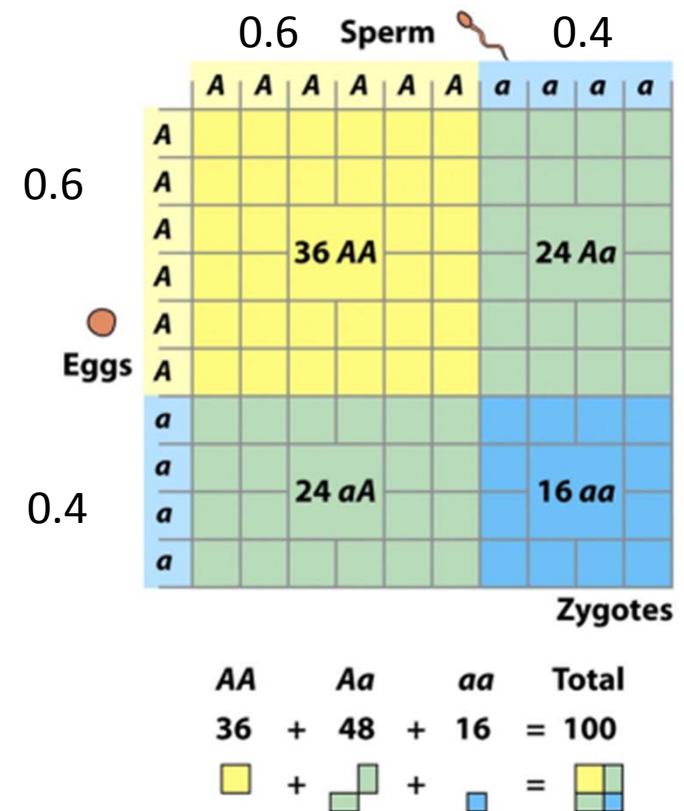
SUPPORT THE HARDY-WEINBERG PRINCIPLE



PRACTICE RANDOM MATING IN INFINITE POPULATIONS

# Self-perpetuates!

- Allele “A” frequency was 0.6 in gametes
- Gametes created 0.36/0.48/0.16 genotype frequencies
- These genotypes produce 0.6 “A” gametes





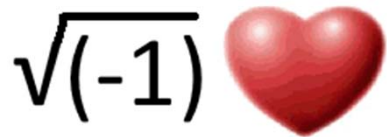
# Hardy / Weinberg / Castle

- Up to 1902, people thought **dominant** alleles would intrinsically increase in a population
- Some assumed **rare** alleles would always be lost eventually
- 1908: Hardy & Weinberg independently showed both assumptions **NOT TRUE**
  - Allele & genotype frequencies stay stable *when some assumptions are made*

Castle  
1903

# Let's formalize the math...

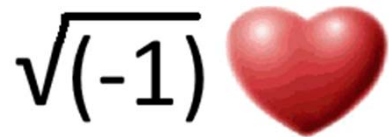
- Frequency of A = p
- Frequency of a = q       $p + q = 1$
- Frequency of AA =
- Frequency of Aa =
- Frequency of aa =



MATH

# Let's formalize the math...

- Frequency of A = p
- Frequency of a = q       $p + q = 1$
- Frequency of AA =  $p^2$
- Frequency of Aa =  $2pq$
- Frequency of aa =  $q^2$

