

# Building Blocks of Quantitative Genetics

## 1) Single gene model

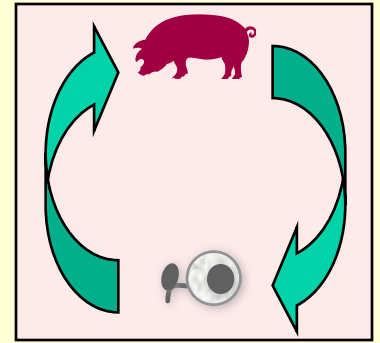
- effect of genotype on quantitative phenotype
- effect of a parent's genotype on quantitative phenotype of its progeny --- **breeding value**

## 2) Multiple gene model

- Functional model for quantitative phenotypes
- Breeding values
- Population distributions of  
phenotypes and breeding values

# Building Blocks of Quantitative Genetics

## Single gene model



$p$  = population gene frequency of B

$q$  = population gene frequency of b

Population Genotype Frequencies under random mating ( ➔ **Hardy Weinberg Equilibrium** )

		Eggs	
		B ( $p$ )	b ( $q$ )
Sperm	B ( $p$ )	$p^2$	$pq$
	b ( $q$ )	$pq$	$q^2$

# Genetic Value

= effect of an animal's genes on its **own** phenotypic value

Genotype	BB	Bb	bb
Average phenotype example	$P_{BB}$ 320	$P_{Bb}$ 310	$P_{bb}$ 280
HWE Frequency p=0.8	$p^2$ 0.64	$2pq$ 0.32	$q^2$ 0.04
Genetic value G = $g_{xy}$ -315.2*	$G_{BB}$ +4.8	$G_{Bb}$ -5.2	$G_{bb}$ -35.2

\* Population mean phenotype =  $p^2 P_{BB} + 2pq P_{Bb} + q^2 P_{bb} = 315.2$

Population mean G =  $p^2 G_{BB} + 2pq G_{Bb} + q^2 G_{bb} = 0$

# Genetic Value in Falconer Notation

(Falconer and Mackay, 1996)

Genotype	BB	Bb	bb
Average phenotype example	$P_{BB}$ 320	$P_{Bb}$ 310	$P_{bb}$ 280
Genetic value = $g_{xy}$ -mean	$G_{BB}$ +4.8	$G_{Bb}$ -5.2	$G_{bb}$ -35.2
Falconer genetic value	+a +20	d +10	-a -20

$a = \text{additive effect} = \frac{1}{2}(P_{BB} - P_{bb}) = +20$

= half the difference between two homozygotes

$d = \text{dominance effect} = P_{Bb} - \frac{1}{2}(P_{BB} + P_{bb}) = +10$

= deviation of heterozygote from homozygote mean

# Genetic Value in Falconer Notation

(Falconer and Mackay, 1996)

bb	0	Bb	BB
-a		d	+a

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$d = 0$       no dominance (additive gene)

$0 < d < a$       partial dominance

$d = a$       complete dominance

$d > a$       overdominance

# Breeding Value (BV)

= **2 x** average effect of animal's alleles on **progeny** phenotype

Parent has 2 alleles (e.g. Bb) but only one is (B/b) passed on to a progeny

**BV = effect of allele 1 + effect allele 2 on progeny phenotype**

## Average effect of allele B

Sperm	Egg	Frequ- ency	Progeny genotype	Genetic value	Mean genetic value progeny
<b>B</b>	<b>B</b>	<b>p</b> [.8]	<b>BB</b>	<b>G<sub>BB</sub></b> [ 4.8]	<b><math>\alpha_B = pG_{BB} + qG_{Bb}</math></b> <b>= .8(4.8) + .2(-5.2) = +2.8</b>
	<b>b</b>	<b>q</b> [.2]	<b>Bb</b>	<b>G<sub>Bb</sub></b> [-5.2]	

## Average effect of allele b

Sperm	Egg	Frequ- ency	Progeny genotype	Genetic value	Mean genetic value progeny
<b>b</b>	<b>B</b>	<b>p</b> [.8]	<b>Bb</b>	<b>G<sub>Bb</sub></b> [-5.2]	<b><math>\alpha_b = pG_{Bb} + qG_{bb}</math></b> <b>= .8(-5.2) + .2(-35.2) = -11.2</b>
	<b>b</b>	<b>q</b> [.2]	<b>bb</b>	<b>G<sub>bb</sub></b> [-35.2]	

