Inheritance

D3.2 · SL and HL

Two similar parents can have a different-looking offspring

Explain transmission before predicting a phenotype

Shared D3.2: controlled crosses, alleles and phenotypes, dominance patterns, human examples, pedigrees, continuous variation and box plots.

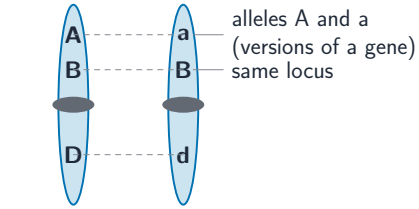
AHL: segregation and dihybrid crosses, database loci, linked phase, recombination and chi-squared tests.

Crosses, families and samples are invented teaching models. Probabilities do not prescribe an offspring sequence.

Track a locus through gametes and fertilization

1. **Diploid parent.** Two homologues normally carry two copies of an autosomal locus. AA and aa are homozygous; Aa is heterozygous.
2. **Gametes.** A normal gamete receives one member of each pair and one **allele** at each ordinary autosomal locus.
3. **Fertilization.** Two haploid contributions restore the diploid complement. Alleles are variants of one gene, not unrelated genes because letters differ.

Homologous chromosomes



a homologous pair
(same length, same genes)

One from each parent

Control the pollen source before interpreting offspring

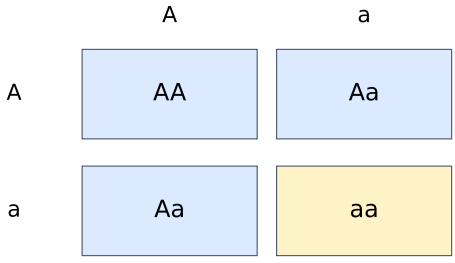
1. **Before release.** Where appropriate remove anthers before self-pollen release; protect a receptive stigma from unintended pollen.
2. **Cross.** Apply selected pollen, label parents and use bagging and suitable controls.
3. **Generations.** P parents produce F1; suitable F1 crosses or selfings produce F2. These names alone do not guarantee homozygous parents.

Separate the inherited information from a measured outcome

Example	**Interpretation**
Ordinary ABO type	Relatively simple genetic contribution in the model
Injury scar	Acquired environmental consequence
Height	Many genes and environment interact
Sun / shade leaves	One **genotype** can develop differently in different conditions
Plasticity	Expression or development changes without requiring a base-sequence change

Read four possible combinations, not four compulsory children

Aa × Aa: four equally likely combinations



Genotypes 1 : 2 : 1; phenotypes 3 : 1

AA and Aa share the dominant phenotype in this model.

An expectation is not a fixed family count

1. **Aa × Aa.** AA:Aa:aa = 1:2:1; dominant:recessive = 3:1 under complete dominance.
2. **Twenty offspring.** Expected aa count = $20 \times 1/4 = 5$; actual counts can differ.
3. **Two specified offspring.** Independent fertilizations: $(1/4) \times (1/4) = 1/16$ for both aa. A previous result does not force the next.

Use a test cross to compare possible parental genotypes

1. **AA × aa.** All Aa under the ordinary model.
2. **Aa × aa.** Half Aa and half aa; a recessive offspring supports a heterozygous parent.
3. **Limit.** A small all-dominant sample does not prove AA. Dominant does not mean common, healthy or stronger.

Connect an enzyme change with an environmental intervention

1. **Normal conversion.** Phenylalanine hydroxylase helps convert phenylalanine to tyrosine.
2. **Reduced activity.** Phenylalanine can accumulate and harm development; phenylalanine is also an essential amino acid.
3. **Inheritance and environment.** Carrier $\times$ carrier predicts $1/4$ affected per pregnancy in the recessive model. Dietary management can alter consequences without changing the **genotype**.

