- 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

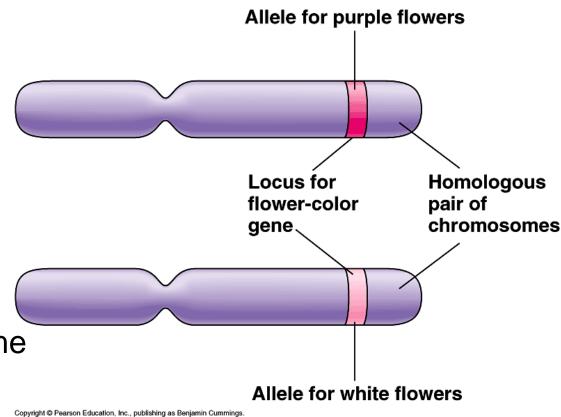
Codes for a specific trait (flower color)

Allele

Specific form of gene (Purple, white)

Locus

Genes' position in genome (plural loci)



Reminder: Locus, gene, allele

Locus for MC1R (Melanocortin 1 receptor) gene:

Complete gene

Chromosome 16: 89912119-89920977

SNP, causing red hair Chromosome 16: 89919736 C>T

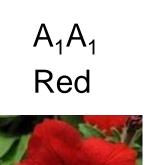
TT red hair



Reminder: Dominant, recessive, codominant, incomplete dominant

Diploid organism

Genotype Phenotype





A₁A₂ Red



 A_2A_2 White

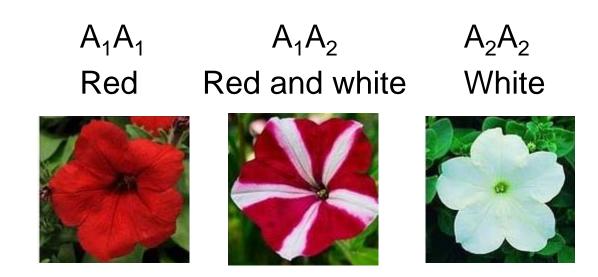


A₁ dominant, A₂ recessive

Reminder: Dominant, recessive, codominant, incomplete dominant

Diploid organism

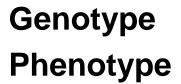
Genotype Phenotype

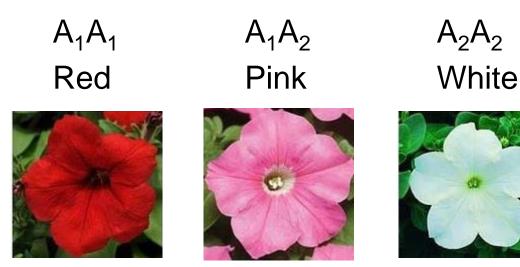


A₁ and A₂ are codominant

Reminder: Dominant, recessive, codominant, incomplete dominant

Diploid organism





Incomplete dominance

Analysis of genetic variation of a gene in an experimental population

Mendels laws in 1866

$\begin{array}{c} \text{True-breeding} \\ \text{parental} \\ \text{generation} \end{array} \\ \begin{array}{c} \text{Spherical} \\ \text{seed} \end{array} \\ \begin{array}{c} \text{Dented} \\ \text{seed} \end{array} \\ \\ F_1 \text{ generation} \\ \end{array} \\ \begin{array}{c} \text{All seeds} \\ \text{spherical} \end{array}$

3/4 Spherical

1/4 Dented

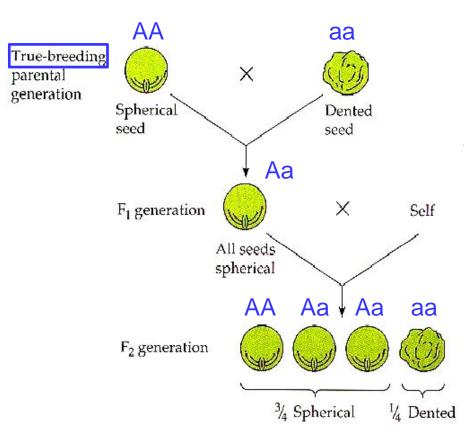
Assumptions:

- 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 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

$$A_{1}A_{2}$$
 P_{12}
22

$$A_{2}A_{2}$$
 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

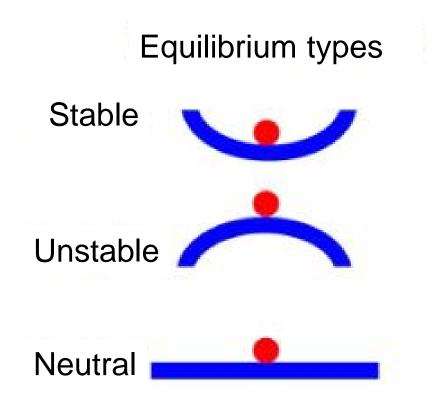
the population is in Hardy-Weinberg equilibrium with the genotype distribution

 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.



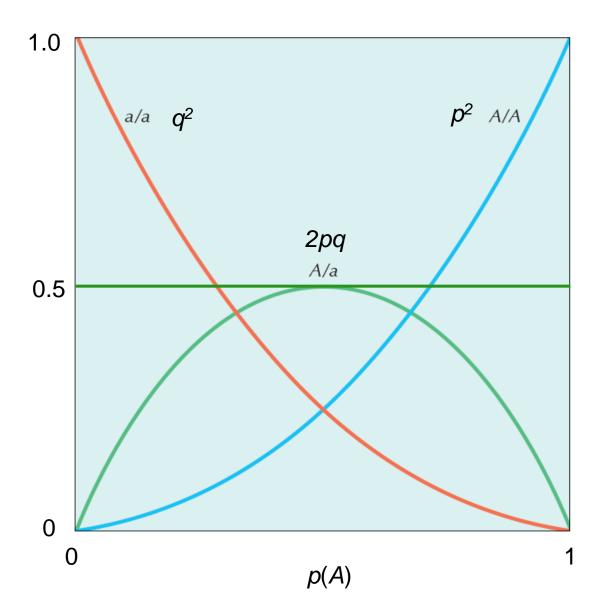
The Hardy-Weinberg equilibrium is neutral with respect to allele frequencies. If the allele frequencies change to p' and q', they will remain there in the future.

$$A_1A_1 \qquad A_1A_2 \qquad A_2A_2$$

$$p^2 \qquad 2p'q' \qquad q^2$$

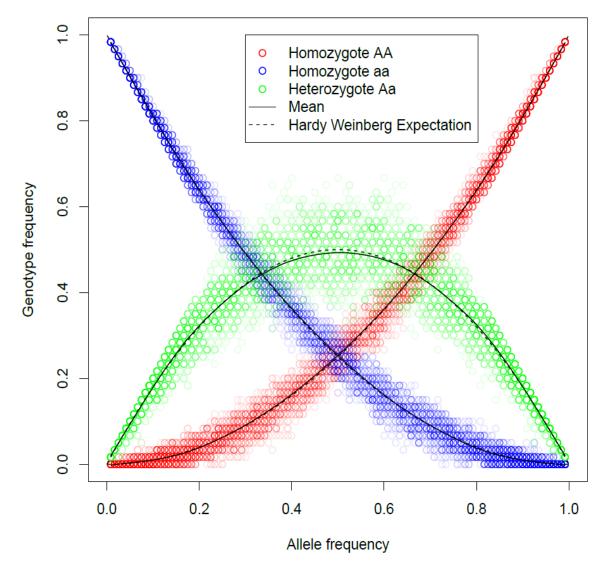
The genotype frequencies for given allele frequencies are stable.

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 ² 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 _i)	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	↑	\
Population admixture	↑	\
Selection	$\uparrow \downarrow$	$\uparrow \downarrow$
Sex-linked polymorphism	↑	\
Assortative mating	$\uparrow \downarrow$	$\uparrow \downarrow$

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

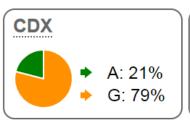
SNP in East Asia population (EAS)

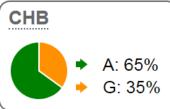
$$F = (2132.84 - 1914)/2132.84$$

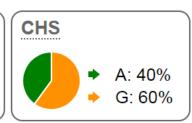
= 0.11

What is the reason for the excess of homozygotes?