# Breeding Value (BV)

Average effect of alleles

$$\alpha_B = pG_{BB} + qG_{Bb} = .8 (4.8) + .2 (-5.2) = +2.8$$

$$\alpha_b = pG_{Bb} + qG_{bb} = .8 (-5.2) + .2 (-35.2) = -11.2$$

Breeding value = Sum of average effects

$$BV_{BB} = \alpha_B + \alpha_B = (+2.8) + (+2.8) = +5.6$$

$$BV_{Bb} = \alpha_B + \alpha_b = (+2.8) + (-11.2) = -8.4$$

$$BV_{bb} = \alpha_b + \alpha_b = (-11.2) + (-11.2) = -22.4$$

14

14

'Value' of each copy of B = +14

$$= \alpha_B + \alpha_b = \alpha$$

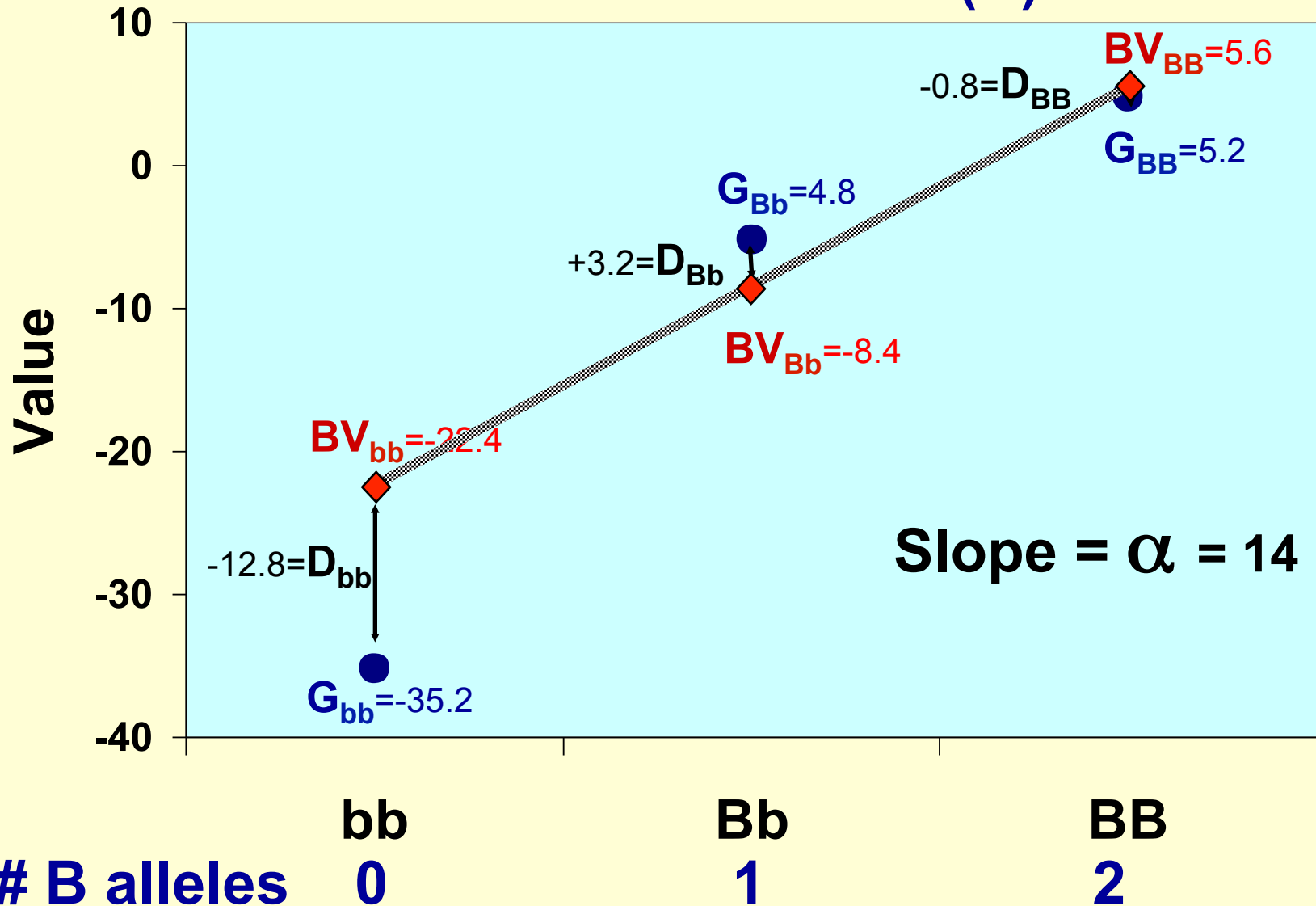
= allele substitution effect

Additive  
effect of genes

Genetic value (G)

Breeding value (BV)

Dominance value (D)  $D=G-BV$





<b>Genotype</b>	<b>BB</b>	<b>Bb</b>	<b>bb</b>
<b>Average phenotype</b> example	$P_{BB}$ 320	$P_{Bb}$ 310	$P_{bb}$ 280
<b>Frequency</b> $p=0.8$	$p^2$ 0.64	$2pq$ 0.32	$q^2$ 0.04
<b>Genetic value</b> $G=g_{xy}-\text{Mean}$	$G_{BB}$ +4.8	$G_{Bb}$ -5.2	$G_{bb}$ -35.2
<b>Breeding value</b> $BV=\alpha_x+\alpha_y$	$BV_{BB}$ +5.6	$BV_{Bb}$ -8.4	$BV_{bb}$ -22.4
<b>Dominance value</b> $D=G-BV$	$D_{BB}$ -0.8	$D_{Bb}$ +3.2	$D_{bb}$ -12.8

Genotype	BB	Bb	bb
Average phenotype example	$g_{BB}$ 320	$g_{Bb}$ 310	$g_{bb}$ 280
Frequency p=0.8	$p^2$ 0.64	$2pq$ 0.32	$q^2$ 0.04
Genetic value $G=g_{xy}$ -Mean	$G_{BB}$ +4.8	$G_{Bb}$ -5.2	$G_{bb}$ -35.2
Breeding value $BV=\alpha_x+\alpha_y$	$BV_{BB}$ +5.6	$BV_{Bb}$ -8.4	$BV_{bb}$ -22.4
Dominance value $D=G-BV$	$D_{BB}$ -0.8	$D_{Bb}$ +3.2	$D_{bb}$ -12.8