A population has several alleles; one individual has two

Type	**Ordinary-model genotypes**
A	$I^A I^A$ or $I^A i$
B	$I^B I^B$ or $I^B i$
AB	$I^A I^B$; both antigen features
O	ii
Dominance	I^A and I^B codominant; each dominates i

Compare two ABO crosses using the actual gametes

1. **Heterozygote A × heterozygote B.** $I^A i \times I^B i$ gives A, B, AB and O each with probability $1/4$.
2. **AB × O.** $I^A I^B \times ii$ gives half type A and half type B.
3. **Limit.** A population can carry more than two alleles at a locus. A SNP need not cause disease, and one diploid person normally has only two autosomal copies.

An intermediate phenotype does not permanently blend alleles

Model	**Heterozygote and offspring**
Mirabilis red / white	Heterozygote pink: incomplete dominance
Pink $\times$ pink	Red:pink:white $= 1{:}2{:}1$
Alleles	Segregate; red and white can reappear
Ordinary ABO AB	Distinguishable contributions of both alleles: codominance
Complete dominance	Heterozygote resembles one homozygote for the defined trait

State the conditioning group for a haemophilia probability

1. **Parents.** $X^H X^h \times X^H Y$ in the simplified X-linked recessive model.
2. **Four equally likely outcomes.** $X^H X^H$, $X^H X^h$, $X^H Y$, $X^h Y$.
3. **Denominator.** Affected sons: $1/2$ of sons, or $1/4$ of all offspring if X/Y-bearing fertilizations are equally likely.

A father transmits different chromosomes to sons and daughters

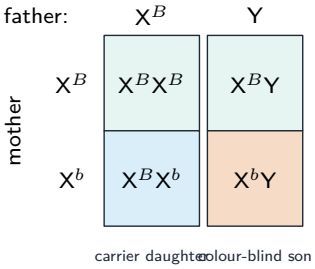
Do not turn the teaching grid into a universal claim about females

In the ordinary XX/XY model, father gives X to daughters and Y to sons; direct father-to-son transmission of his X-linked allele is absent.

X carries more genes than Y; a Y symbol does not supply an alternative haemophilia allele.

Females can have haemophilia and heterozygotes can have bleeding symptoms, including through X-inactivation. The simplified model has limits.

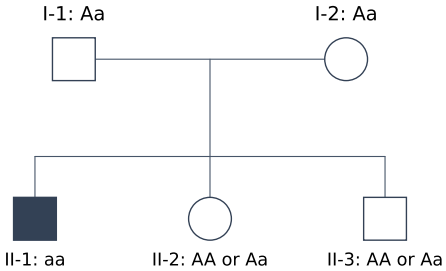
An X-linked cross



> Sons get their X from their mother

Name the relationship and symbol before inferring a genotype

Invented family: test an autosomal recessive model



Square: male; circle: female; filled: affected

Fully penetrant autosomal recessive model; no new mutation.

Condition on an unaffected sibling rather than all offspring

1. **Parents.** An aa child of two unaffected parents requires Aa $\times$ Aa under the stated model.
2. **Unaffected possibilities.** AA, Aa, Aa: two of three are carriers. Conditional probability $= 2/3$.
3. **Reasoning.** Model choice from family patterns is induction; required genotypes follow deductively once the model and assumptions are accepted.

A small pedigree can fit more than one biological mechanism

Keep the model separate from its conditional deductions

An affected child of unaffected parents contradicts a simple fully penetrant dominant model without new mutation; real families may involve new variants or incomplete penetrance.

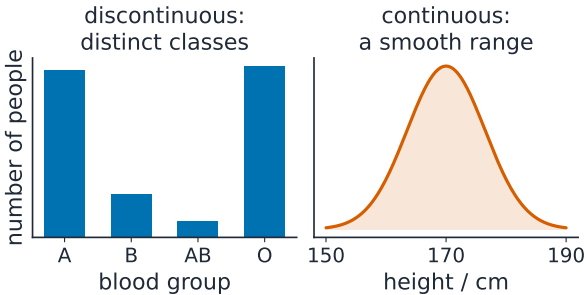
Missing affected sons in a small family does not prove X linkage. Male-to-male transmission argues against ordinary direct X linkage.

