# Review of quantitative genetics

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Evangelina López de Maturana & Oscar González-Recio

Something you need to carefully look at, or that may impair your GWP

Something to do, or that optimizes your GWP

Don’t. Discourage to use this.

Smart tip. Something that makes the trick.

Advanced. Something to dive in.

# Challenges

What you need to know from this lecture

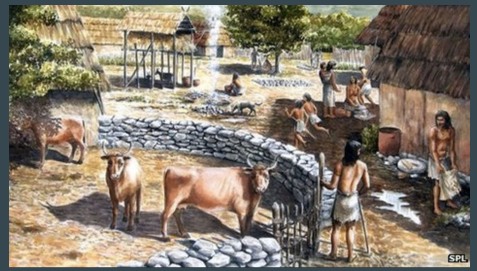
Basic concepts

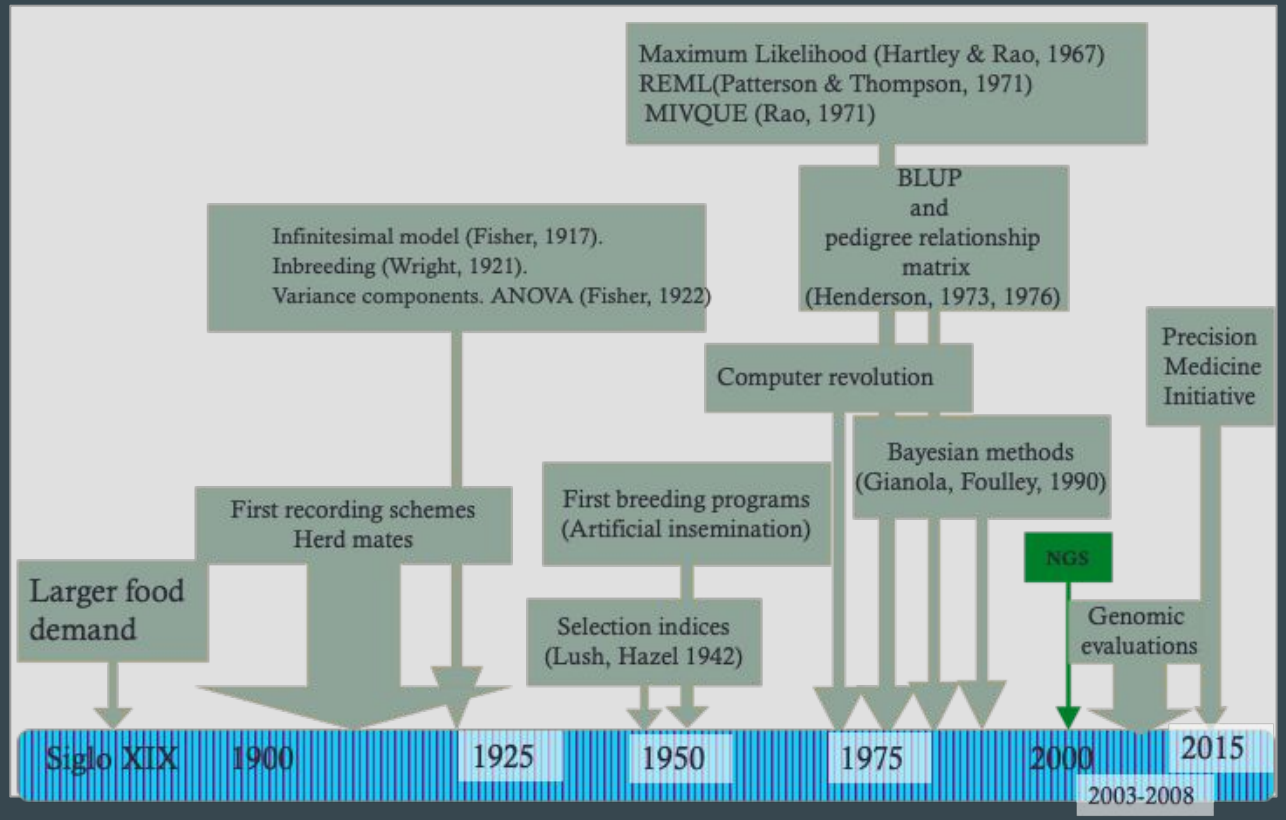
How genes and environment modulate the phenotype

