- Description of variation at one gene
  - Genotype/allele frequencies
- The Hardy-Weinberg principle
  - Autosomal gene with 2 codominant alleles
  - Statistical test
  - Sex-linked genes
  - Autosomal gene with a dominant allele
  - Graphical test for multiple diallelic genes

## Reminder: Locus, gene, allele

#### Gene

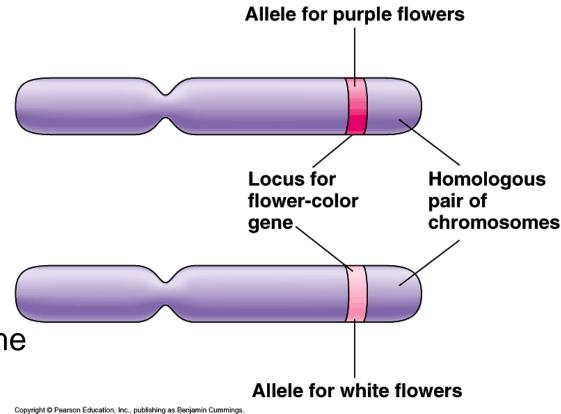
Codes for a specific trait (flower color)

#### **Allele**

Specific form of gene (Purple, white)

#### Locus

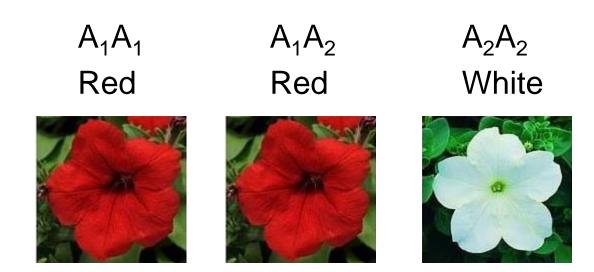
Genes' position in genome (plural loci)



## Reminder: Dominant, recessive, codominant, incomplete dominant

### **Diploid organism**

Genotype Phenotype

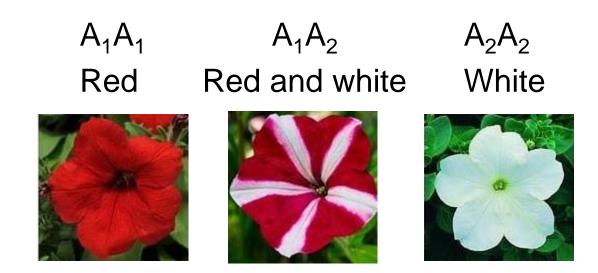


A<sub>1</sub> dominant, A<sub>2</sub> recessive

## Reminder: Dominant, recessive, codominant, incomplete dominant

### **Diploid organism**

Genotype Phenotype



A<sub>1</sub> and A<sub>2</sub> are codominant

## Reminder: Dominant, recessive, codominant, incomplete dominant

### **Diploid organism**

Genotype Phenotype





 $A_1A_2$ 

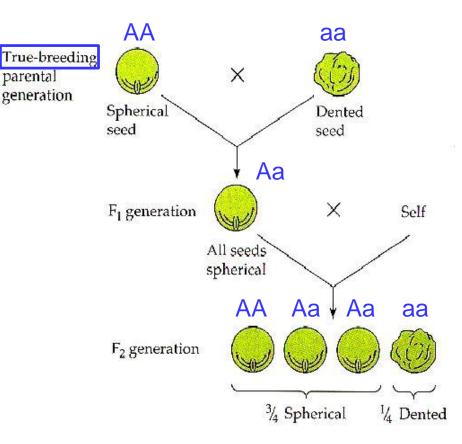




Incomplete dominance

# Analysis of genetic variation of a gene in an experimental population

#### Mendels laws in 1866



### Assumptions:

- 1) diploid organism
- 2) autosomal gene
- 3) 2 alleles
- 4) dominance among alleles
- 5)  $3 + 4 \Rightarrow 2$  phenotypes



# Analysis of genetic variation of a gene in a natural population

In a plant species the color of the flowers is determined by two alleles, one is dominant and the other recessive.

In a population of this species, 75% of the individuals carry red flowers and 25% white flowers.

What is the frequency of the allele coding for white flowers?

# Analysis of genetic variation at a locus in a natural population

SNP (Single Nucleotide Polymorphism)

```
Allele 1 ... GATCCGTACTGATGGGATGG...
```

Allele 2 ... GATCCGTACTGGTGGGATGG...

