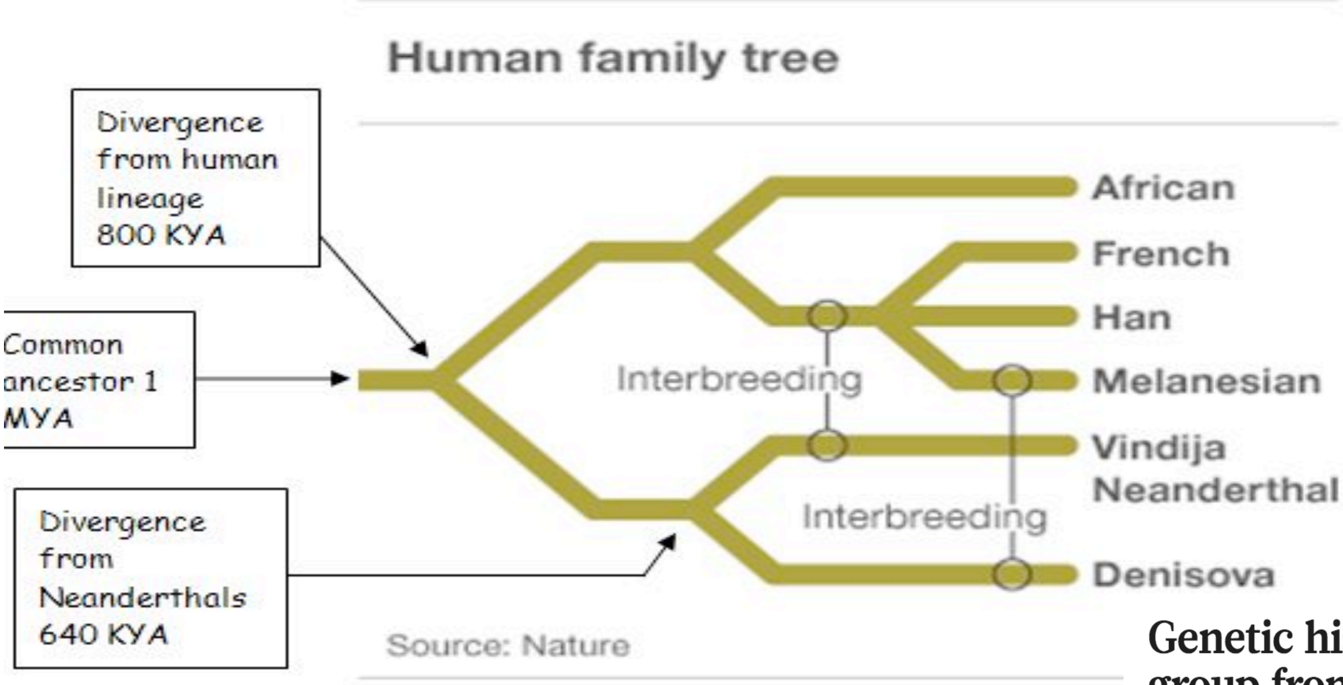

https://www.flickr.com/photos/hmnh/3033749380/


Human family tree

Divergence from human lineage 800 KYA

Common ancestor 1 MYA

Divergence from Neanderthals 640 KYA

Source: Nature

Genetic history of an archaic hominin group from Denisova Cave in Siberia

David Reich[1,2]*, Richard E. Green[3,4]*, Martin Kircher[3]*, Johannes Krause[3,5]*, Nick Patterson[2]*, Eric Y. Durand[6]*, Bence Viola[3,7]*
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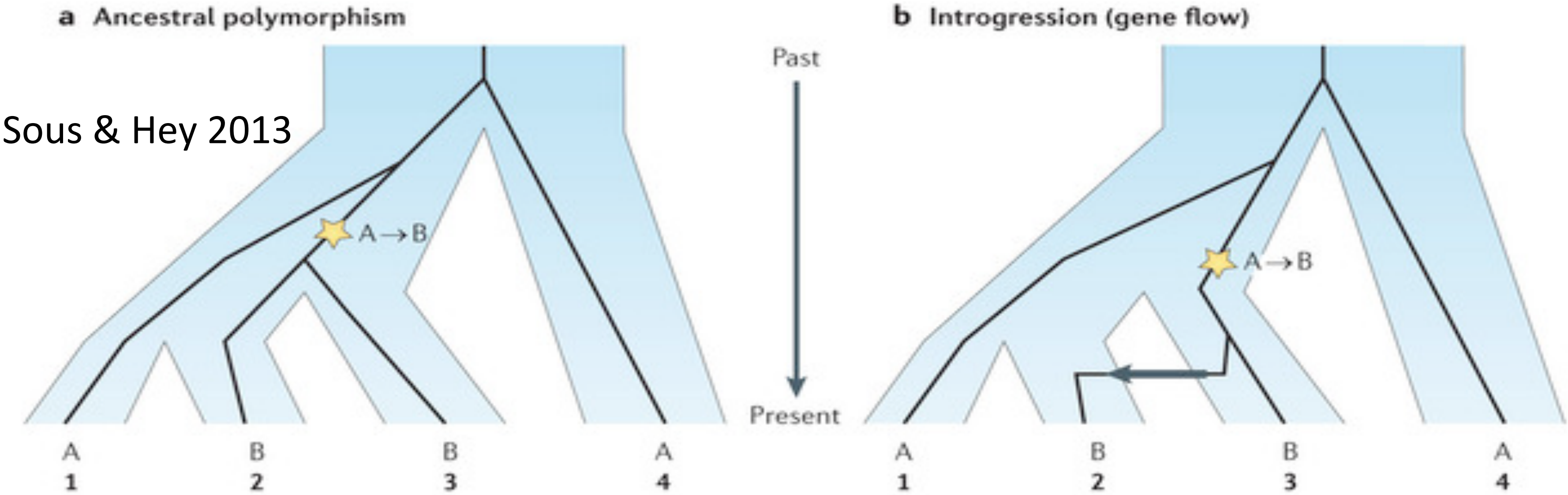
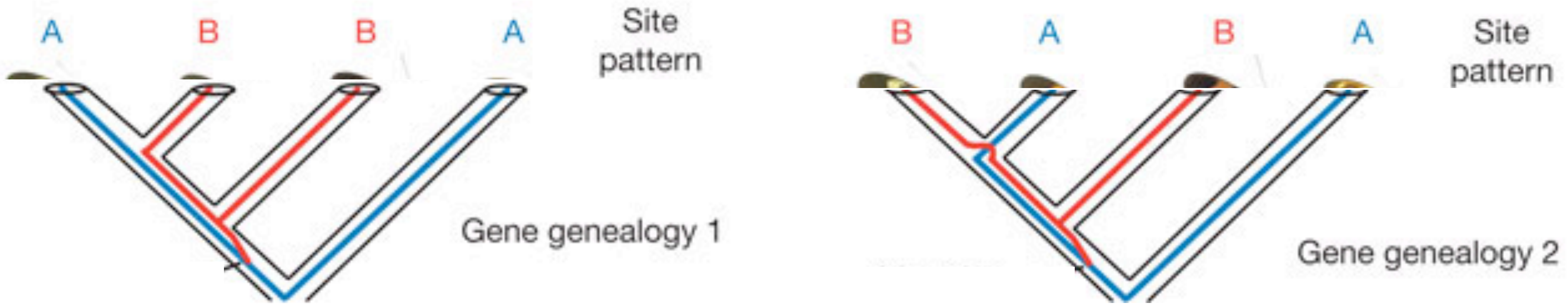
Michael Richards[7,13], Sahra Talamo[7], Michael V. Shunkov[14], Anatoli P. Derevianko[14], Jean-Jacques Hublin[7], Janet Kelso[3],
Montgomery Slatkin[6] & Svante Pääbo[3]