What is genomic heritability and how it affects GWP

Interpret what a GWP implies

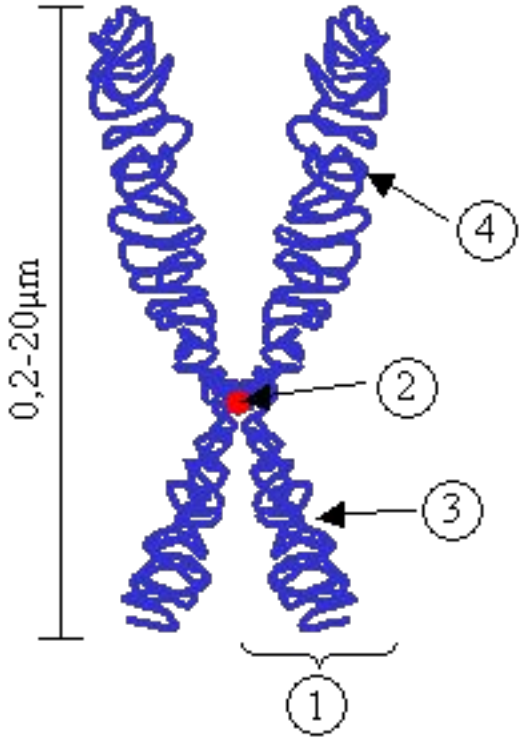
# A bit of history





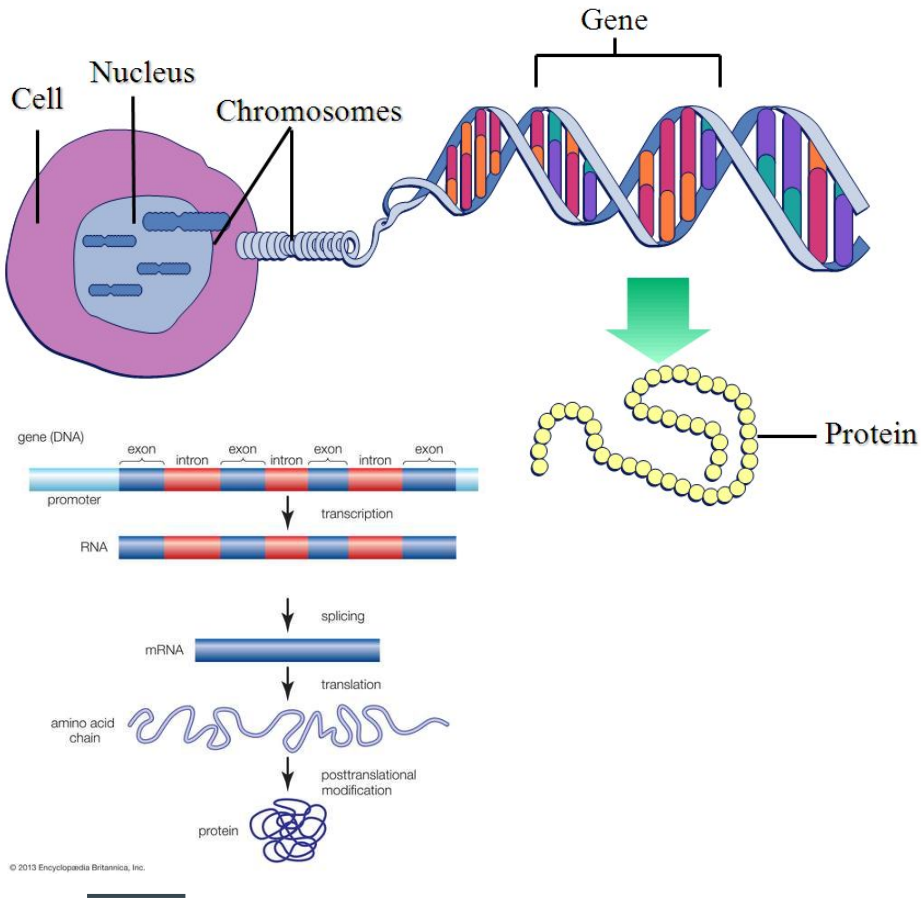
# Locus, loci

A specific physical location of a gene, DNA sequence or genetic marker on a chromosome; like a genetic street address