**Population variance** =  $\sum$  frequency \* (value-mean)<sup>2</sup>

**Additive genetic variance**

$$\sigma_A^2 = p^2 * BV_{BB}^2 + 2pq * BV_{Bb}^2 + q^2 * BV_{bb}^2 = 2pq\alpha^2 = 62.72$$

**Dominance variance**

$$\sigma_D^2 = p^2 * D_{BB}^2 + 2pq * D_{Bb}^2 + q^2 * D_{bb}^2 = (2pqd)^2 = 10.24$$

**Total genetic variance**

$$\sigma_G^2 = p^2 * G_{BB}^2 + 2pq * G_{Bb}^2 + q^2 * G_{bb}^2 = \sigma_A^2 + \sigma_D^2 = 72.96$$

# Building Blocks of Quantitative Genetics

## 1) Single gene model

- effect of genotype on quantitative phenotype
- effect of a parent's genotype on quantitative phenotype of its progeny --- breeding value

## 2) Multiple gene model

- Functional model for quantitative phenotypes
- Breeding values
- Population distributions of  
phenotypes and breeding values

# Building Blocks of Quantitative Genetics

## Multiple gene models

Quantitative phenotype is affected by  
many genes plus environment

$$P = \mu + G + E$$

$\mu$  = mean (systematic environmental effects)

$G$  = collective genetic value of *all* genes

=  $\sum G_i$        $G_i$  = Genetic value of  $i^{\text{th}}$  gene

$E$  = collective effect of all environmental factors

# Multiple gene models

$$P = \mu + G + E$$

$$P = \mu + \underbrace{BV + D + I}_{G} + E$$

**BV** = collective **breeding value** of *all* genes

$$= \sum BV_i \quad BV_i = \text{Breeding value for } i^{\text{th}} \text{ gene}$$

**D** = collective **dominance value** of *all* genes

$$= \sum D_i \quad D_i = \text{Dominance value for } i^{\text{th}} \text{ gene}$$

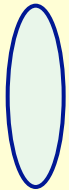
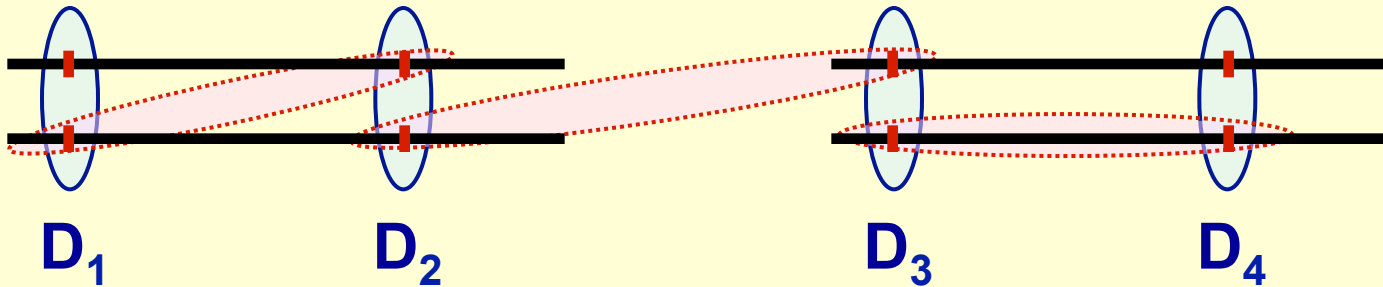
**I** = collective effect of **epistatic interactions**  
among genes

$$= \sum I_{ij} \quad I_{ij} = \text{Interaction between genes } i \text{ and } j$$