Gene tree-species tree conflict can result from introgression or incomplete lineage sorting

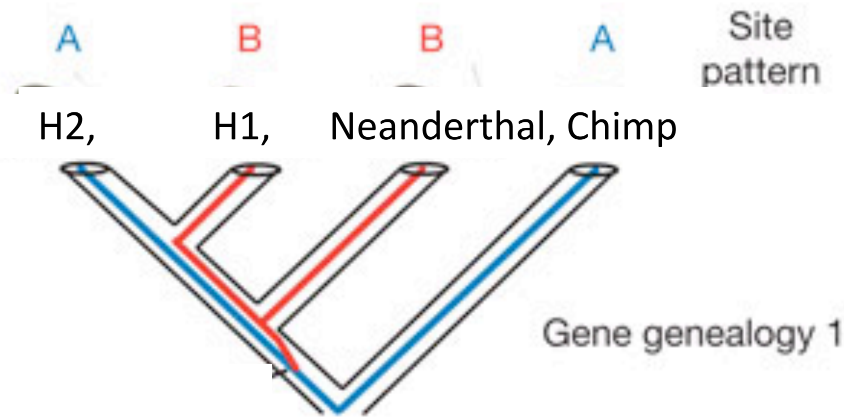


Sous & Hey 2013



Distinguishing incomplete lineage sorting from introgression (ABBA-BABA statistic)
Under incomplete lineage sorting & no introgression
Number of ABBA loci =Number of BABA loci
D = (#(ABBA) – #(BABA))/C,   C= #(ABBA) + #(BABA)

Green et al 2010, Nature



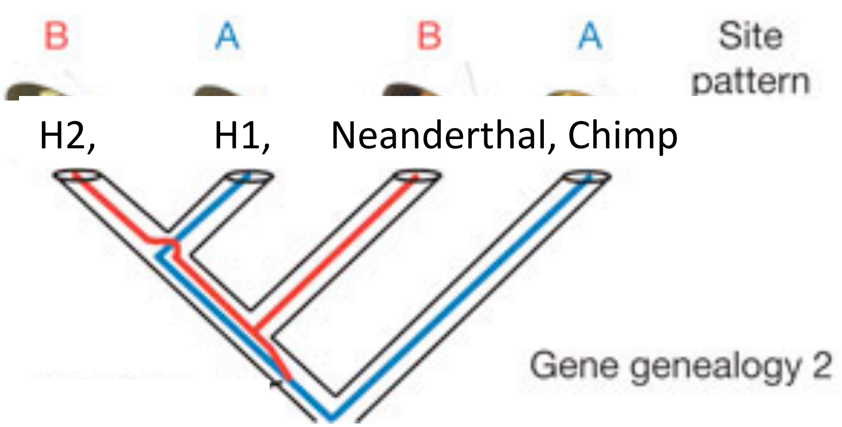


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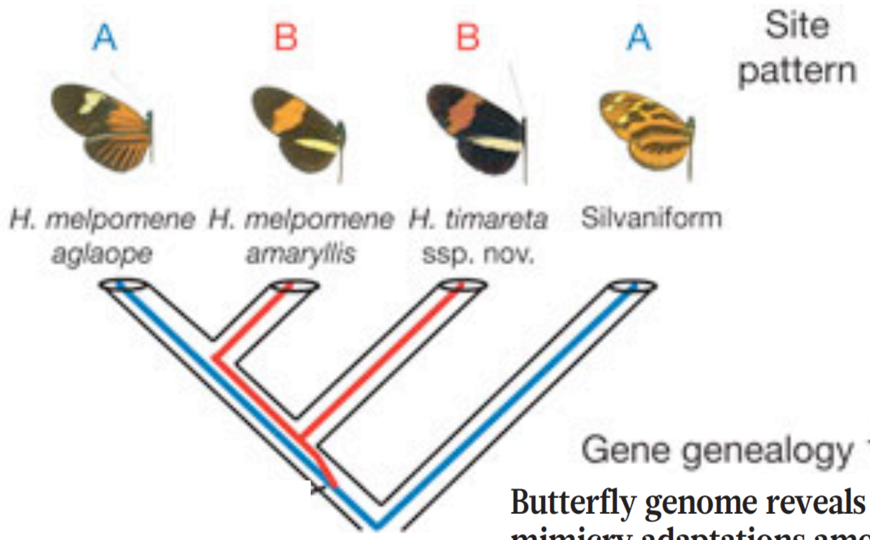
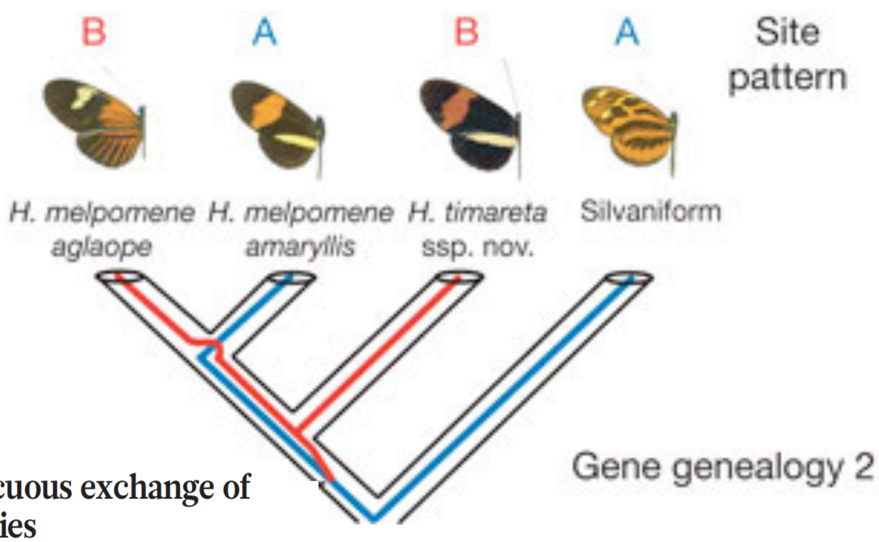
Table 1 | Sharing of derived alleles between present-day and archaic hominins

Sample H_1	Sample H_2	$D(H_1, H_2$, Neanderthal, chimpanzee)					$D(H_1, H_2$, Denisova, chimpanzee)				
		n_{BABA}	n_{ABBA}	D (%)	s.e. (%)	Z-score	n_{BABA}	n_{ABBA}	D (%)	s.e. (%)	Z-score
African/African*											
San	Yoruba	23,690	23,855	−0.3	0.6	−0.6	39,042	39,019	0.0	0.5	0.1
Eurasian/African*											
French	San	25,242	22,982	4.7	0.6	7.6†	39,838	38,495	1.7	0.5	3.4†
French	Yoruba	21,794	19,890	4.6	0.7	6.9†	34,262	33,078	1.8	0.5	3.6†
Han	San	25,081	22,470	5.5	0.6	8.5†	38,815	37,439	1.8	0.5	3.4†
Han	Yoruba	21,741	19,412	5.7	0.7	7.9†	33,182	32,184	1.5	0.5	2.8
Eurasian/Melanesian*											
French	Papuan	15,523	15,548	−0.1	0.8	−0.1	23,509	25,470	−4.0	0.7	−5.7†
Han	Papuan	15,059	14,677	1.3	0.9	1.5	22,262	24,198	−4.2	0.7	−5.8†
Melanesian/African*											
Papuan1	San	21,985	20,366	3.8	0.7	5.1†	35,923	32,841	4.5	0.6	7.2†
Papuan1	Yoruba	19,107	17,646	4.0	0.8	4.9†	30,995	28,186	4.7	0.6	7.4†