# Analysis of genetic variation at a locus in a natural population

SNP (Single Nucleotide Polymorphism)

Example from

Exome Aggregation Consortium (ExAC) database (n > 60,000)

Exome: part of the genome composed of exons (1% of genome, ≈ 30,000,000 bp)

SNP rs509360 located on Chromosome 11: 61781087

Population: East Asians

## Genotype and allele frequencies

Genotype	AA	AG	GG	Sum
Number	968	1914	1424	4316
Frequency	0.2243	0.4434	0.3323	1
Frequency	$P_{AA}$	$P_{AG}$	$P_{GG}$	1

### Allele frequencies

$$p = (2 \times 968 + 1914)/(2 \times 4316) = 0.446$$
  
 $q = (2 \times 1424 + 1914)/(2 \times 4316) = 0.554$ 

$$p = P_{AA} + P_{AG}/2$$
$$q = P_{GG} + P_{AG}/2$$

$$p + q = 1$$

What is the genotype distribution at an autosomal locus in a natural population?

The principle was derived in 1908

G.H. Hardy, English mathematician (1877–1947)



W. Weinberg, German physician (1862–1937)



- · Diploid organism, animal
- Autosomal locus, 2 alleles
- Identical genotype distribution in males and females
- Non-overlapping generations
- Infinite population
- No mutation
- No migration
- No selection
- Random mating (panmictic)
- Mendelian segregation

Genotype	
Adults	
Offspring	

$$A_{1}A_{1}$$
 $P_{11}$ 
??

$$A_{1}A_{2}$$
 $P_{12}$ 
??

$$A_{2}A_{2}$$
 $P_{22}$ 
??

### Sperm

$$fr(A_1) = p$$
  $fr(A_2) = q$ 

$$fr(A_1) = p$$

Eggs

$$fr(A_2) = q$$

$$fr(A_1A_1)$$
$$= p^2$$

$$fr(A_2A_1) = qp$$

$$fr(A_1A_2)$$

$$fr(A_2A_2) = q^2$$

Zygotes

Genotype 
$$A_1A_1$$
  $A_1A_2$   $A_2A_2$  Adults  $P_{11}$   $P_{12}$   $P_{22}$  Offspring  $p^2$   $2pq$   $q^2$ 

Allele frequency among the offspring

$$p' = (p^2 + 2 pq/2)$$
  
=  $(p^2 + pq)$   
=  $p(p+q)$   
=  $p$ 

Allele frequency is constant

Independent of the genotype frequencies in a population,

after one generation with random mating and Mendelian segregation

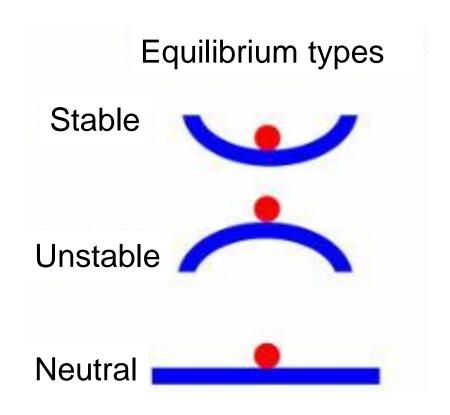
the population is in Hardy-Weinberg equilibrium with the genotype distribution

 $A_1A_1$   $A_1A_2$   $A_2A_2$   $p^2$  2pq  $q^2$ 

and remains there

The Hardy-Weinberg equilibrium is a mixed equilibrium.

The Hardy-Weinberg equilibrium is neutral with respect to allele frequencies.

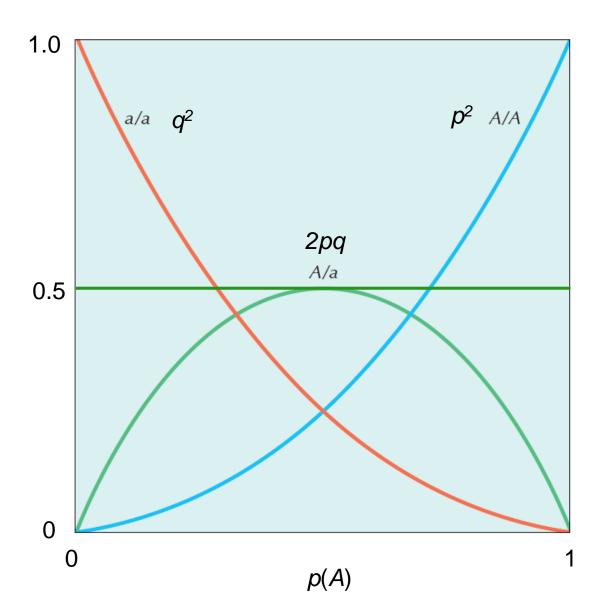


The Hardy-Weinberg equilibrium is neutral with respect to allele frequencies. If the allele frequencies change to p' and q', they will remain there in the future.