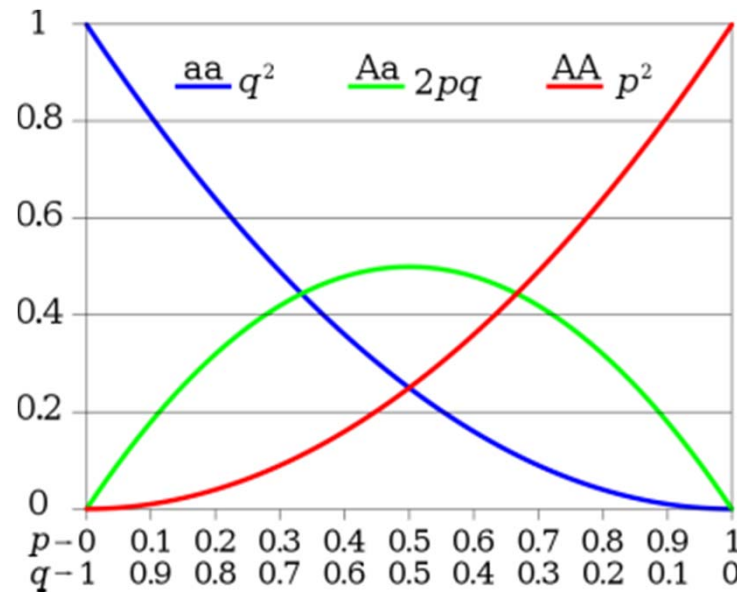


MATH

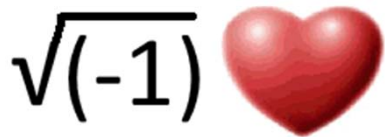
$$p^2 + 2pq + q^2 = 1$$

# Let's formalize the math...

- Frequency of A = p
- Frequency of a = q
- Frequency of AA =  $p^2$
- Frequency of Aa =  $2pq$
- Frequency of aa =  $q^2$



$$p^2 + 2pq + q^2 = 1$$



MATH

Allow you to infer genotype frequencies from allele frequencies,  
BUT certain conditions must be met...

**Important point 1:**

**You can ALWAYS know genotype frequencies  
from genotype counts**



## Important point 1:

**You can ALWAYS know genotype frequencies from genotype counts**

- AA: 8
  - Aa: 64
  - aa: 128
- 
- 1) Add 'em up for total
  - 2) Divide by total





## Important point 1:

**You can ALWAYS know genotype frequencies from genotype counts**

- AA: 8
- Aa: 64
- aa: 128
- **TOTAL** =  $8 + 64 + 128 = 200$
- 1) Add 'em up for total
- 2) Divide by total



## Important point 1:

**You can ALWAYS know genotype frequencies from genotype counts**

- AA: 8  $\rightarrow 8/200 = 0.04$
- Aa: 64  $\rightarrow 64/200 = 0.32$
- aa: 128  $\rightarrow 128/200 = 0.64$
- **TOTAL** = 8 + 64 + 128 = 200
- 1) Add 'em up for total
- 2) Divide by total



## Important point 1:

**You can ALWAYS know genotype frequencies  
from genotype counts**

- AA: 8  $\rightarrow 8/200 = 0.04$
- Aa: 64  $\rightarrow 64/200 = 0.32$
- aa: 128  $\rightarrow 128/200 = 0.64$
- **TOTAL** =  $8 + 64 + 128 = 200$
- 1) Add 'em up for total
- 2) Divide by total

Quick check—  
Confirm they add  
Up to 1.00

**Important point 2:**

**You can ALWAYS know allele frequencies  
from genotype frequencies**



## Important point 2:

**You can ALWAYS know allele frequencies  
from genotype frequencies**

- AA: 0.04
- Aa: 0.32
- aa: 0.64
  
- All of homozygote +  
½ of heterozygote



## Important point 2:

**You can ALWAYS know allele frequencies  
from genotype frequencies**

- AA: 0.04      $p(A) = 0.04 + \frac{1}{2}(0.32) = 0.20$
- Aa: 0.32      $q(a) = 0.64 + \frac{1}{2}(0.32) = 0.80$
- aa: 0.64
  
- All of homozygote +  
½ of heterozygote



## Important point 2:

**You can ALWAYS know allele frequencies  
from genotype frequencies**

- AA: 0.04      $p(A) = 0.04 + \frac{1}{2}(0.32) = 0.20$
- Aa: 0.32      $q(a) = 0.64 + \frac{1}{2}(0.32) = 0.80$
- aa: 0.64
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½ of heterozygote

Quick check—  
Confirm they add  
Up to 1.00



### Important point 3:

**You CANNOT always know genotype frequencies from allele frequencies**





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- Let's say  $p(A) = 0.5$  and  $q(a) = 0.5$



### Important point 3:

**You CANNOT always know genotype frequencies from allele frequencies**

- Let's say  $p(A) = 0.5$  and  $q(a) = 0.5$
- Could have:
  - AA: 0.25
  - Aa: 0.50
  - aa: 0.25 (HW expected)



### Important point 3:

**You CANNOT always know genotype frequencies from allele frequencies**

- Let's say  $p(A) = 0.5$  and  $q(a) = 0.5$
- Could have:
  - AA: 0.25                      AA: 0.45
  - Aa: 0.50                      Aa: 0.10
  - aa: 0.25 (HW expected)      aa: 0.45



