Natural selection

D4.1 · SL and HL

An environment can favour an existing inherited difference

Connect variation, differential reproduction and transmission

Shared D4.1: selection, mutation and sexual variation, competition, abiotic pressures, fitness, heritability, sexual selection and guppy evidence.

AHL: gene pools, real human allele data, three selection patterns, Hardy–Weinberg calculations and deliberate breeding.

Numerical plant models are invented. Endler's published guppy means are real source data, not examination questions.

Explain change without giving plants an intention

1. **Inherited variation.** Plants differ in root depth; some of the difference is inherited.
2. **Pressure and contribution.** During a drought, some obtain more water and leave more viable, fertile offspring.
3. **Transmission.** Contributing alleles can become more frequent. The drought need not instruct an individual to produce a useful allele.

A theory supplies a tested explanatory framework

Selection is a mechanism rather than a promise of perfection

Darwin explained how differential survival and reproduction can produce evolutionary change. Selection contributed to biodiversity over immense timescales.

The selection framework differed from simply inheriting acquired improvements through use and disuse. A paradigm shift replaces an influential explanatory framework.

A scientific theory does not graduate into a law. Modern evolution includes mechanisms besides selection; a changed average alone does not identify the cause.

Separate the origin of alleles from new combinations

Process	Contribution and limit
Mutation	Can create new alleles; useful changes are not induced by need
Crossing over	Recombines alleles between homologous chromosomes
Assortment	Produces different combinations at suitably unlinked loci
Fertilization	Combines gametes; does not explain every new allele

Visible differences are not automatically inherited DNA differences

Ask what was inherited and what environment contributed

Deep roots may reflect genotype, soil conditions or an interaction. Selection acts on phenotypes; evolutionary response requires a heritable contribution.

Mutation can occur before or during pressure. Random with respect to need does not mean equal mutation probability at every site.

Sexual reproduction reshuffles existing variation; a useful phenotype is not evidence that an organism chose a mutation.

Resource competition can occur without fighting

1. **Potential increase.** Many more seeds can be produced than establish and reproduce.
2. **Shared requirements.** Same-species plants compete for water, light, minerals and space; reproductive adults may compete for mates.
3. **Selective condition.** Mortality alone is insufficient. A heritable difference must affect contribution to later generations for that feature to respond evolutionarily.

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A density-independent event can still discriminate among genotypes

State a pressure, a feature and the reproductive consequence

Frost or drought can affect a population without depending on crowding. Genotypes can still differ in their physiological response.

Predators, pathogens and competitors also affect success. A trait's advantage depends on the particular environment.

Reduced stomatal opening conserves water but restricts carbon dioxide entry. Deep roots consume resources that could support other growth or reproduction.

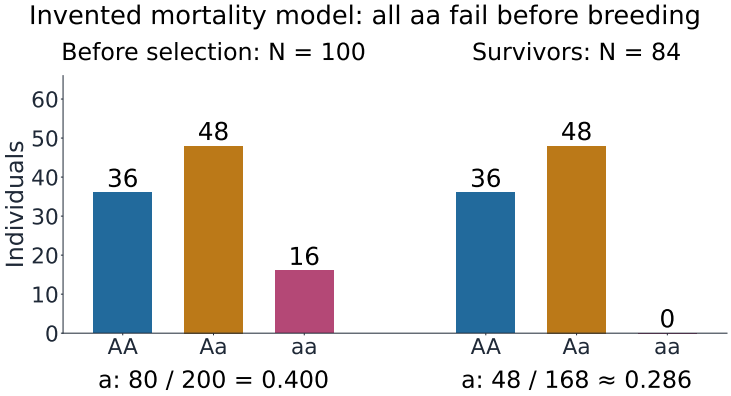
Compare offspring contribution per equivalent starting parent

1. **Invented comparison.** Twenty parents of each genotype: 60 versus 40 offspring reach the defined reproductive stage.
2. **Calculation.** Mean contributions 3 versus 2 per parent. Relative fitness, with first set to one: 1 versus $2/3 \approx 0.667$.
3. **Evaluation.** Raw totals mislead when starting numbers differ. Survival, lifespan or strength alone do not measure reproductive contribution.

Design a test that separates family and growing conditions

1. **Common conditions.** Compare offspring from contrasting parents at comparable ages in controlled soil and water conditions.
2. **Independent replication.** Use independent families and replicate pots. One family in one pot confounds family with pot conditions.
3. **Stronger inference.** Reciprocal environments test interactions. Common conditions do not remove every parental effect; connect inheritance with function and reproductive success.

Count copies again after mortality changes the population



A changed denominator matters; survivors are not yet a new generation.

Track both copies in each ordinary diploid genotype

1. **Before.** AA 36, Aa 48, aa 16; $N = 100$. $A = 120/200 = 0.60$; $a = 80/200 = 0.40$.
2. **Survivors.** All aa fail: $N = 84$. $A = 120/168 = 5/7$; $a = 48/168 = 2/7 \approx 0.286$.
3. **Transmission.** No surviving genotype changed. Equal gamete contribution alone need not lower a again; continuing selection or another process is needed for systematic further change.