$$A_1A_1$$
  $A_1A_2$   $A_2A_2$   $p^2$   $2p'q'$   $q'^2$ 

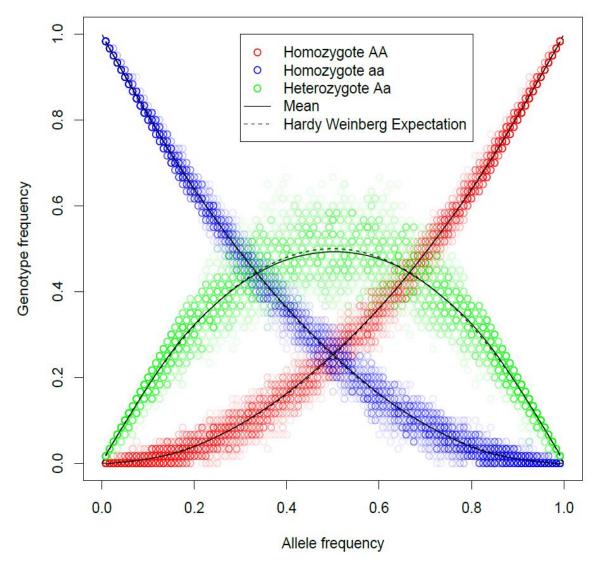
The genotype frequencies for given allele frequencies are stable.

## Hardy-Weinberg proportions



## Hardy-Weinberg proportions

6000 SNPs from HapMap (YRI)



YRI: Yoruba in Ibadan, Nigeria N = 60

## Test of Hardy-Weinberg proportions

Genotype	AA	AG	GG	Sum
Observed $(O_i)$	968	1914	1434	4316
Expected $(E_i)$	p <sup>2</sup> N	2pqN	$q^2N$	4316
Expected $(E_i)$	858.58	2132.84	1324.58	4316

#### **Test**

$$\chi^2 = \Sigma(O_i - E_i)^2 / E_i$$
  
=  $(968 - 858.58)^2 / 858.58$   
+  $(1914 - 2132.84)^2 / 2132.84 + (1434 - 1324.58)^2 / 1324.58$ 

$$= (109.42)^{2} / 858.58 + (-218.84)^{2} / 2132.84 + (109.42)^{2} / 1324.58$$

= 45.44

## Test of Hardy-Weinberg proportions

### Degrees of freedom

$$H_0$$
 Genotypes  $A_1A_1$   $A_1A_2$   $A_2A_2$  Sum Degrees of freedom  $P_{11}$   $P_{12}$   $P_{22}$  1 2  $P_{23}$  1 1 1 1 1 Genotypes  $p^2$   $2pq$   $q^2$ 

Test (difference in degrees of freedom between hypotheses)

If  $X^2 > 3.84$ , the test is significant at the 5% level (df = 1).

## Test of Hardy-Weinberg proportions

Genotype	AA	AG	GG	Sum
Observed (O <sub>i</sub> )	968	1914	1434	4316
Expected $(E_i)$	$p^2N$	2pqN	$q^2N$	4316
Expected $(E_i)$	858.58	2132.84	1324.58	4316

#### **Test**

$$\chi^2 = \Sigma(O_i - E_i)^2 / E_i$$
  
= 45.44

```
R > pchisq(45.44, df=1, lower.tail=FALSE) [1] 1.57387e-11
```

# Interpreting a test for Hardy-Weinberg proportions

Accepting a hypothesis that an observed genotype distribution is in accordance with Hardy-Weinberg proportions,

does **NOT** indicate that the population is in a Hardy-Weinberg equilibrium

# Hardy-Weinberg proportions, but NO Hardy-Weinberg equilibrium

$A_1A_1$	$A_1A_2$	$A_2A_2$
Sterile	Fertile	Sterile
1/4	1/2	1/4

Characterising deviations from Hardy-Weinberg proportions:

Definition of inbreeding coefficient

$$F = (H_e - H_o)/H_e$$
  
=  $(2pq - P_{12})/(2pq)$   
=  $(2f_A f_a - f_{Aa})/(2f_A f_a)$   
therefore,

$$P_{12} = 2pq(1 - F)$$

 $H_o$  Observed freq. of heterozygotes  $H_e$  Expected freq. of heterozygotes (Nielsen & Slatkin notation)

With inbreeding or population admixture (F > 0): deficiency of heterozygotes compared to HW and excess of homozygotes compared to HW

Characterising deviations from Hardy-Weinberg proportions:

	Homozygotes	Heterozygotes
Inbreeding	<b>↑</b>	<b>\</b>
Population admixture	<b>↑</b>	<b>\</b>
Selection	$\uparrow \downarrow$	$\uparrow \downarrow$
Sex-linked polymorphism	<b>↑</b>	<b>\</b>
Assortative mating	$\uparrow \downarrow$	$\uparrow \downarrow$

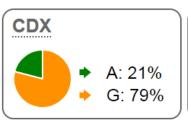
Genotype	AA	AG	GG	Sum
Observed (O <sub>i</sub> )	968	1914	1434	4316
Expected $(E_i)$	$p^2N$	2pqN	$q^2N$	4316
Expected $(E_i)$	858.58	2132.84	1324.58	4316

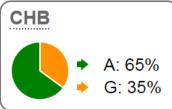
### SNP in East Asia population (EAS)

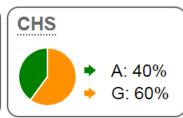
$$F = (2132.84 - 1914)/2132.84$$
  
= 0.11

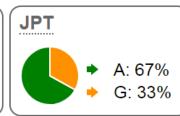
What is the reason for the excess of homozygotes?

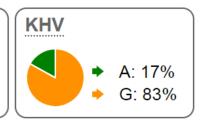
#### EAS subpopulations











-Three Chinese populations ——

Japan

Vietnam

Wahlund effect

Males  $X^AY$   $X^aY$ 

Allele frequencies  $X^A$ : p

 $X^a$ : q

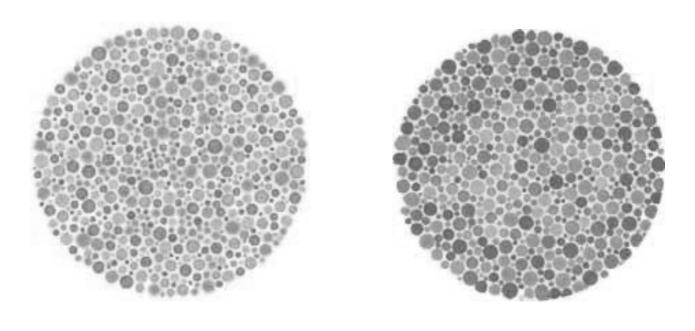
Assumption: same allele frequencies in both sexes

Assumptions: Random union of gametes Mendelian segregation

				Eggs		
				XA	Xa	
				р	q	
	1/2	XA	p	$p^2$	pq	
Sperm	/2	Xa	q	qp	$q^2$	
	1/2	Y		p	q	

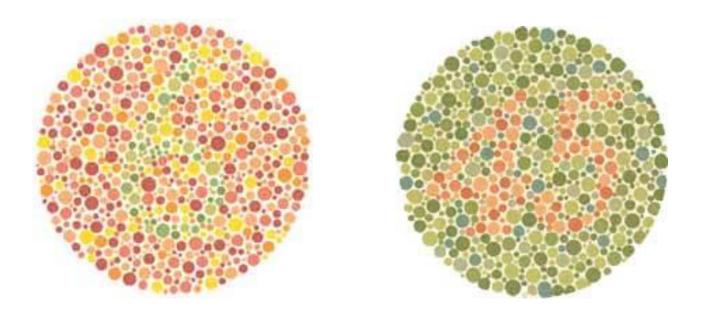
Females	1/2	$X^AX^A$	X <sup>A</sup> X <sup>a</sup>	XaXa
		$p^2$	2pq	$q^2$
Males	1/2	XAY		X <sup>a</sup> Υ
		p		q

Which numbers can you see?



Example: Colour blindness is recessive in females

Which numbers can you see now?