# Gene

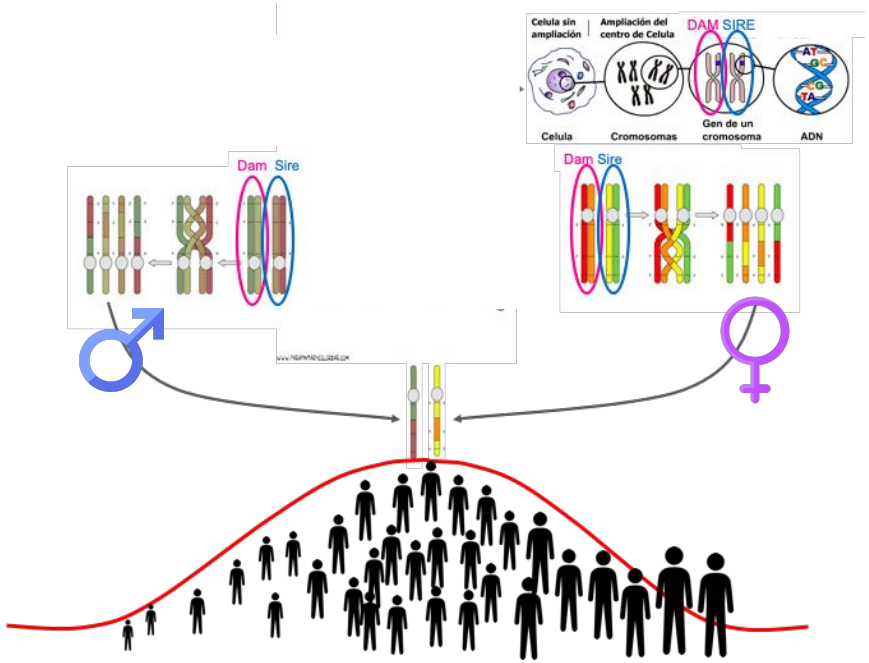
Gene, unit of hereditary information that occupies a fixed position (locus) on a chromosome. Genes achieve their effects by directing the synthesis of proteins.




Genome-wide prediction

# Mendelian effect

Deviation from the expected parent average




$$a_i = \frac{1}{2}a_p + \frac{1}{2}a_m + \phi_i$$

$$\phi_i \sim N(0, \sigma_a^2 / d_i)$$

Genome-wide prediction

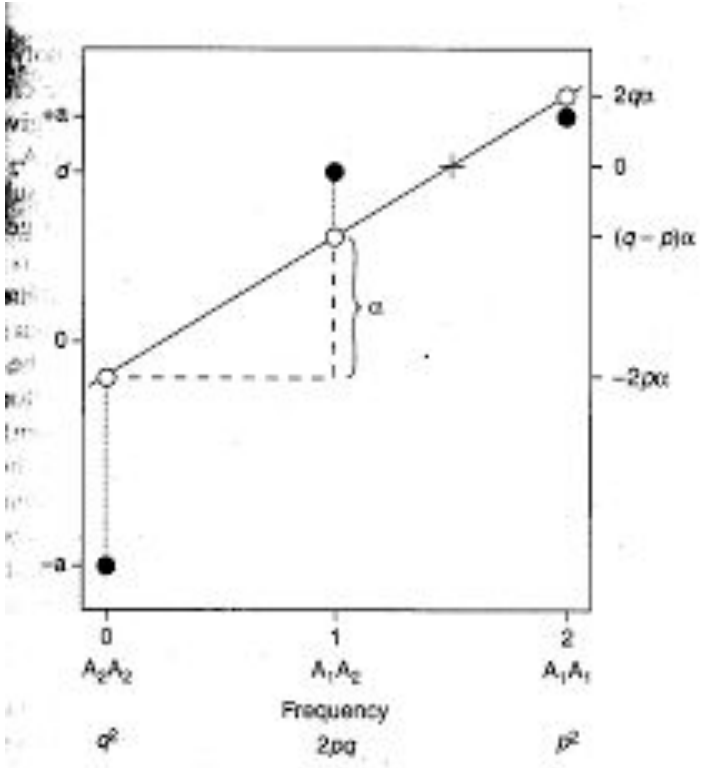
# Pedigree index

Parent average

$$1/2\ EBV_{sire} + 1/2\ EBV_{dam}$$

# ⚠ Allele substitution effect

The effect that the presence of a copy of an allele has on the phenotype (regarding the reference allele).