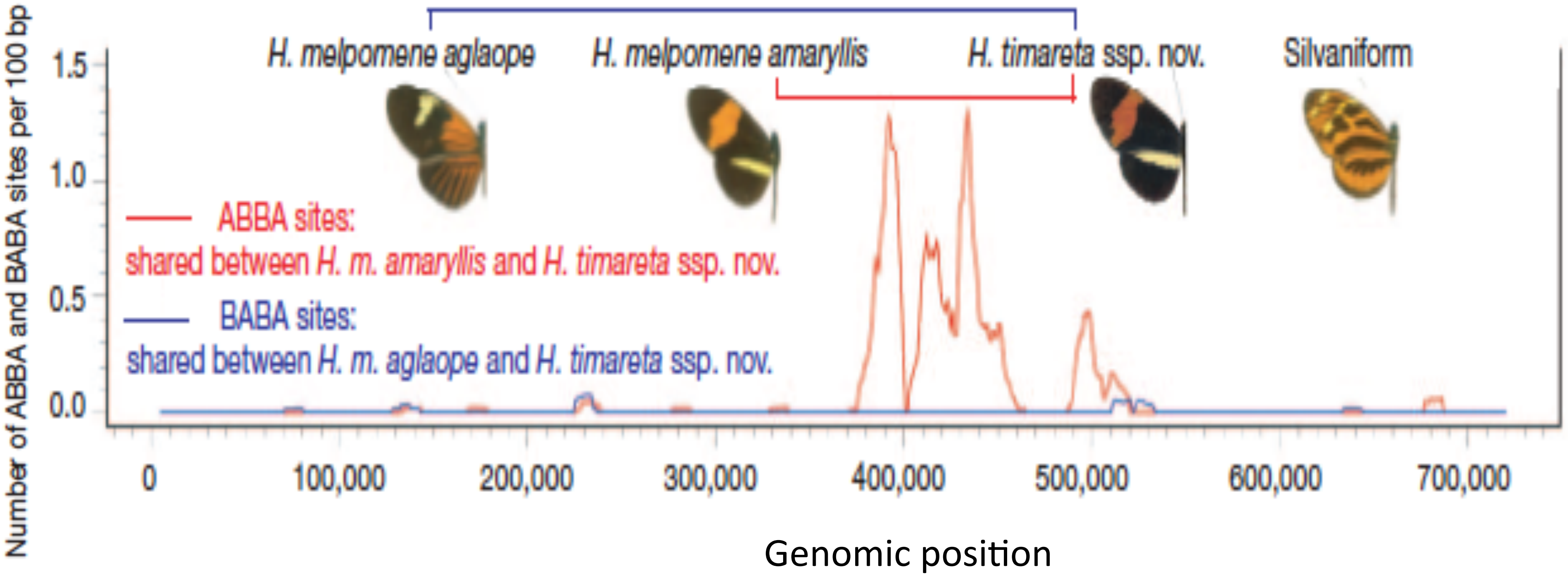
Butterfly genome reveals promiscuous exchange of mimicry adaptations among species

The *Heliconius* Genome Consortium*



Under incomplete lineage sorting
D = (#(ABBA) – #(BABA))/C

D=0.037 ± 0.003 (two-tailed D = 0, P = 1 × 10^{-40})

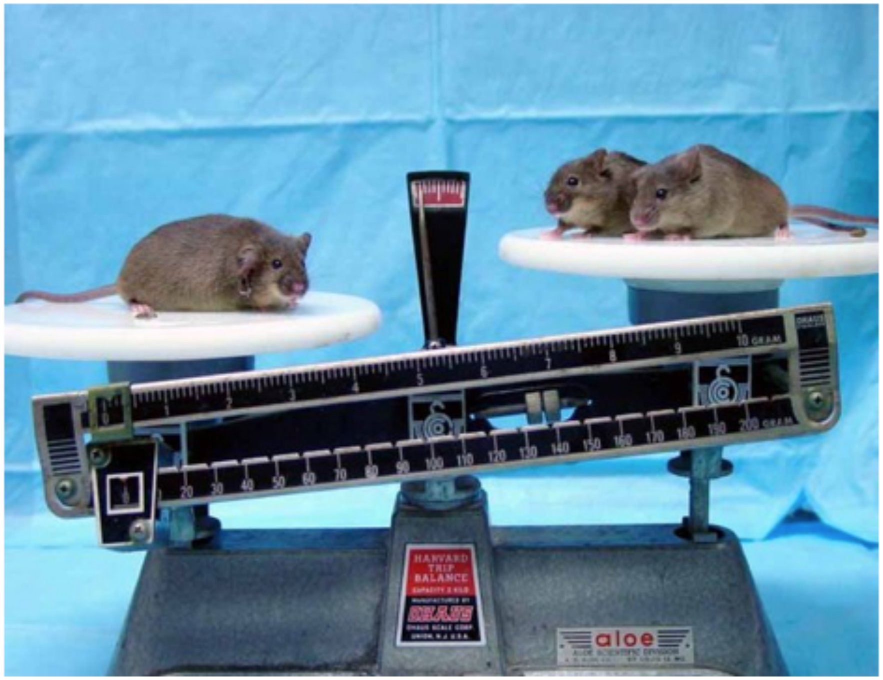


Do your genes make you a criminal?

In the US a murderer is claiming his crime was the tragic consequence of being born a killer. Steve Connor reports on new arguments over whether some people are destined to be bad