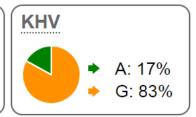
EAS subpopulations











-Three Chinese populations —

Japan

Vietnam

Wahlund effect

Males $X^A Y$ $X^a Y$

Allele frequencies X^A : p

 X^a : q

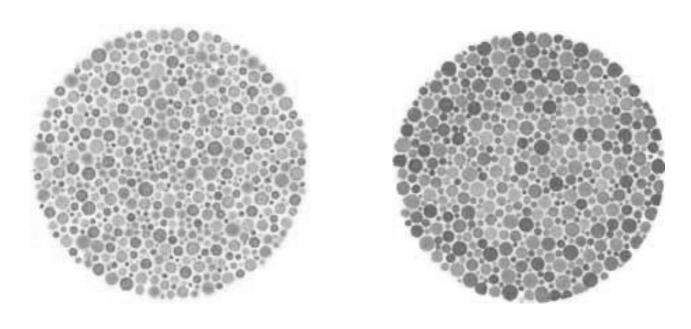
Assumption: same allele frequencies in both sexes

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

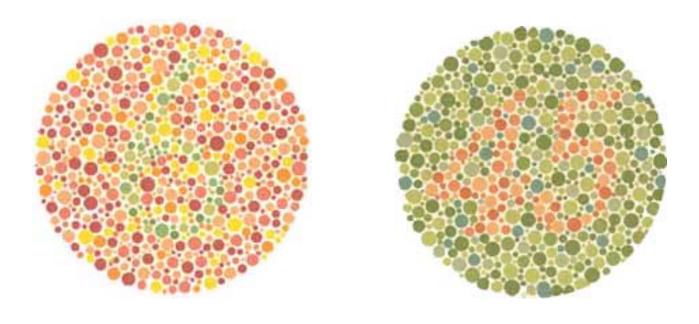
Females	X^AX^A	X ^A X ^a	X ^a X ^a
	p^2	2pq	q^2
Males	XAY		XaΥ
	p		q

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 ^A Y		Χ ^a Υ
	p		q
	0.92		0.08

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

Genotype TT Tt tt

Phenotype T- tt

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

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

Assuming HW:

38



A white-phase next to a black bear (British Columbia, Canada)

Recessive variant in melanocortin 1 receptor gene (mc1r)

missense variant A893G: GG white, AA, AG normal Tyr298Cys

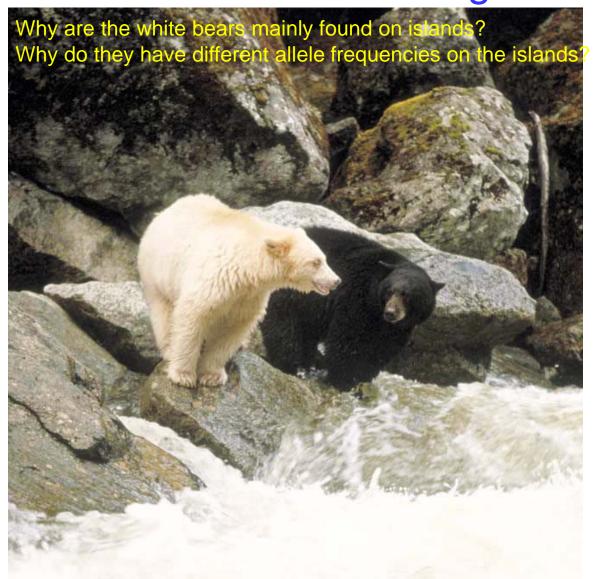
Humans C478T TT red hair



Phenotype frequencies (western Canada)

$$q = \sqrt{N_{tt}/N}$$

Island localities	Norm	al White	Sum	q	
Gribbell	13	10	23	0.66	
Princess Royal	43	9	52	0.42	
Roderick	10	2	12	0.41	
Mainland localities					Many Sugar syrve
East of Princess Royal	25	0	25	0	
North of Roderick	11	1	12	0.29	
Don Peninsula	24	0	24	0	
Terrace	21	0	21	0	40
Sum	81	1	82	0.11	Ritland et al. (2001)