f(A)= mean(Aa)-mean(aa)

# Pleiotropy

the phenomenon in which a single locus affects two or more apparently unrelated phenotypic traits

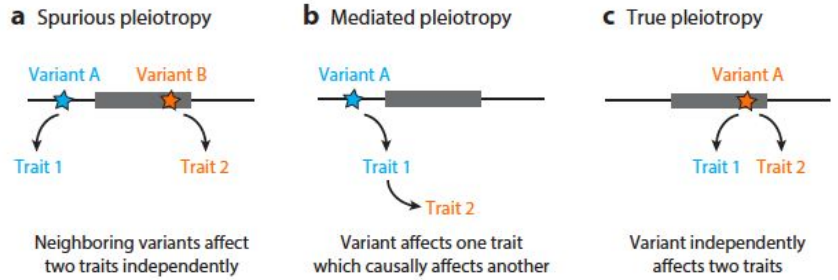



**Figure 4**

Diagrams illustrating (*a*) spurious pleiotropy, in which two neighboring, separately causal variants (*blue* and *orange stars*) are mistakenly inferred to be pleiotropic because they cannot be statistically distinguished; (*b*) mediated pleiotropy, in which a variant is statistically associated with two traits because it has a causal effect on one trait that in turn causally impacts another; and (*c*) true pleiotropy, in which a single unambiguous causal variant is separately biologically causal for two independent traits.