STEVE CONNOR | Sunday 12 February 1995

Overweight? Maybe You Really Can Blame Your Genes



Phenotypic Resemblance between relatives

- Covariance

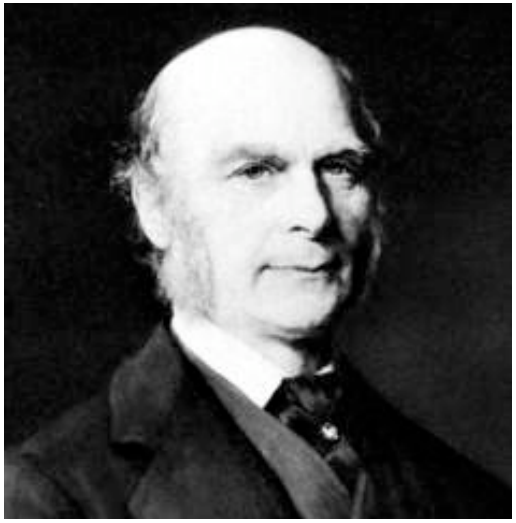
- Correlation

- Slope of linear regression

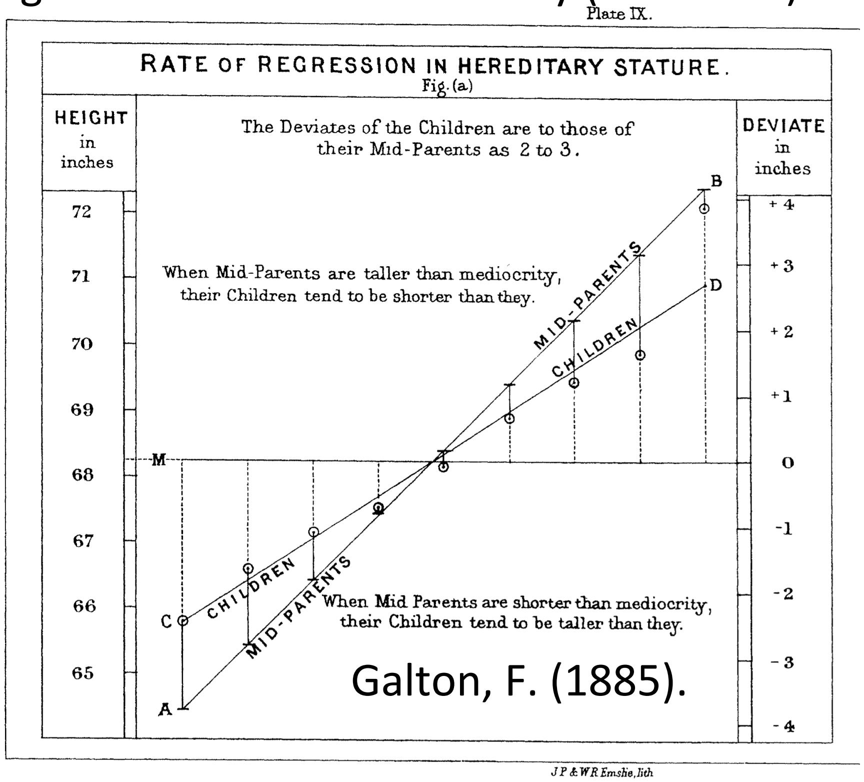
Francis Galton

Phenotypic variation with a population is usually continuous, often has a normal distribution.

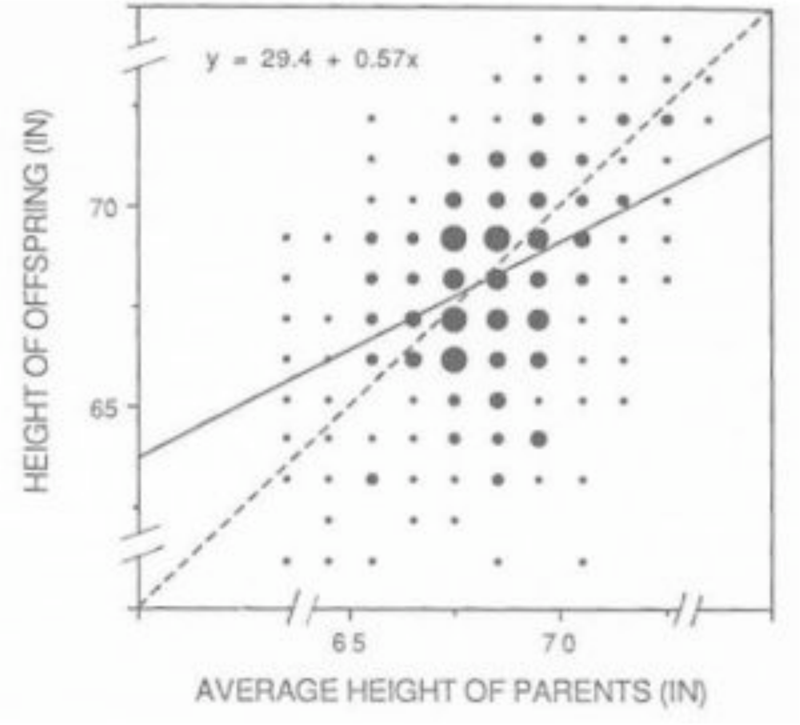
Inheritance is the blending together of parental phenotypes.



Regression towards mediocrity (the mean)



Galton, F. (1885).



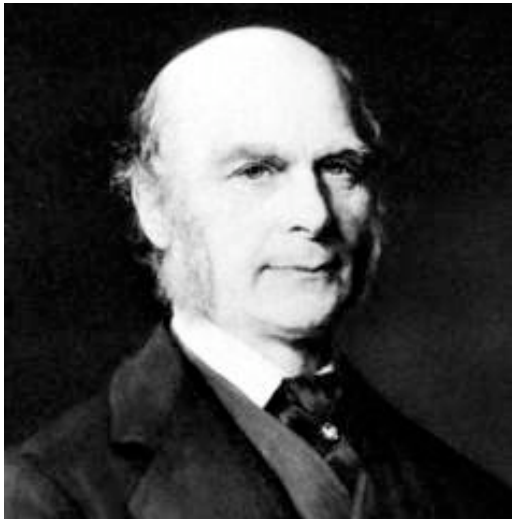
Resemblance between relatives

Gregor Mendel

And the Mendelians
e.g.Bateson

Galton

And the Biometricians
e.g. Pearson and
Weldone



R.A. Fisher (1918)

"The correlations between relatives on the supposition of Mendelian inheritance"

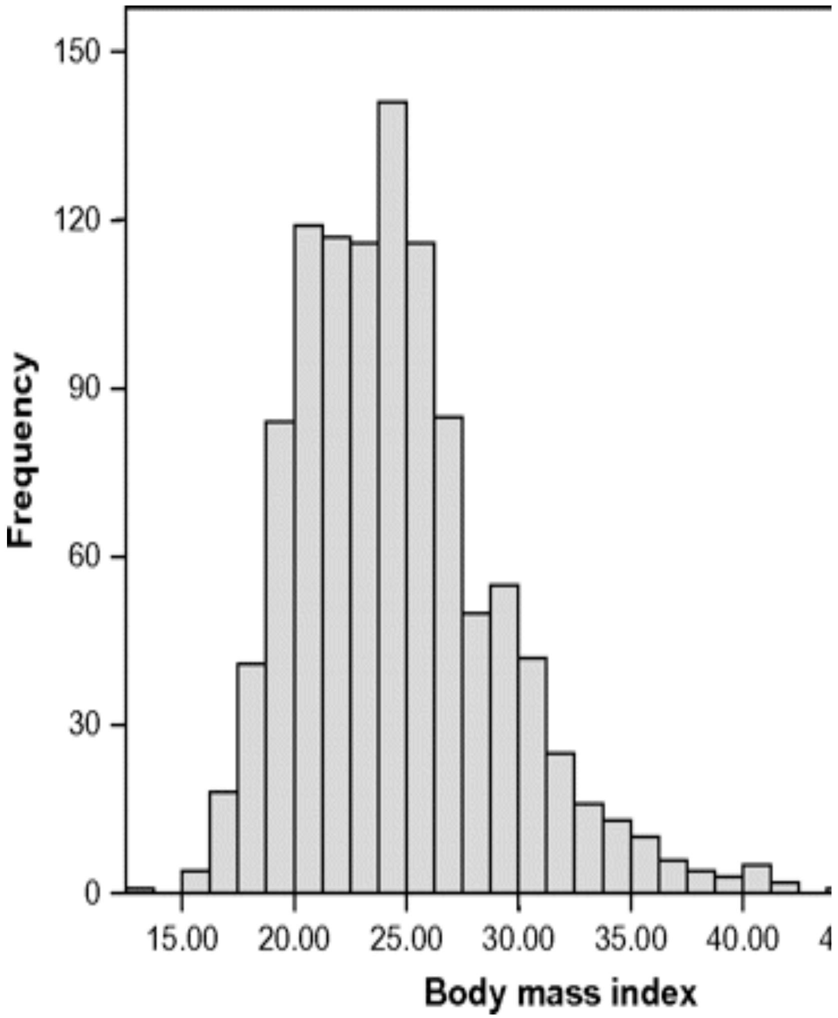
- Reconciled these two views by showing that the mendelian inheritance of many alleles, each of small effect, gave rise to:

--Resemblance between relatives.

--regression towards the mean.