### Important point 3:

**You CANNOT always know genotype frequencies from allele frequencies**

- Let's say  $p(A) = 0.5$  and  $q(a) = 0.5$

- Could have:

– AA: 0.25	AA: 0.45	AA: 0.5
– Aa: 0.50	Aa: 0.10	Aa: 0
– aa: 0.25 (HW expected)	aa: 0.45	aa: 0.5





## Bottom line:

- CAN always calculate allele frequencies from genotype frequencies
  - Alleles are *ingredients* of genotypes
- CANNOT always calculate genotype frequencies from allele frequencies
  - Genotypes are *specific combinations* of alleles
  - Many combinations are possible





# What about Hardy-Weinberg?

- HW allows prediction of genotype frequencies from allele frequencies **under certain conditions**



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  - Random mating (multiplying probabilities rule)



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  - Infinite population size – no “genetic drift”



# What about Hardy-Weinberg?

- HW allows prediction of genotype frequencies from allele frequencies **under certain conditions**
  - Random mating (multiplying probabilities rule)
  - No selection / migration / mutation at that locus
  - Infinite population size – no “genetic drift”

Hardy-Weinberg predicts a  
“**boring**” population that  
could never exist...?





# Hardy-Weinberg provides a **NULL HYPOTHESIS**

- By seeing **HOW** natural populations deviate from the HW expected genotype frequencies, we infer what interesting evolutionary forces are operating!





## Example 1: Is this at HW?

- AA 245
  - Aa 210
  - aa 45
- 
- 1) Figure out “true” genotype frequencies
  - 2) Figure out “true” allele frequencies
  - 3) Figure out HW “expected” genotype freq
  - 4) Does “true” freq = “expected” freq?



## Example 1: Is this at HW?

- AA 245       $245/500 = \frac{\text{TRUE}}{0.49}$
- Aa 210       $210/500 = 0.42$
- aa 45         $45/500 = 0.09$

TOTAL=500

- 1) Figure out “true” genotype frequencies
- 2) Figure out “true” allele frequencies
- 3) Figure out HW “expected” genotype freq
- 4) Does “true” freq = “expected” freq?



## Example 1: Is this at HW?

- AA 245       $245/500 = \overset{\text{TRUE}}{0.49}$
- Aa 210       $210/500 = 0.42$
- aa 45         $45/500 = 0.09$

TOTAL=500

$$p(A) = 0.49 + \frac{1}{2} \overset{\text{TRUE}}{0.42} = 0.7$$
$$q(a) = 0.09 + \frac{1}{2} 0.42 = 0.3$$

- 1) Figure out “true” genotype frequencies
- 2) Figure out “true” allele frequencies
- 3) Figure out HW “expected” genotype freq
- 4) Does “true” freq = “expected” freq?



## Example 1: Is this at HW?

- AA 245       $245/500 = \overset{\text{TRUE}}{0.49}$
- Aa 210       $210/500 = 0.42$
- aa 45         $45/500 = 0.09$

TOTAL=500

$$p(A) = 0.49 + \frac{1}{2} 0.42 = 0.7$$
$$q(a) = 0.09 + \frac{1}{2} 0.42 = 0.3$$

$$\overset{\text{HW EXPECTED}}{p^2 = 0.7^2 = 0.49}$$
$$2pq = 2(0.7)(0.3) = 0.42$$
$$q^2 = 0.3^2 = 0.09$$

- 1) Figure out “true” genotype frequencies
- 2) Figure out “true” allele frequencies
- 3) Figure out HW “expected” genotype freq
- 4) Does “true” freq = “expected” freq?



## Example 2: Is this at HW?

- AA 400
  - Aa 200
  - aa 400
- 
- 1) Figure out “true” genotype frequencies
  - 2) Figure out “true” allele frequencies
  - 3) Figure out HW “expected” genotype freq
  - 4) Does “true” freq = “expected” freq?





## **Example 2: Is this at HW?**

AA 400, Aa 200, aa 400



# Hardy-Weinberg provides a **NULL HYPOTHESIS**

- By seeing **HOW** natural populations deviate from the HW expected genotype frequencies, we infer what interesting evolutionary forces are operating!



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