# Dominance vs. Epistasis

Chromosome pair 1  
gene 1      gene 2

Chromosome pair 2  
gene 3      gene 4

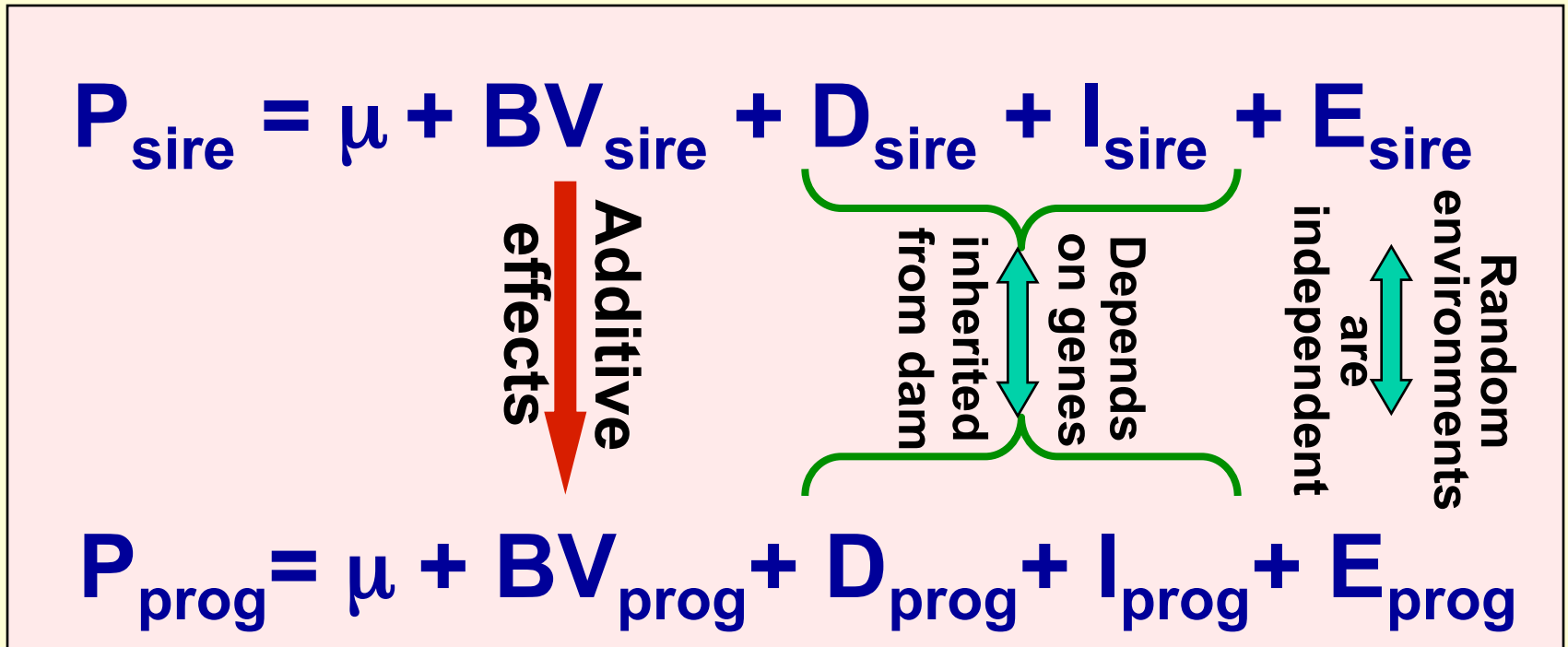


**Dominance** = interaction between alleles  
at the **same** locus/gene



**Epistasis** = interaction between alleles  
at the **different** loci/genes

# How does a Parent's phenotype relate to phenotype of its Progeny?

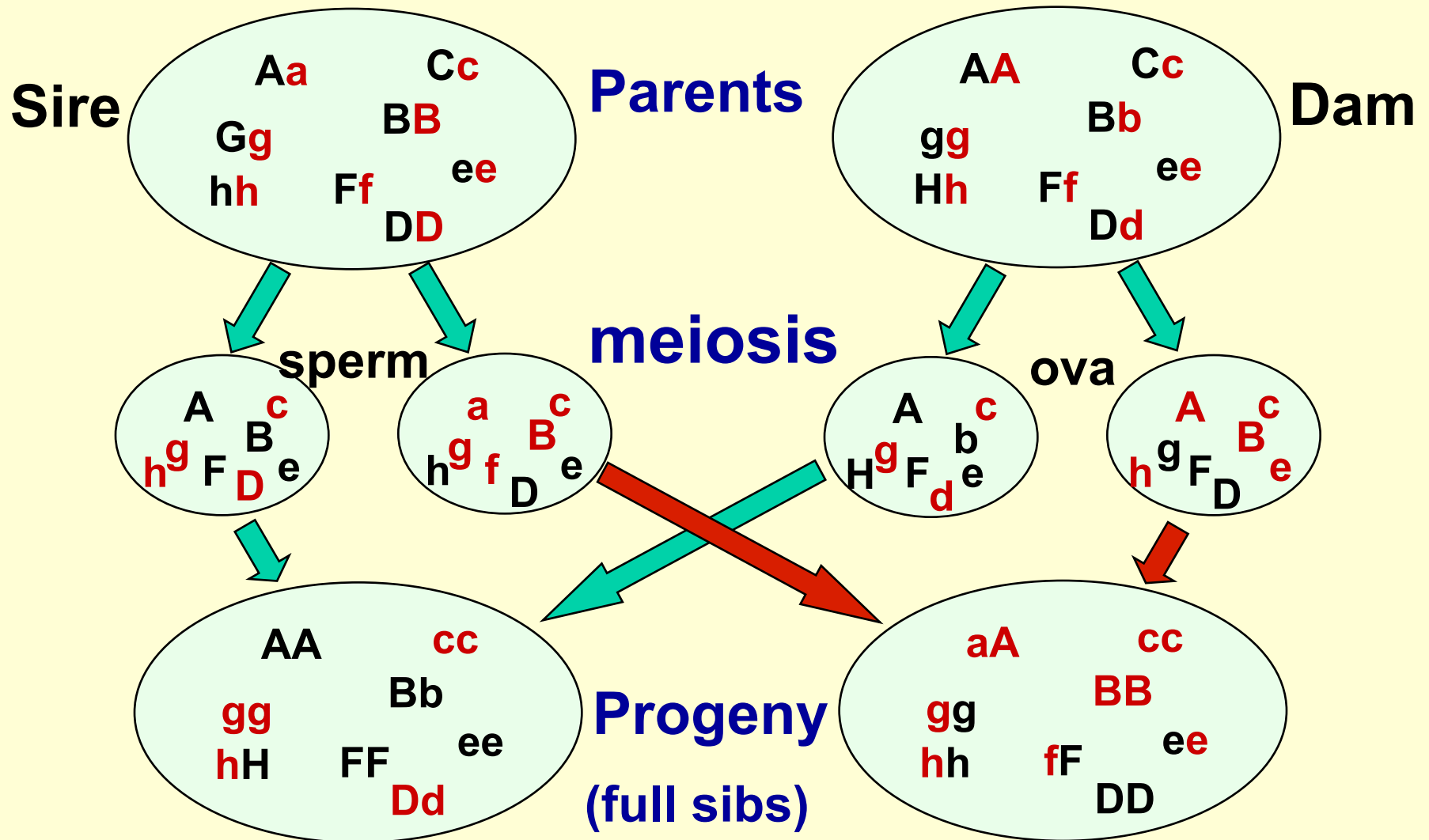