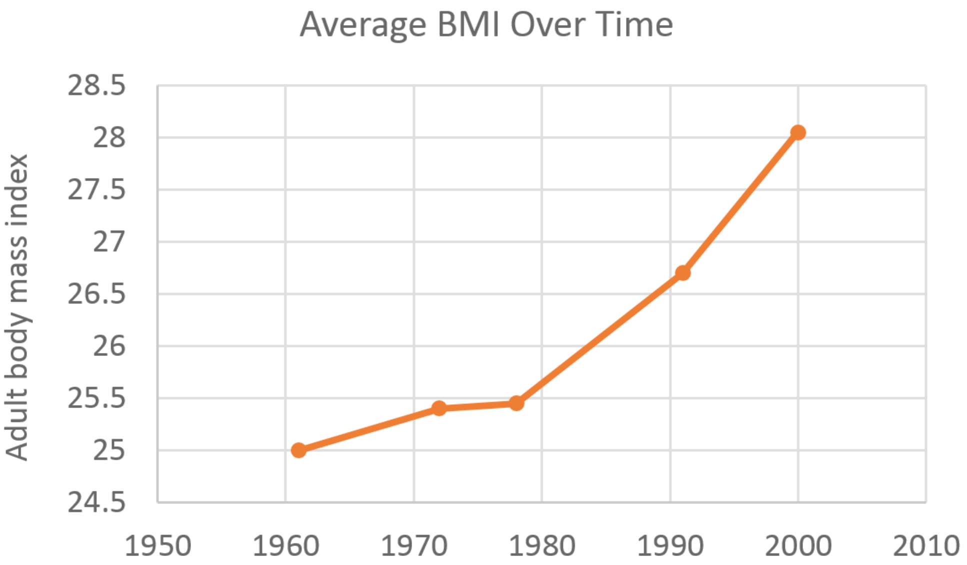
The apparent 'blending' of traits is due to inheritance ½ alleles from Mum and ½ from Dad.

To what extent is my weight genetic?

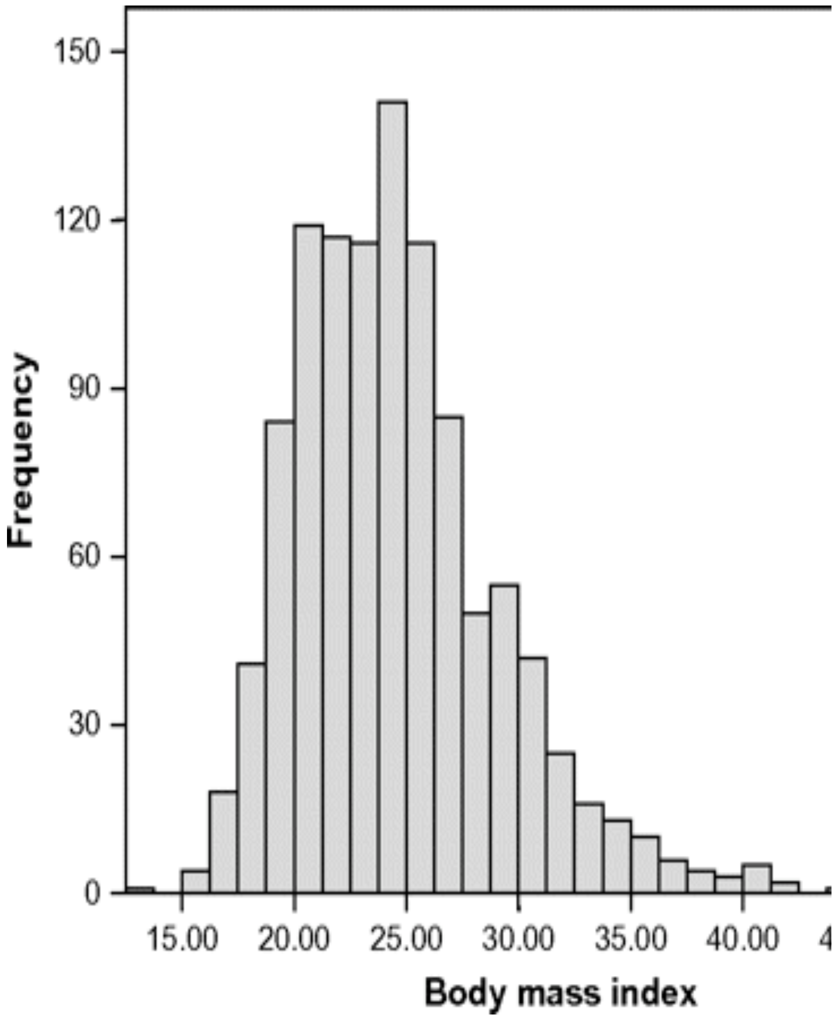


Histogram from Barratt et al 2007

My height ~6 foot
My weight ~160 pounds
My BMI 21.7



Phenotypes are always due to the interaction of genes and environments.



Histogram from Barratt et al 2007

My BMI is 22.4

Top 6 Alleles associated with BMI:

SNP name	My Genotype	Avg. Effect on BMI*
rs3751812	GT	0.33 for each T
rs10871777	AA	0.2 for each G
rs13130484	CC	0.19 for each T
rs4788102	GG	0.15 for each A
rs10838738	AA	0.07 for each G
rs3101336	CT	0.1 for each C

There are likely to be hundreds more genetic variants contributing to BMI.

*Calculated by 23&Me.