Example: Colour blindness is recessive in females

Females	$X^AX^A$	$X^AX^a$	XaXa
	$p^2$	2pq	$q^2$
	0.846	0.147	0.0064
Males	X <sup>A</sup> Y		XaΥ
	p		q
	0.92		0.08

Assumption: same allele frequencies in both sexes Example: Colour blindness is recessive in females q in Denmark is  $\approx 0.08$ 

# Hardy-Weinberg principle with dominance interaction among alleles

Genotype TT Tt tt

Phenotype T- tt

Number 
$$N_{T-}$$
  $N_{tt}$   $N$  (total)

$$\frac{p^2}{p^2 + 2pq} \frac{2pq}{q^2} \frac{q^2}{q^2}$$

**Assuming HW:** 

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# Analysis of genetic variation at a locus in a natural population

In a plant species the color of the flowers is determined by two alleles, one is dominant and the other recessive.

In a population of this species, 75% of the individuals carry red flowers and 25% white flowers.

What is the frequency of the allele coding for white flowers?

## Exercise 1 to 3

## Graphical test for multiple diallelic loci

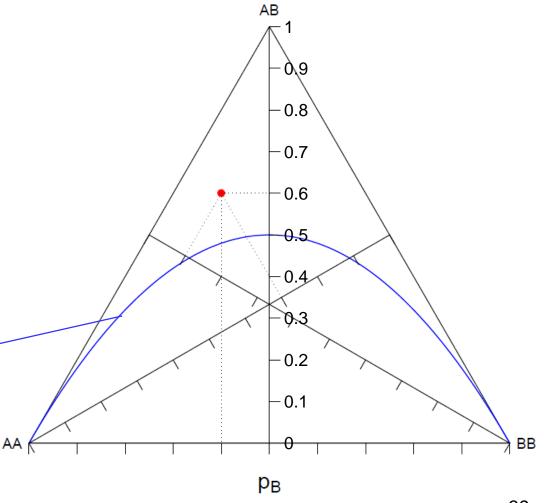
De Finetti diagram

$$f_{AA} = 0.3$$

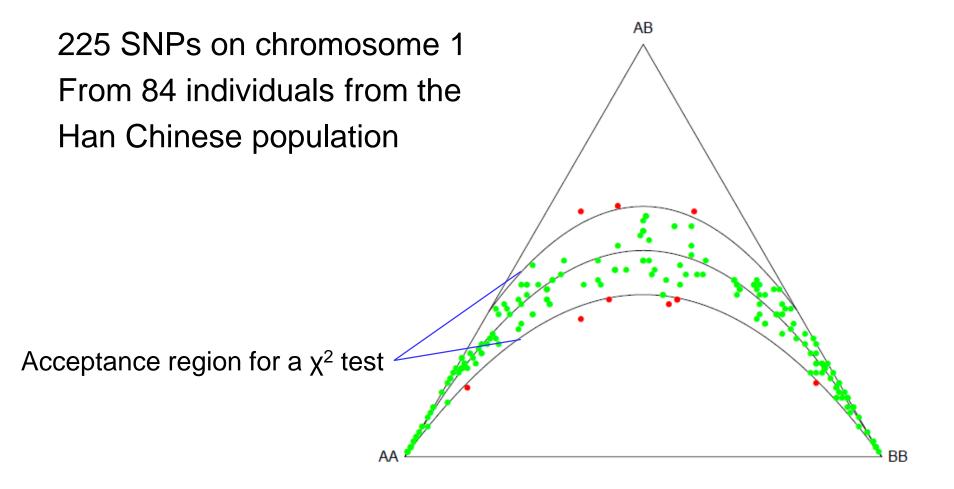
$$f_{AB} = 0.6$$

$$f_{BB} = 0.1$$

Hardy-Weinberg proportions

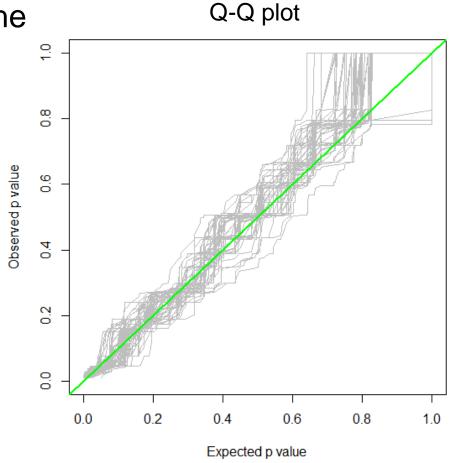


## Graphical test for multiple diallelic loci



## Graphical test for multiple diallelic loci

225 SNPs on chromosome 1 From 84 individuals from the Han Chinese population



Concluding remarks

No models are correct.

But some are extremely useful.

We relax the assumptions
Infinite population
No mutation
No migration
No selection