**Only Additive Effects of genes (=Breeding Value) are transmitted from a parent to its progeny**

(regardless of mating)

**Dominance and Epistatic effects depend on mating**

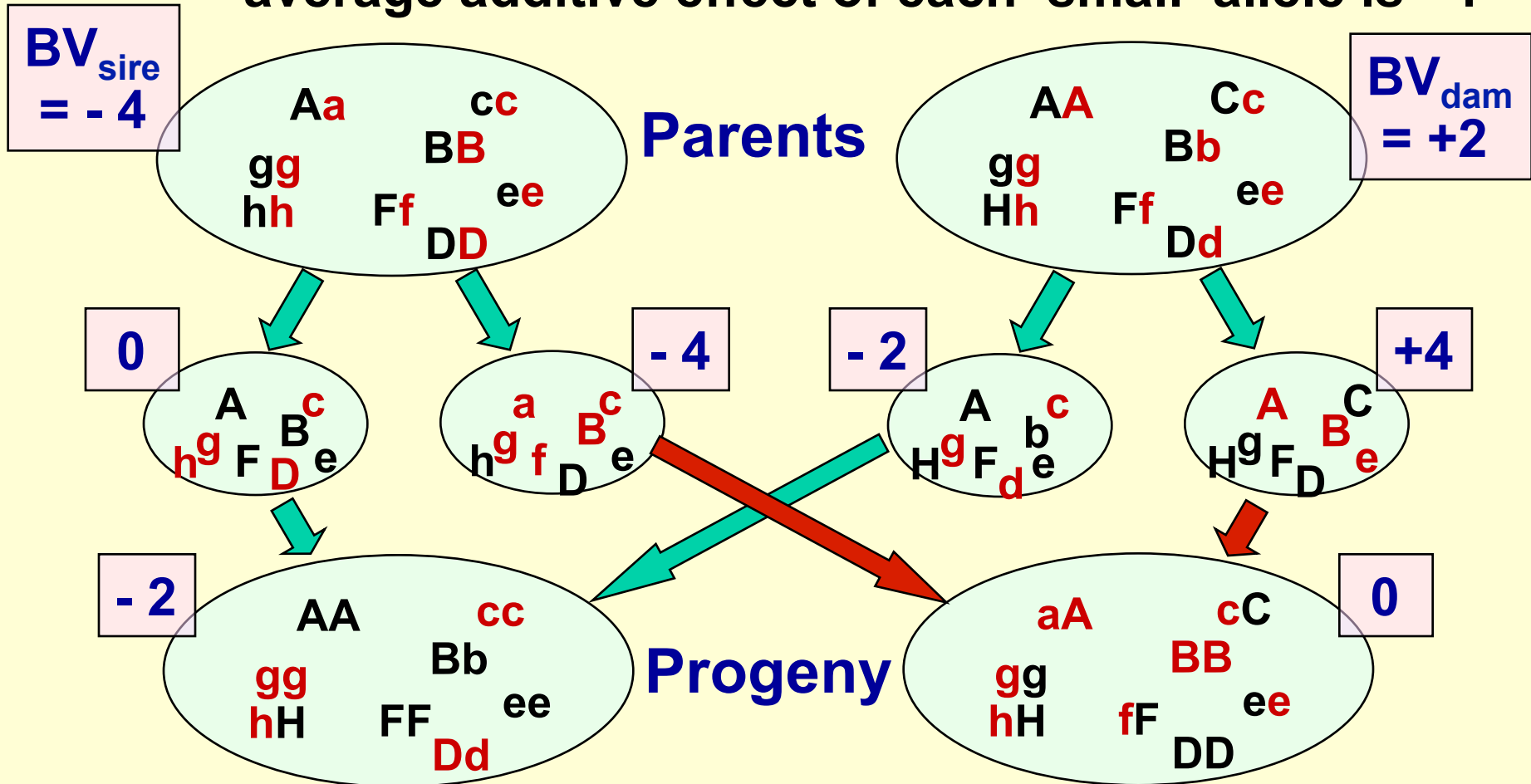
# Parents pass a sample half of their alleles to progeny





# Parents pass a sample half of their Breeding Value to progeny

E.g.: average additive effect of each capital allele is +1  
 average additive effect of each small allele is -1