The heritability BMI (h^2) in Europeans is between 0.5 and 0.70

Resemblance between relatives in Quantitative traits

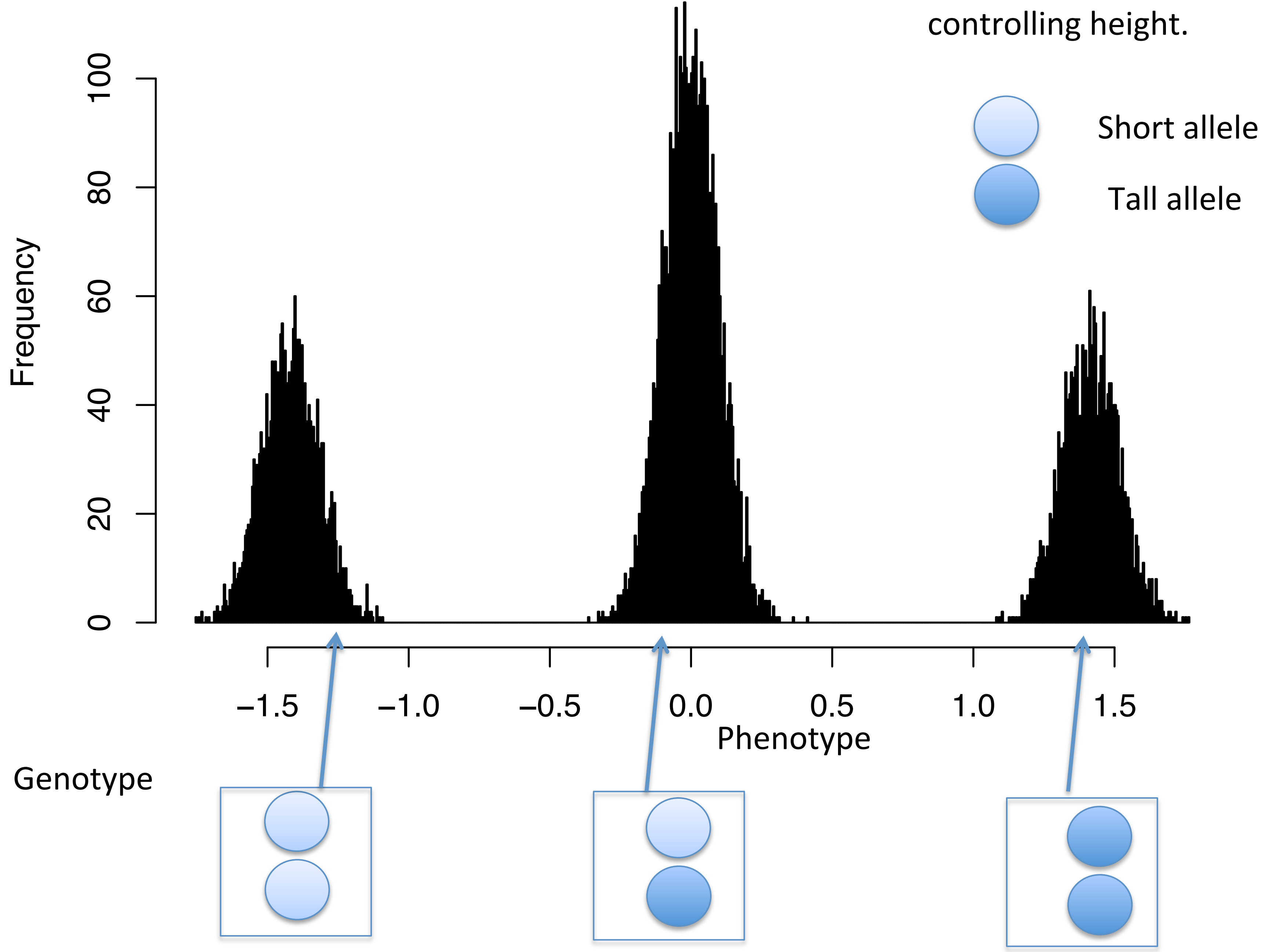
- A trait with L loci

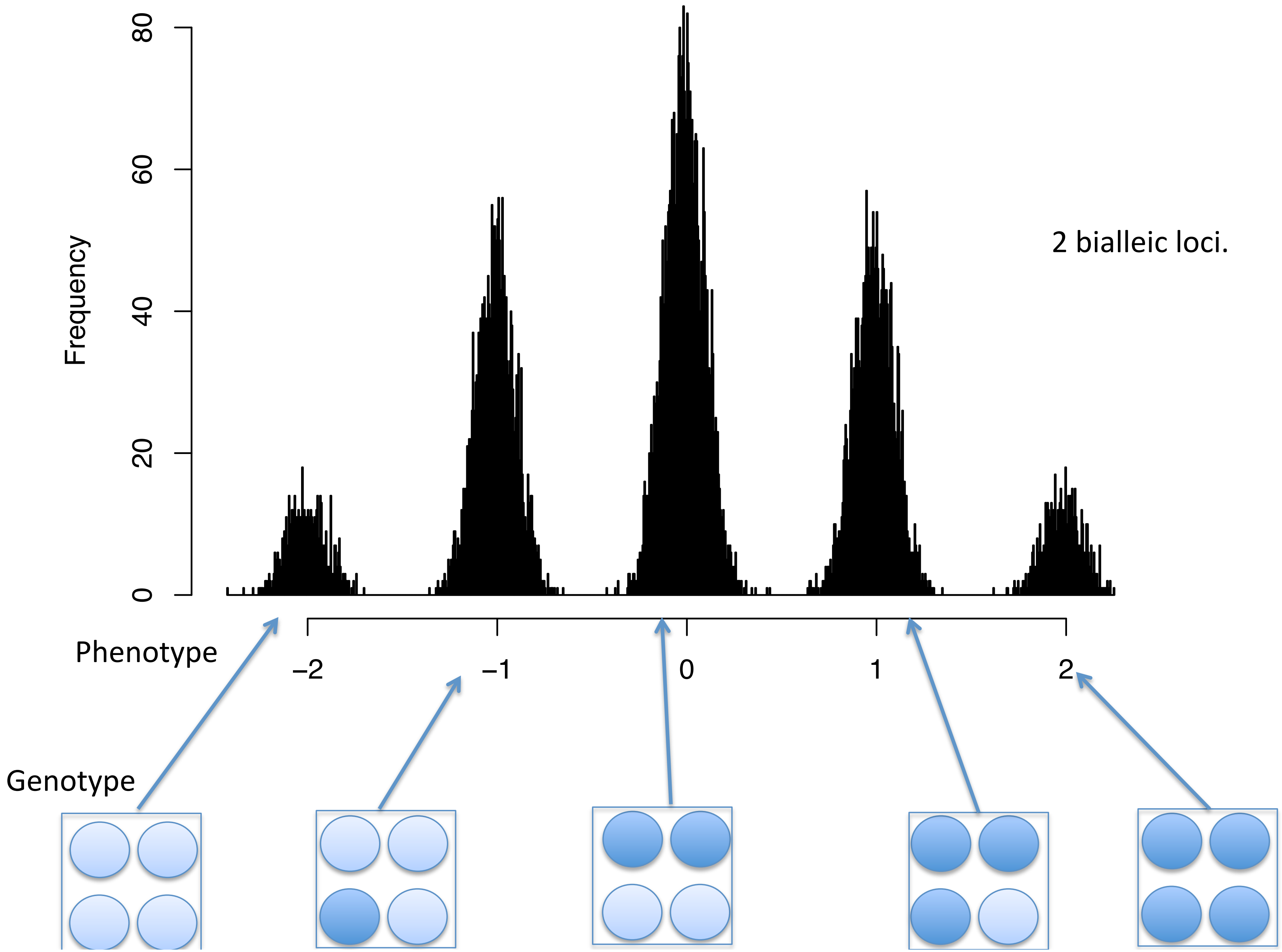
- Each segregating an allele A_1 at freq. p_l

- Each copy of the A_1 allele at a locus increasing our phenotype by a_l, i.e. additively, around mean.
- Our genotype at locus l is 0,1,2
- w.p. p_l^2,$2p_l(1-p_l)$, $(1-p_l)^2$

- An individual's phenotype, X_p, is made up of
  - $X_P = X_A + X_E$

Two alleles at a single locus controlling height.