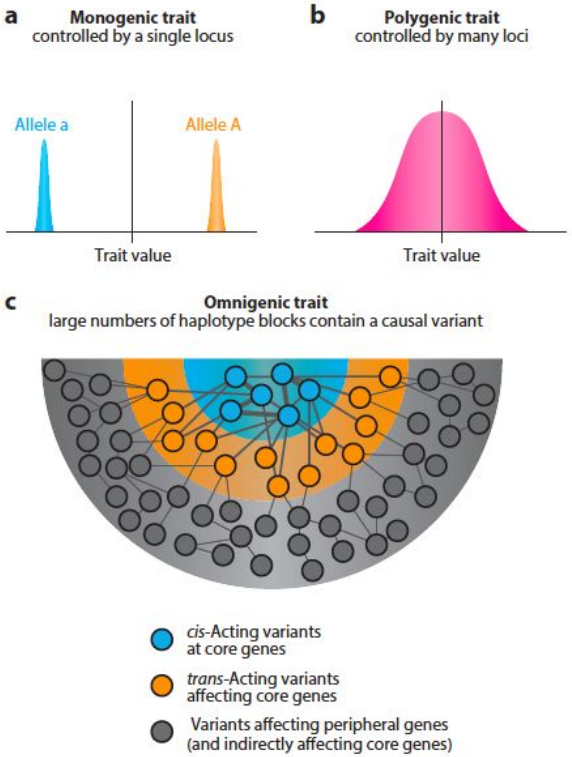


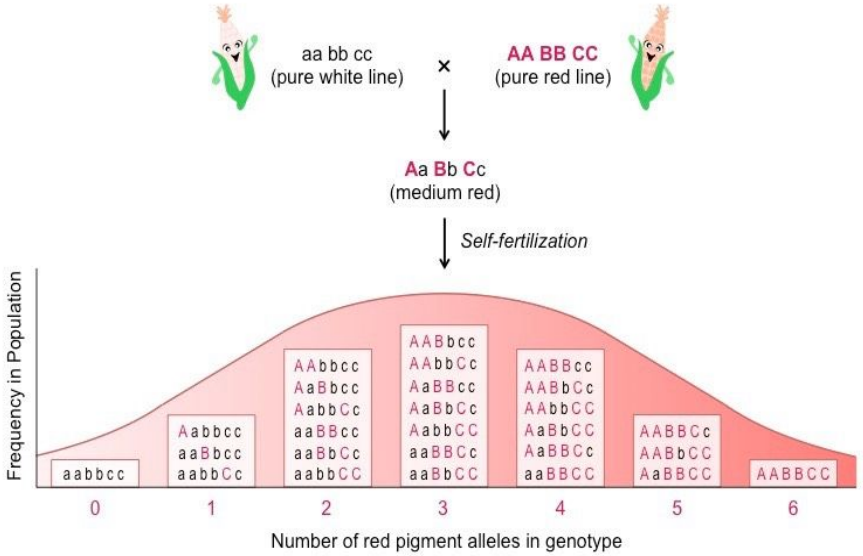

**Figure 1**

(*a*) A bimodal trait distribution for a monogenic trait controlled by a single genetic locus, as compared to (*b*) a continuous trait distribution for a polygenic trait controlled by many genetic loci. (*c*) Schematic of one possible architecture for an omnigenic trait, in which several large-effect *cis*-acting and many smaller-effect *trans*-acting variants modulate a set of core genes, as does a much larger ensemble of *cis*- and *trans*-acting variants impacting peripheral genes that only indirectly modulate the phenotype.

Genome-wide prediction

# Infinitesimal model

A quantitative trait is influenced by an infinitely large number of genes, each of which makes an infinitely small (infinitesimal) effect, as well as by environmental factors. Random sampling of alleles at each gene produces a continuous, normally distributed phenotype in the population (at least around the average of that of the individual's parents).

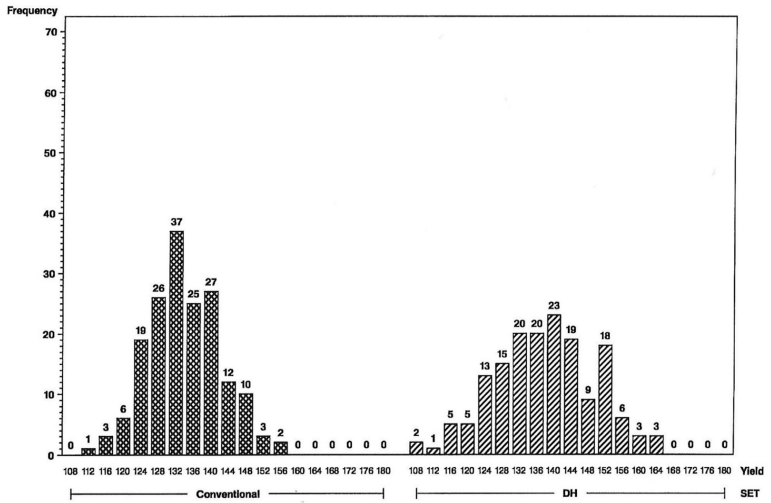



*Probability of j major alleles in k biallelic loci* $\Rightarrow$

$$\Rightarrow \binom{2k}{j} = \left(\frac{1}{2}\right)^{2k} \frac{2k!}{j!\,(2k-j)!}$$

# Genetic variance

Phenotype deviation from the mean phenotype caused by the combination of alleles inherited from parentals and these alleles independent effects on the specific phenotype