# Relationship between BV of parents and progeny

**Average** value of sample  
half of genes from

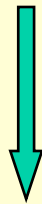
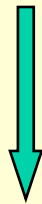
**sire**

**dam**

Mendelian sampling  
(Random Assortment)  
effect from

**sire**

**dam**



$$BV_{\text{prog}} = \underbrace{\frac{1}{2}BV_{\text{sire}} + \frac{1}{2}BV_{\text{dam}}}_{\text{Increased by using parents with high BV}} + \underbrace{RA_{\text{sire}} + RA_{\text{dam}}}_{\text{Random and uncontrollable}}$$

Increased by using  
parents with high BV  
Common to full sibs

Random and  
uncontrollable  
Differs between full sibs

# Quantitative Trait Parameters

$$P = \mu + BV + D + I + E$$
$$\sigma_P^2 = \sigma_A^2 + \sigma_D^2 + \sigma_I^2 + \sigma_E^2$$

## Heritability in the BROAD sense $H^2$

= fraction of phenotypic variance due to genetics

$$H^2 = \frac{\sigma_A^2 + \sigma_D^2 + \sigma_I^2}{\sigma_P^2} = \frac{\sigma_G^2}{\sigma_P^2}$$

## Heritability in the NARROW sense $h^2$

= fraction of phenotypic variance due to **additive** genetics

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2}$$

# Population Variances

$$P = \mu + BV + D + I + E$$

$$\sigma_P^2 = \sigma_A^2 + \sigma_D^2 + \sigma_I^2 + \sigma_E^2$$

Phenotypic  
variance

Additive  
genetic  
variance

Dominance  
variance

Epistatic  
variance

Environ-  
mental  
variance

Genetic  
variance

$$\sigma_G^2 = \sigma_A^2 + \sigma_D^2 + \sigma_I^2$$

$$G = BV + D + I$$

# Between and Within Family Variances

$$\mathbf{BV}_{\text{prog}} = \mathbf{1/2BV}_{\text{sire}} + \mathbf{1/2BV}_{\text{dam}} + \mathbf{RA}_{\text{sire}} + \mathbf{RA}_{\text{dam}}$$

$$\sigma_A^2 = \mathbf{1/4\sigma_A^2} + \mathbf{1/4\sigma_A^2} + \mathbf{1/4\sigma_A^2} + \mathbf{1/4\sigma_A^2}$$

Between  
sire  
variance

Between  
dam  
variance

Within family  
additive variance

# Correlations between Traits

## Phenotypic correlation ( $r_p$ )

= correlation between phenotypes for traits 1 and 2 observed on the same individuals

Causes for existence of a phenotypic correlation:

- 1) Some genes can have effects on both traits  
= Pleiotropy

→ genetic correlation ( $r_g$ )

- 2) Some environmental factors can affect both traits

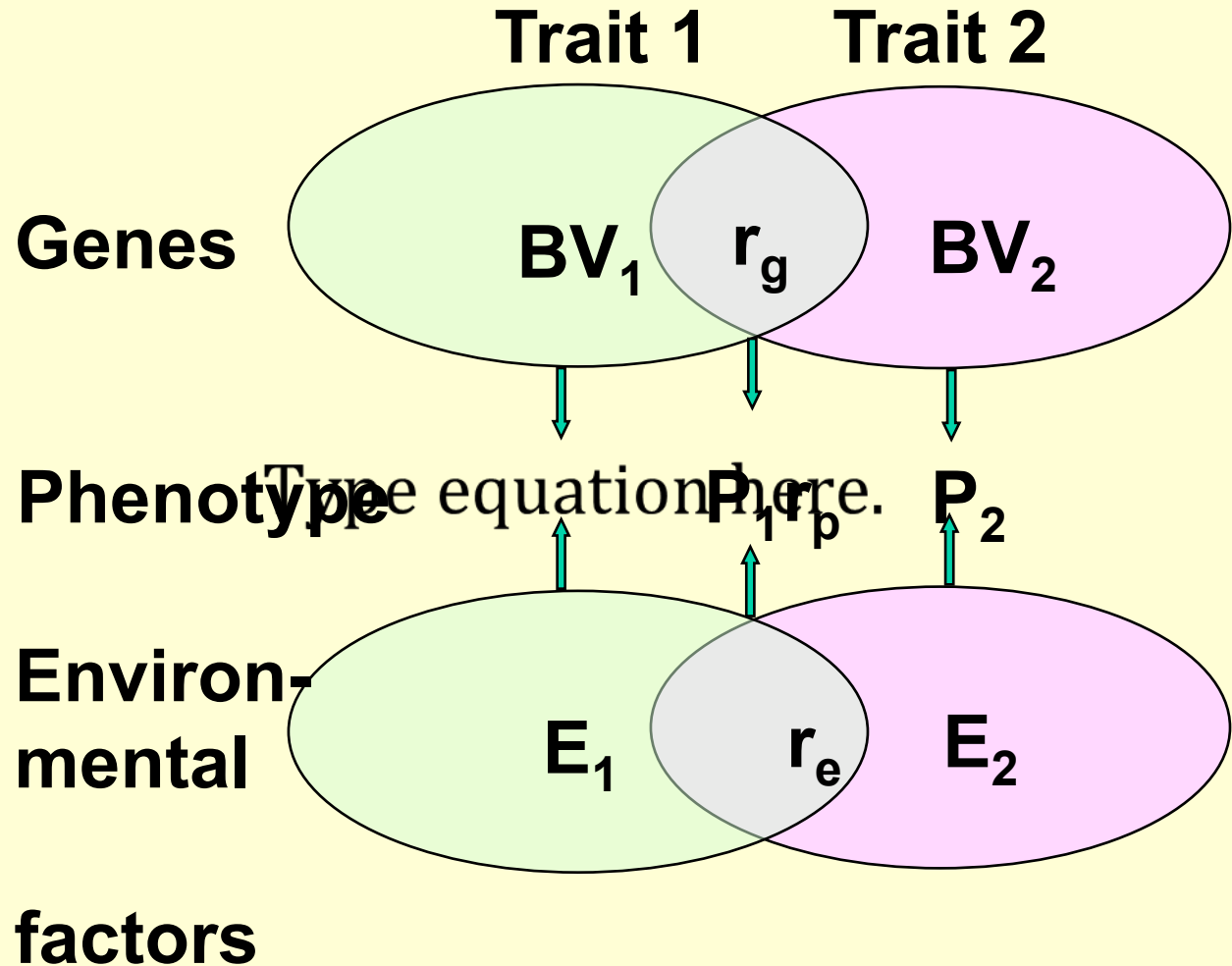
→ environmental correlation ( $r_e$ )