Close relatives may share a rare recessive allele from common ancestry. Increased homozygous risk does not mean every child must be affected.

Compare measures of centre for an invented height sample

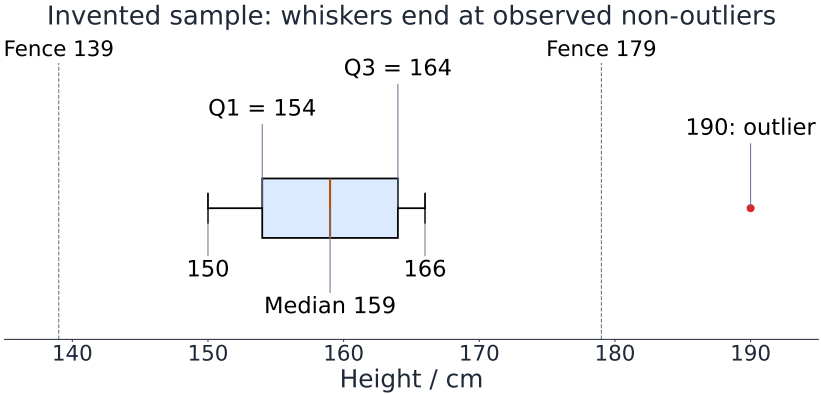
1. **Data / cm.** 150, 152, 154, 156, 158, 160, 162, 164, 166, 190.
2. **Calculate.** Sum 1612; mean 161.2 cm. Middle two are 158 and 160: median 159 cm. No mode.
3. **Interpret.** The high observation affects the mean more than the median. Rounding height does not change its underlying continuous nature.

Discontinuous and continuous variation



Many genes and the environment give continuous variation

Separate quartiles, fences and observed extremes



The maximum is 190 cm; the upper whisker is 166 cm.

Use the stated quartile convention and the actual observations

1. **Median of halves.** Q1 = 154, Q3 = 164 cm; IQR = 10 cm.
2. **Fences.** $154 - 15 = 139$; $164 + 15 = 179$ cm. The 190 cm observation lies beyond the upper fence.
3. **Whiskers.** Most extreme observed non-outliers: 150 and 166 cm. A fence is not automatically a whisker endpoint; retain the underlying data.

Each cell combines one gamete from each parent

AaBb × AaBb: independent assortment model

	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AaBb
Ab	AABb	AAbb	AaBb	Aabb
aB	AaBB	AaBb	aaBB	aaBb
ab	AaBb	Aabb	aaBb	aabb
	A_B_: 9	A_bb: 3	aaB_: 3	aabb: 1

Independent assortment and complete dominance give $9:3:3:1$.

Explain the ratio from meiosis and fertilization

1. **Gametes.** Segregation separates alleles. Independent orientation of different chromosome pairs gives AB, Ab, aB and ab each 1/4.
2. **F2.** AaBb $\times$ AaBb gives 16 equally likely combinations: 9 A_B_, 3 A_bb, 3 aaB_, 1 aabb.
3. **Different outcome.** AaBb **genotype** has probability 1/4, not 9/16. AaBb $\times$ aabb instead gives 1:1:1:1 under independence.

An expected phenotype ratio has biological assumptions

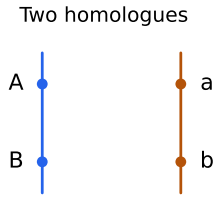
1. **Counts.** For 160 F2 offspring: 90, 30, 30 and 10 expected in the four classes.
2. **Assumptions.** Independent assortment, complete dominance at both loci, random fertilization and no relevant survival or scoring bias.
3. **Physical map.** Distant loci on one chromosome can behave approximately independently. A 50% recombination result does not prove different chromosomes.