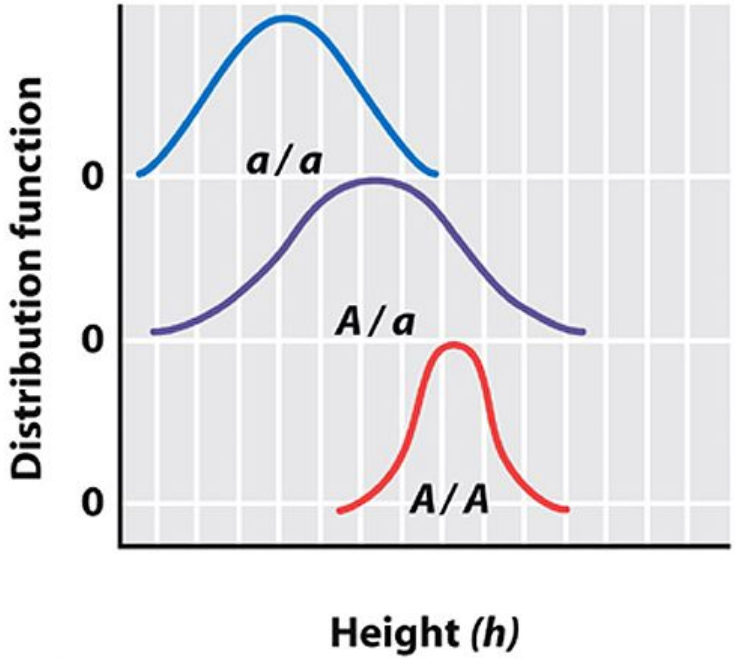



Genome-wide prediction

# Phenotype decomposition

Phenotype is affected by genetic (additive +dominance +epistasis), environment and their interactions.

$$P = G + E$$



# Heritability

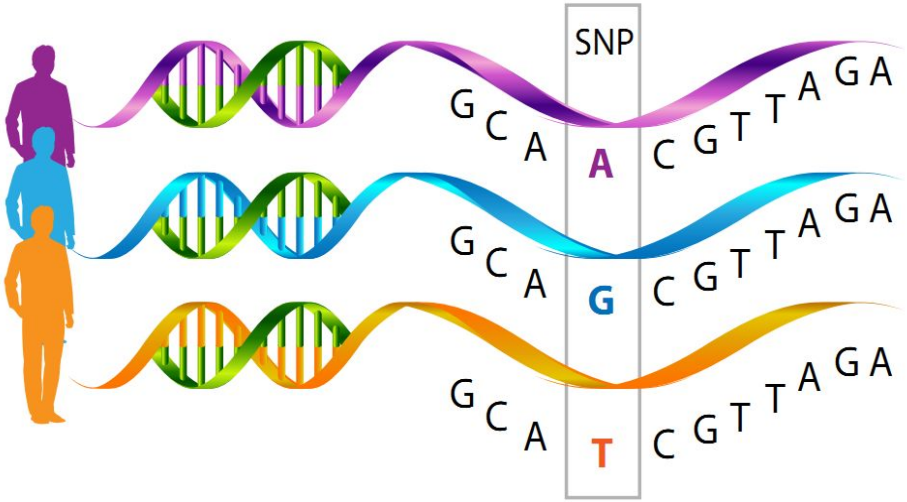
The amount of phenotypic (observable) variation in a population that is attributable to individual genetic differences

“Narrow and broad sense”

$$H^2 = \frac{V_g}{V_g + V_e}$$

# Genetic marker

DNA sequence with a known location on a chromosome that can be used to identify individuals or species. It can be described as a variation (which may arise due to mutation or alteration in the genomic loci) that can be observed



# Marker variance

Phenotype deviation from the mean phenotype caused by the inheritance of a particular allele from parentals and this allele's independent effect on the phenotype

| Notation | Variance component | Genotype coding |
|---|---|---|
| $V_A$ | $2pq[a + d(p - q)]^2$ | $x_A \in \{0, 1, 2\}$ |
| $V_D$ | $(2pqd)^2$ | $x_D \in \{0, 2p, 2(p - q)\}$ |
| $V'_D$ | $\frac{4pq^2}{1+q}(a + dq)^2$ | $x'_D \in \{0, 2, 2\}$ |
| $V'_A$ | $\frac{2p^2q}{1+q}(a - d)^2$ | $x'_A \in \{0, \frac{1-q}{1+q}, \frac{-2q}{1+q}\}$ |
| $V''_{AA}$ | computed numerically | $x''_{AA} \in (x_{A,1} - 1)(x_{A,2} - 1)$ |

# Genomic variance

The amount of variance explained by marker effects (<genetic variance, because of incomplete LD with QTLs or missingness)

$$
\begin{aligned}
Var(\beta' x_i) &= \beta' Cov(x_i, x_i') \beta \\
&= \beta' \Sigma_x \beta \\
&= \alpha' \Sigma_{zx} \Sigma_x^{-1} \Sigma_x \Sigma_x^{-1} \Sigma_{xz} \alpha \\
&= \alpha' \Sigma_{zx} \Sigma_x^{-1} \Sigma_{xz} \alpha
\end{aligned}
$$