Graphical test for multiple diallelic loci

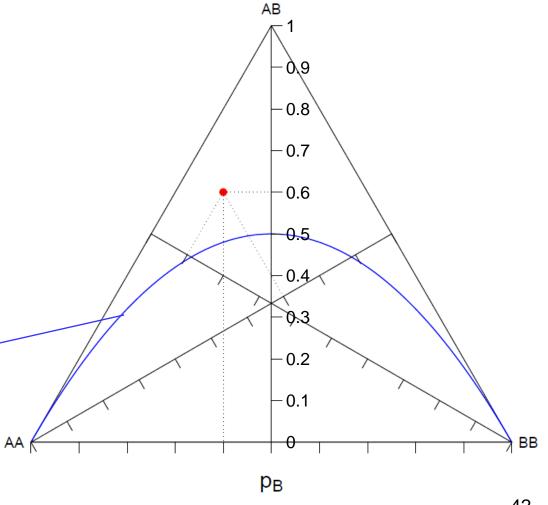
De Finetti diagram

$$f_{AA} = 0.3$$

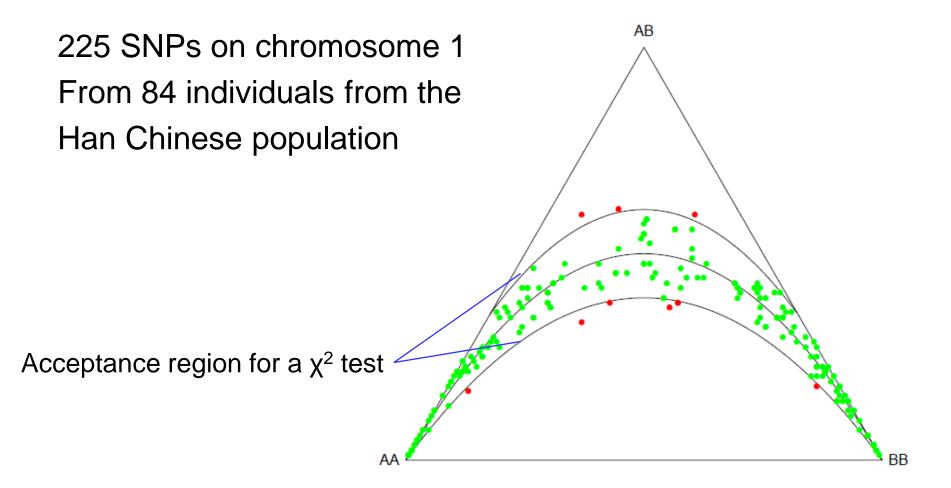
$$f_{AB} = 0.6$$

$$f_{BB} = 0.1$$

Hardy-Weinberg proportions

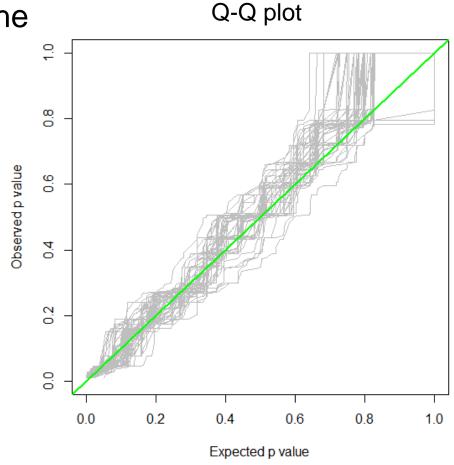


Graphical test for multiple diallelic loci



Graphical test for multiple diallelic loci

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



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?

Concluding remarks

No models are correct.

But some are extremely useful.

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