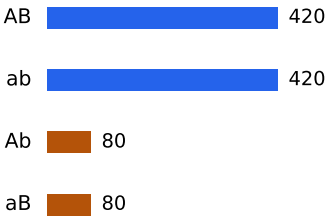
Check organism, assembly, locus and product together

Human loci	Database-backed comparison
ABO / HBB	Chromosomes 9 / 11; glycosyltransferase / beta-globin
APOE / APOC1	Nearby chromosome 19 loci; apolipoprotein E / C-I
GRCh38 APOE	44,905,796–44,909,393
GRCh38 APOC1	44,914,325–44,919,346
Limit	Coordinates alone do not specify a universal recombination frequency

Read parental phase before counting recombinants

Invented coupling-phase test cross: AB/ab × ab/ab





160 / 1000 = 16% recombinant

Parental AB and ab differ from recombinant Ab and aB.

Recover the gametes from a coupling-phase test cross

1. **Invented cross.** AB/ab $\times$ ab/ab: 420 AaBb, 420 aabb, 80 Aabb, 80 aaBb.
2. **Frequency.** Recombinants $= 80 + 80 = 160$ of 1000, giving 16%. Gametes AB 42%, ab 42%, Ab 8%, aB 8%.
3. **Phase and limit.** Repulsion Ab/aB reverses parental identities. Recombinant frequency is not the fraction of meioses with any crossover; multiple events can be hidden.

Compute expected counts from the stated null prediction

1. **Invented F2.** Observed 90, 34, 26, 10; null 9:3:3:1; expected 90, 30, 30, 10.
2. **Statistic.** $\chi^2 = 0 + 16/30 + 16/30 + 0 \approx 1.067$; four fully specified categories give df $= 3$.
3. **Decision.** Below critical 7.815 at 5%: do not reject. This does not prove the ratio uniquely true or assign 95% probability to the null.

A test cross can reject independence without proving every assumption

1. **Null.** The 420, 420, 80, 80 test cross predicts 250 in each class under independence.
2. **Calculate.** $\chi^2 = 4(170^2/250) = 462.4$, above 7.815: reject 1:1:1:1.
3. **Interpret.** Known phase and unbiased outcomes support linkage. In real investigations consider scoring and survival bias; use independent counts with adequate expected sizes.

Attempt the handout before revealing the numerical checks

Start with parentage, model, gametes and phenotype key

Explain controlled plant crosses, phenotype plasticity, PKU, ABO, incomplete dominance, X linkage and conditional pedigree inference.

Calculate centres, quartiles, fences and observed whiskers. Compare continuous characteristics with discrete categories.

AHL: derive dihybrid ratios, inspect named loci, analyse linked phase and use a chi-squared decision with bounded conclusions.

Check the shared probabilities and descriptive statistics

1. **Monohybrid / X linkage.** Expected aa among twenty $= 5$; two specified aa $= 1/16$. Affected X-linked probability: $1/2$ of sons, $1/4$ of all offspring.
2. **Pedigree.** Unaffected parents of aa child: Aa and Aa. Carrier probability conditional on unaffected $= 2/3$.
3. **Height.** Mean 161.2, median 159, no mode; quartiles 154/164, IQR 10; fences 139/179; whiskers 150/166; maximum 190 cm.

AHL answers: phase and a second chi-squared sample

1. **Practice linkage.** 360, 360, 140, 140: recombinants $280/1000 = 28\%$; AB/ab each 36%, Ab/aB each 14%.
2. **Phase check.** The same counts called repulsion give 72% recombinants, strongly conflicting with the maximum expected 50%. Sample proportions fluctuate; investigate assumptions.
3. **Practice F2.** 100, 20, 30, 10 versus 90, 30, 30, 10: $\chi^2 = 40/9 \approx 4.444 < 7.815$; do not reject at 5%.

Check yourself

A probability needs a model and a denominator

Genotype is not phenotype; dominance is not allele frequency. An expected ratio does not force the next offspring outcome.

Identify the conditioning group in pedigrees and X-linked probabilities. Distinguish box-plot fences from observed whiskers.

AHL: write phase before identifying recombinants. Give expected counts, degrees of freedom, decision and limitations for chi-squared.