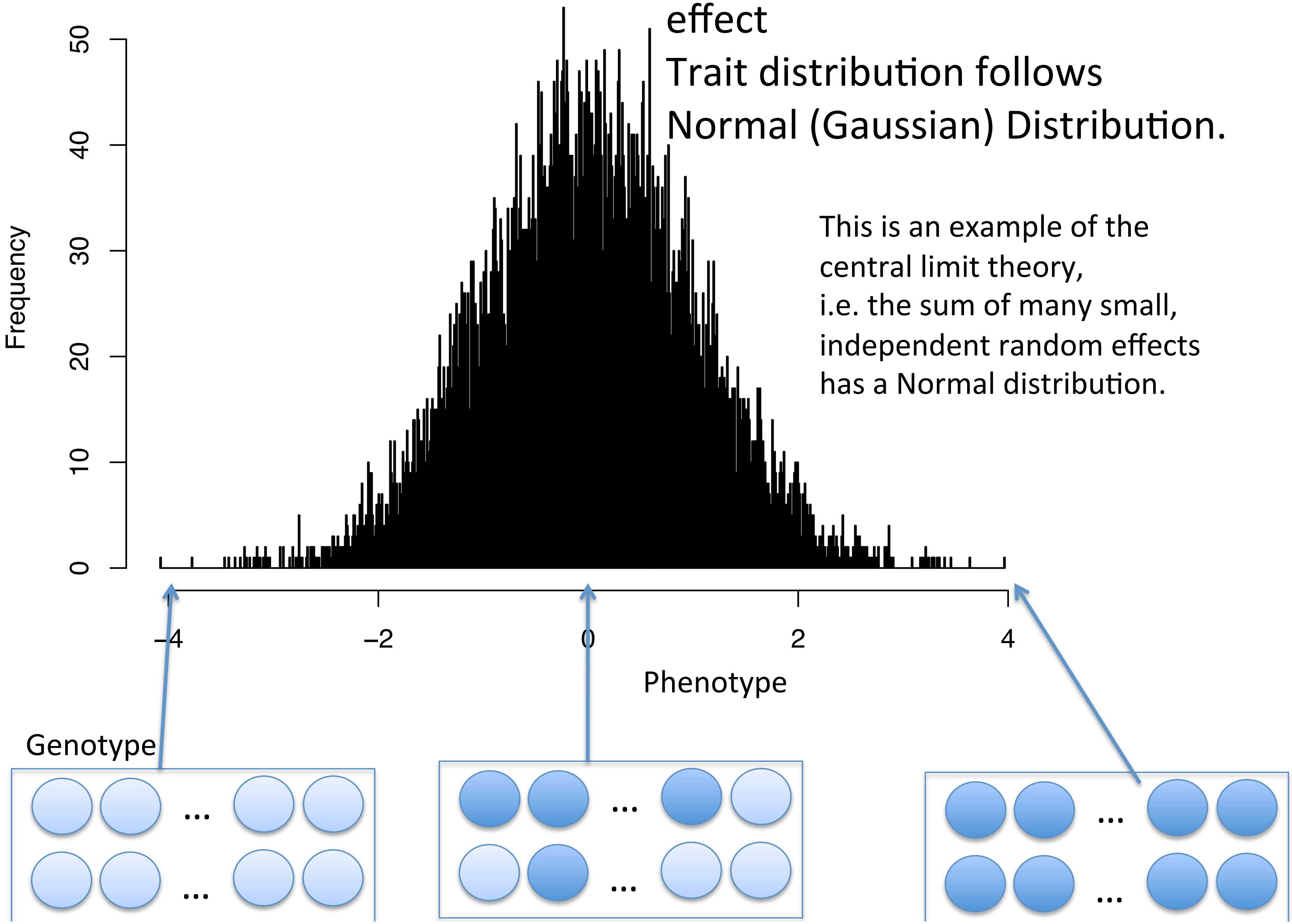




2 bialleic loci.

100 loci with equal additive effect

Trait distribution follows Normal (Gaussian) Distribution.



This is an example of the central limit theory,
i.e. the sum of many small, independent random effects has a Normal distribution.

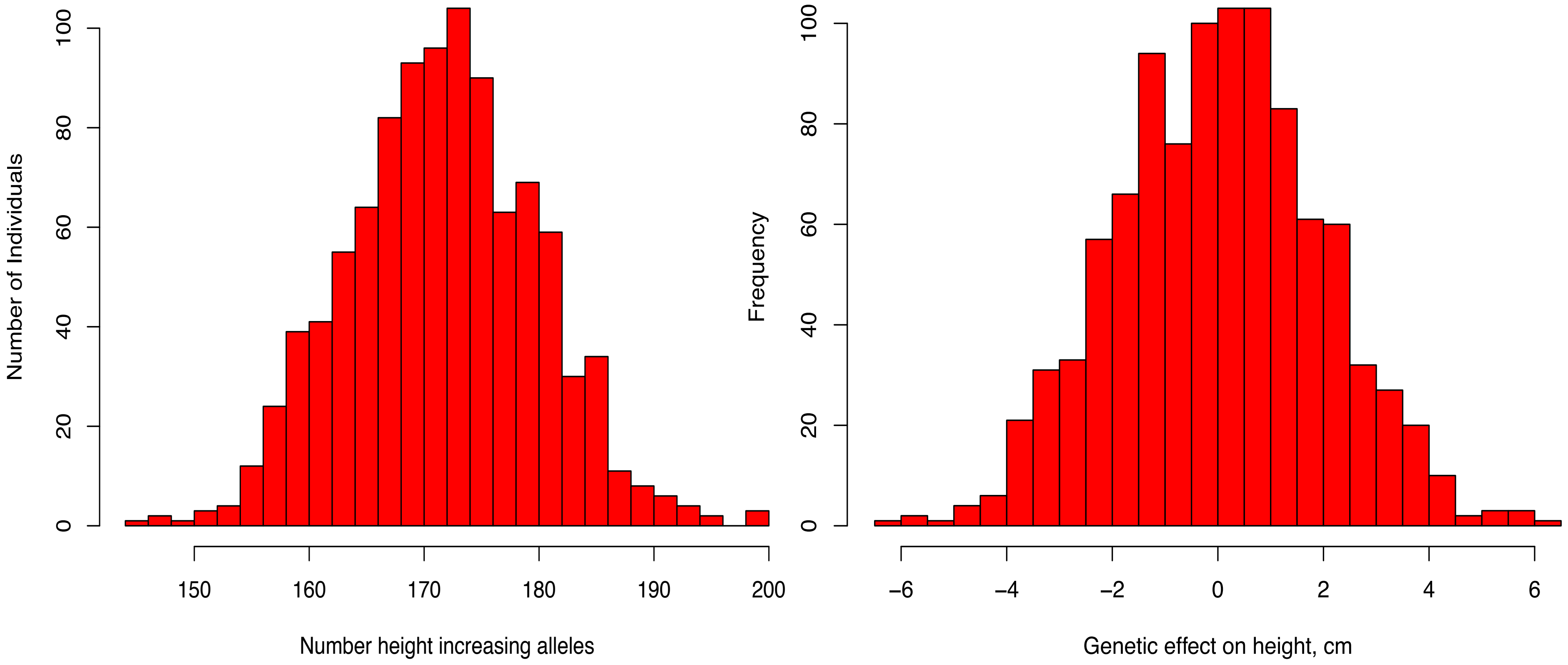
163 loci
Mean additive
effect on height at a locus: 0.24cm

Mean allele frequency:
52% in French population

doi:10.1038/nature09410

Hundreds of variants clustered in genomic loci and biological pathways affect human height

A full list of authors and their affiliations appears at the end of the paper.



An individual's phenotype, X_p, is made up of
$X_P = X_A + X_E$

X_A Genetic contribution to phenotype has a normal distribution $N(0, V_A)$
--Follows from the Central Limit Theory