# Genomic heritability

The proportion of variance of a trait that can be explained (in the population) by a linear regression on a set of markers

$$h_g^2 = \frac{\sigma_g^2}{\sigma_y^2} = \frac{\sigma_a^2}{\sigma_y^2}\frac{\sigma_g^2}{\sigma_a^2} = h^2\frac{\sigma_g^2}{\sigma_a^2}$$

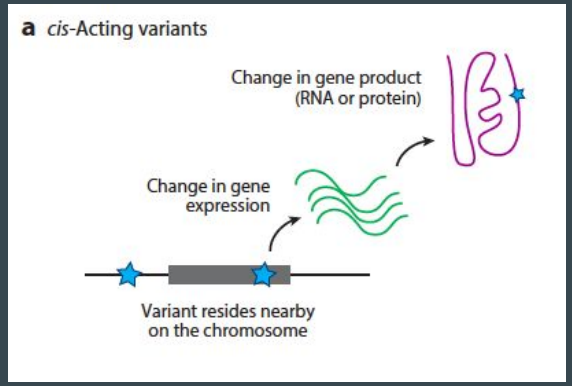
$h^2_g <= h^2$

# Missing heritability

The problem of missing heritability, that is to say the gap between heritability estimates from genotype data and heritability estimates from twin data

**The case of the missing heritability**

When scientists opened up the human genome, they expected to find the genetic components of common traits and diseases. But they were nowhere to be seen. Brendan Maher shines a light on six places where the missing loot could be stashed away.



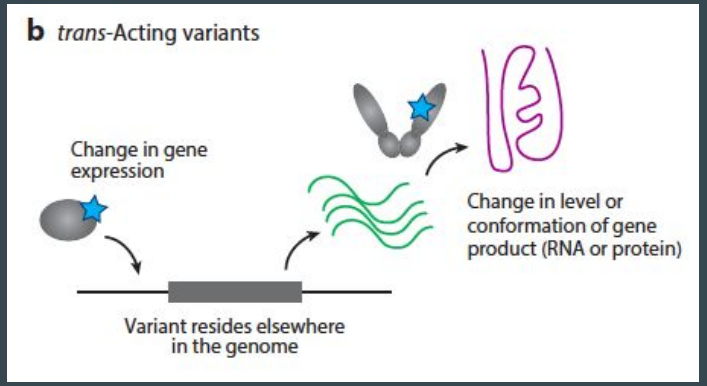
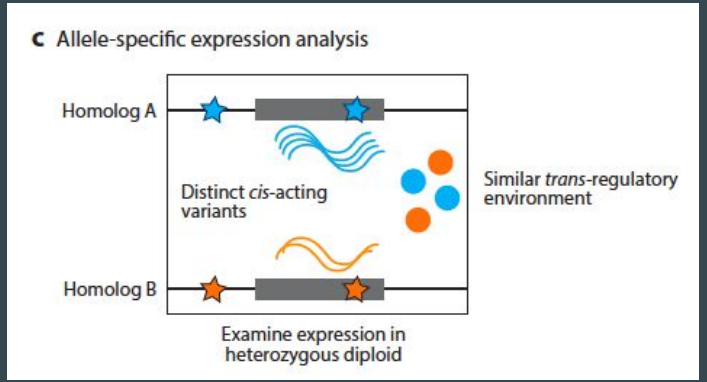




**Figure 2**

(*a*) *cis*-Acting variants that impact the expression of a gene immediately proximal on the chromosome. (*b*) *trans*-Acting variants that impact a gene product originating from a distal genetic locus. (*c*) Schematic of an experimental design to measure allele-specific mRNA levels. Due to the presence of both parental alleles in the $F_0$ heterozygote, *cis*-acting regulatory activity is inferred from differential expression of the messenger RNA attributable to one of the two homologous loci. This is because both homologs exist in an essentially equivalent *trans*-regulatory environment; any difference in abundance must therefore be due to a nearby *cis*-acting variant.




Jakobson and Jarosz, 2020