# Correlations between Traits

$$r_g = \frac{\text{Cov}(BV_1, BV_2)}{\sigma_{BV_1} \sigma_{BV_2}}$$

$$r_P = \frac{\text{Cov}(P_1, P_2)}{\sigma_{P_1} \sigma_{P_2}}$$

$$r_E = \frac{\text{Cov}(E_1, E_2)}{\sigma_{E_1} \sigma_{E_2}}$$



# (Additive) Genetic Relationship

$a_{xy}$  = additive genetic relationship  
between  $x$  and  $y$

$a_{xy}$  = fraction of genes  $x$  and  $y$  share due  
to common ancestry

= probability that a randomly chosen allele  
at a locus (gene) in  $y$  is also present in  $x$

$a_{\text{parent-offspring}} = 1/2$  Parent passes on half of its genes

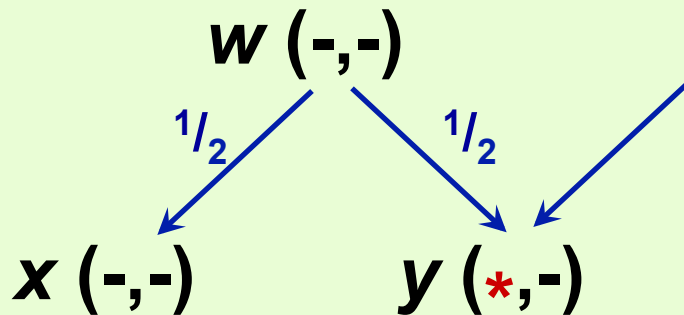
$a_{\text{grandparent-offspring}} = 1/4$  Grand sire  $\xrightarrow{1/2}$  Sire  $\xrightarrow{1/2}$  Progeny



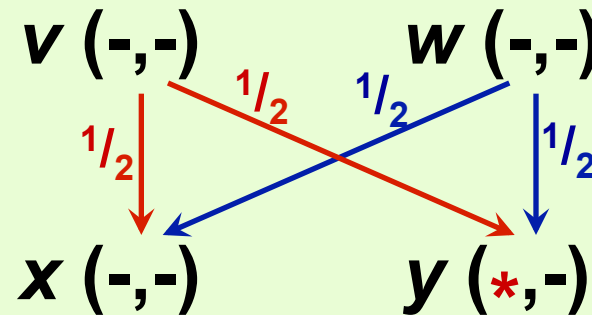
# (Additive) Genetic Relationship

$a_{xy}$  = fraction of genes  $x$  and  $y$  share due to common ancestry  
= probability that a randomly chosen allele at a locus (gene) in  $y$  is also present in  $x$

$$a_{\text{half-sibs}} = \frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$$

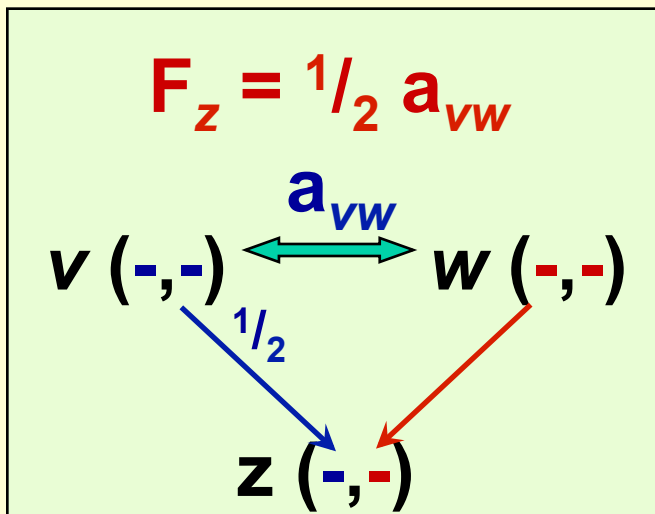


$$a_{\text{full-sibs}} = 2\left(\frac{1}{2} \times \frac{1}{2}\right) = \frac{1}{2}$$