Assume that X_E has a normal distribution $N(\mu_E, V_E)$

Thus X_P has a normal distribution

$$N(\mu_A + \mu_E, V_P) \qquad V_P = V_E + V_A$$

$$\text{*Heritability} = h^2 = V_A / V_P$$

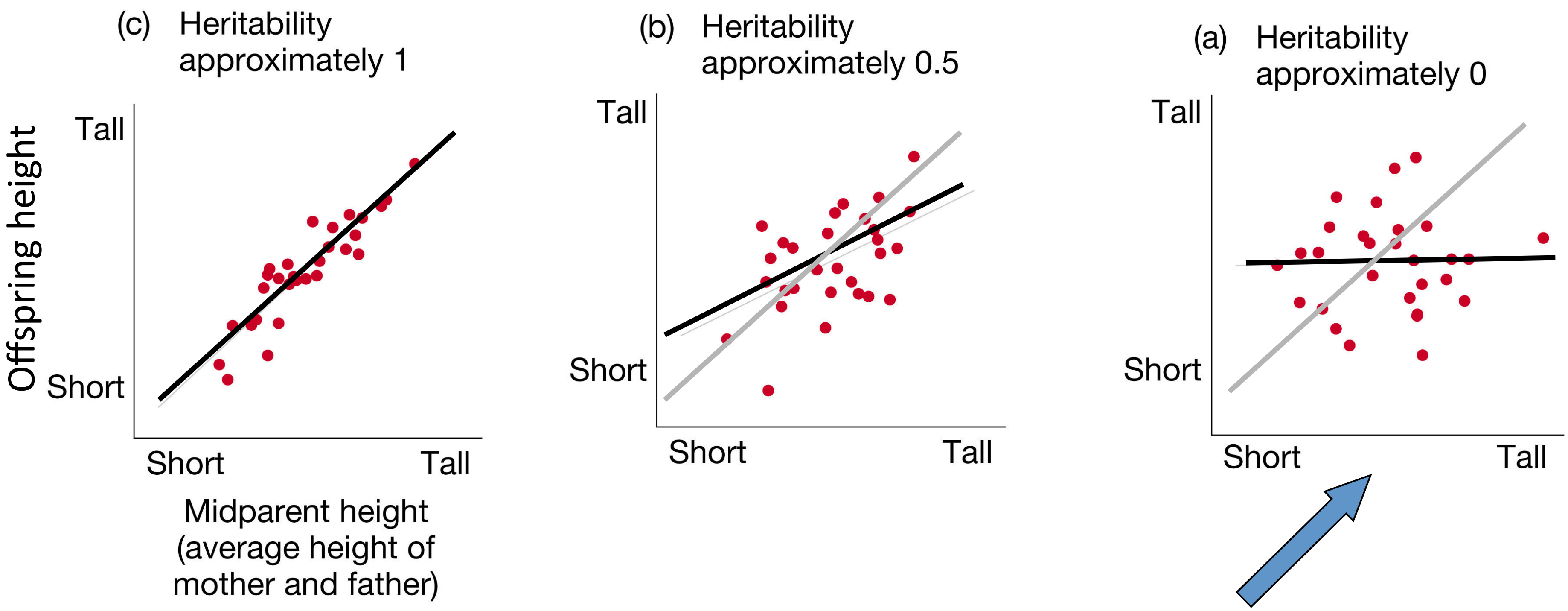
*NARROW SENSE

Resemblance between relatives in Quantitative traits

- Individual 1’s phenotype = X_1
- Individual 2’s phenotype =X_2
- Want to know the cov(X_1,X_2)
- = Cov((X_{1M}+X_{1P}+X_{1E}), (X_{2M}+X_{2P}+X_{2E}))

Heritability is estimated from mid-parent-offspring analysis as the slope of the regression line

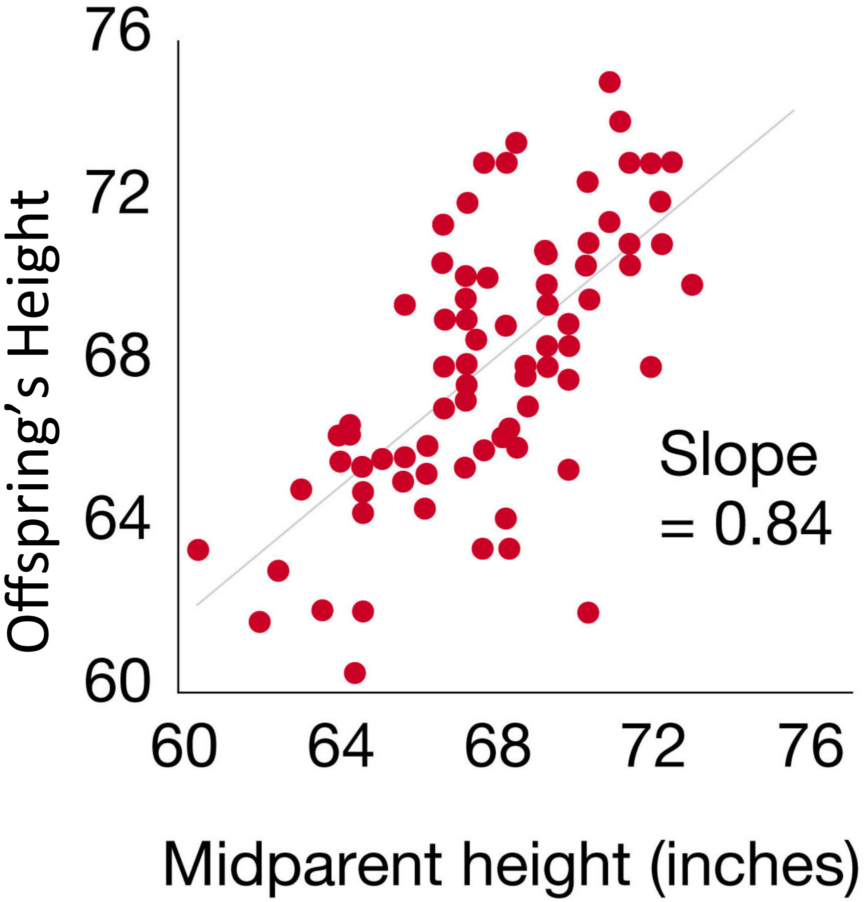
$$\text{Slope} = \text{Cov}(X,Y)/\text{Var}(X) = (V_A/2)/(V_P/2) = h^2$$

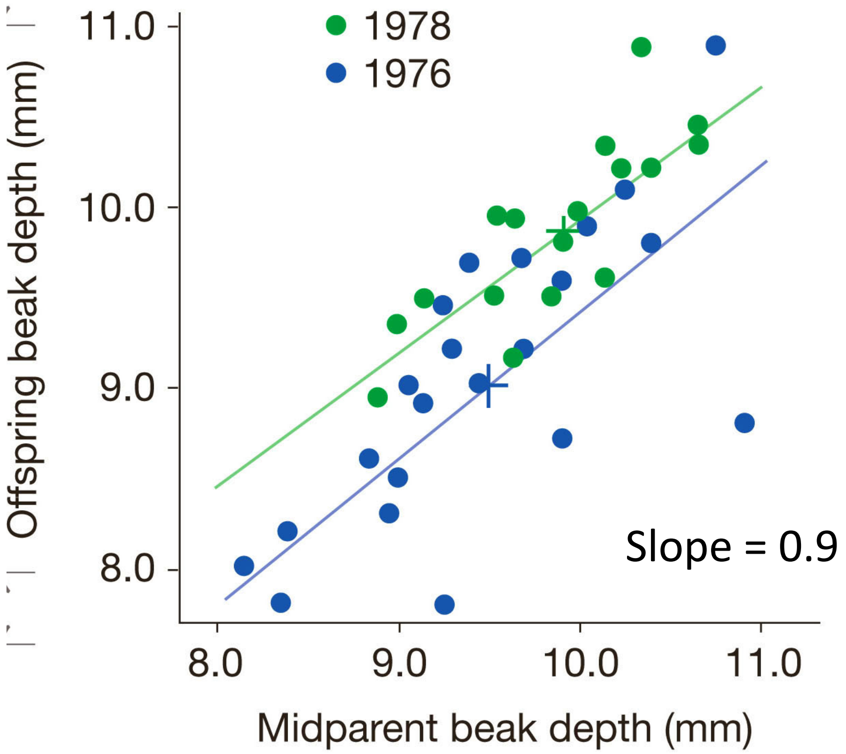


Offspring's phenotype predicted by parental mean

When mid-parental values does not influence offspring phenotype.

(d) Students and their parents





the effect of shared environment

- Need to eliminate the covariance

of relatives due to shared environment.

- This is hard but doable

through careful experiments.

- E.g. cross fostering,

or common garden experiments

Or by use of other pairings of relatives.