# Coefficient of Inbreeding

$F_z$  = probability that, for a random locus, the allele  $z$  received from its sire is **identical by descent** to the allele  $z$  received from its dam  
=  $1/2$  of the genetic relationship between the sire and dam of  $z$



$$\begin{aligned} a_{zz} &= 1 + F_z \\ &= 1 + 1/2 a_{vw} \end{aligned}$$

# Coefficients of Inbreeding for simple pedigrees

Mating (non- inbred parents)		$a_{\text{parents}}$	$F_{\text{progeny}}$
sire	x daughter	$1/2$	$1/4$
sire	x grand-daughter	$1/4$	$1/8$
half-sib	x half-sib	$1/4$	$1/8$
full-sib	x full-sib	$1/2$	$1/4$
clone	x clone	1	$1/2$

**Assumes parents are themselves NOT inbred**

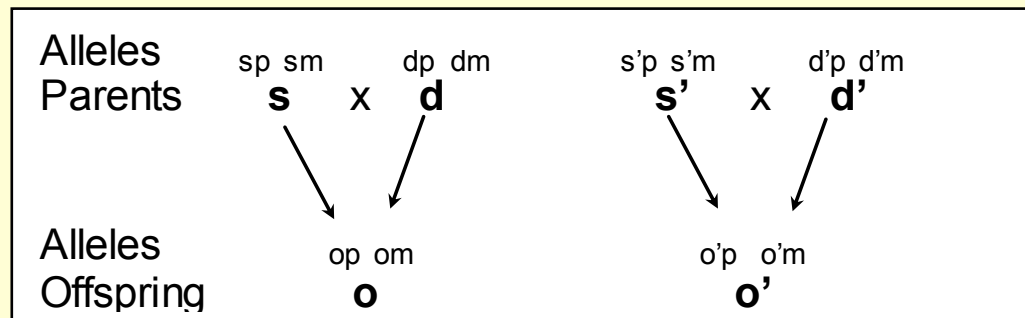
## Are two alleles the same? Identity By State (IBS) versus Identity By Descent (IBD)

- **IBS**: if we can genotype individuals  $o$  and  $o'$  for this locus (QTL), then we can directly determine whether the alleles the two individuals carry are indeed the same
  - if they are the same, this is referred to as the alleles being **IBS**.
- **IBD**: if we cannot genotype the locus (ie. the usual case), then we cannot determine IBS directly but, if  $o$  and  $o'$  have a **common ancestor**, then we can determine the **probability** that the two alleles are identical because they may have originated from a common ancestor

### IBD probabilities from pedigree:

$$\text{Prob}(o_p \text{ is IBD to } o'_p) = P(o_p \equiv o'_p)$$

= **probability that alleles  $o_p$  and  $o'_p$  originated from the same allele of the common ancestor**



### Example IBD probabilities, coefficients of coancestry and additive and dominance coefficients

Individual $o - o'$	IBD probabilities for pairs of alleles				Coancestry coefficient	Additive relationship coefficient	Dominance relationship coefficient
	$o_p - o'_p$	$o_m - o'_m$	$o_p - o'_m$	$o_m - o'_p$			
Sire( $o$ ) – Offspring( $o'$ )	$\frac{1}{2}$	0	0	$\frac{1}{2}$	$\frac{1}{4}$	$\frac{1}{2}$	0
Dam – Offspring	0	$\frac{1}{2}$	$\frac{1}{2}$	0	$\frac{1}{4}$	$\frac{1}{2}$	0
Paternal half-sibs	$\frac{1}{2}$	0	0	0	$\frac{1}{8}$	$\frac{1}{4}$	0
Full sibs	$\frac{1}{2}$	$\frac{1}{2}$	0	0	$\frac{1}{4}$	$\frac{1}{2}$	$\frac{1}{4}$
Identical twins	1	1	0	0	$\frac{1}{2}$	1	1

**Example IBD probabilities, coefficients of coancestry and additive and dominance coefficients**

Individual o – o'	IBD probabilities for pairs of alleles				Coancestry coefficient	Additive relationship coefficient	Dominance relationship coefficient
	op–o'p	om–o'm	op–o'm	om–o'p			
Sire(o) – Offspring(o')	1/2	0	0	1/2	1/4	1/2	0
Dam – Offspring	0	1/2	1/2	0	1/4	1/2	0
Paternal half-sibs	1/2	0	0	0	1/8	1/4	0
Full sibs	1/2	1/2	0	0	1/4	1/2	1/4
Identical twins	1	1	0	0	1/2	1	1

**Some side notes:**

**Coefficient of coancestry** (also coeff. of kinship or consanguinity) between **o** and **o'**

=  $f_{oo'}$  = probability that an allele drawn at random from **o** is IBD to an allele drawn random from **o'**  
 = average of the 4 possible IBD probabilities between alleles at **o** and **o'**

$r_{oo'}$  =  $2f_{oo'}$  = **coefficient of relationship = additive genetic relationship coefficient**

**NOTE:**  $f_{oo'}$  is also equal to the **coefficient of inbreeding** of a progeny produced by **o** and **o'**  
 = probability that an individual's alleles are IBD