Keep percentage points separate from relative percentage change

1. **Invented records.** 90, then 120, then 140 of 200 copies: 45%, 60%, 70%.
2. **Different comparisons.** $45 \to 60$ is $+15$ percentage points; relative increase $= 15/45 \times 100 \approx 33.3\%$. The next rise is $+10$ percentage points.
3. **Causation.** Migration, drift, sampling and changed population boundaries can also alter records. Frequency change alone does not uniquely establish selection.

Mating advantage and survival cost can act in different directions

Bird-of-paradise plumage and courtship provide a context

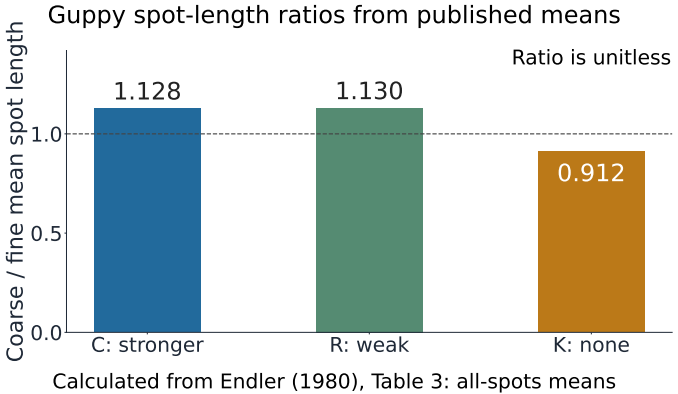
Mate choice and competition can change mating or fertilization success. Inherited traits associated with greater contribution can spread.

Elaborate plumage and display consume resources and may increase predator exposure. The most conspicuous male need not always leave most offspring.

Preferences and environments vary. Control background, illumination and other cues when evaluating mate responses; do not infer an intentional inherited colour change.

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Compare gravel effects within each predator regime



Coarse/fine ratios exceed one with predators and fall below one without.

Interpret a descriptive ratio before claiming a mechanism

1. **Published data.** Endler (1980), Table 3 all-spots means; stronger C, weaker R, no-predator K regimes.
2. **Pattern.** C 1.128; R 1.130; K 0.912. Mean spot length relates differently to gravel background without predators.
3. **Evaluation.** Pond, not each fish, is the independent treatment unit. Ratios alone give no significance test or unique causal explanation; control allocation and measurement matter.

Inheritance explains how variation persists rather than blending away

Neo-Darwinism connects selection with genetics

A gene pool comprises genes and alleles present in a population. It is not one individual's genotype or only the common alleles.

Selection changes contributions linked to heritable differences. Mutation, gene flow and drift can also change allele frequencies.

Population boundaries matter: pooling distinct groups can hide variation and alter observed genotype proportions.

Use the same variant, allele orientation and dataset

1000 Genomes phase 3 group	**Ensembl rs671 allele-copy record**
CHB: Han Chinese in Beijing	A 33; G 173; A frequency $33/206 \approx 0.1602$
CEU: Utah, NW European ancestry	G 198; no A observed; A frequency $0/198$
Denominators	206 and 198 allele copies, not people
Interpretation	Sample contrast does not uniquely distinguish selection from demographic history

Geographical separation can restrict gene flow without complete isolation

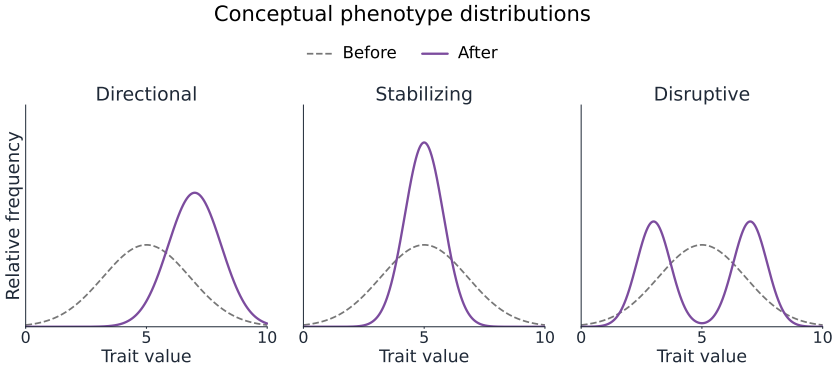
A finite sample is not an entire country or ancestry category

Record rs671, the A/G allele orientation, release, group, count and denominator before comparing. Do not mix releases or denominators.

These are sampled groups. Zero observed copies does not establish complete absence; human populations exchange genes and vary internally.

Frequency differences can reflect selection, drift, gene flow and population history. Additional evidence is needed to identify the mechanism.

A stable mean can hide a change in variation



Phenotype distributions do not directly report allele frequencies.

Predict distributional change without promising a new species

Pattern	**Model outcome and limit**
Directional	One end favoured; mean can shift until costs or conditions change
Stabilizing	Intermediate favoured; **variation** can narrow with little mean change
Disruptive	Both ends favoured; two peaks can develop
Boundary	Disruption alone does not guarantee reproductive isolation or speciation

Combine independent gamete probabilities

Independent gametes combine at random

	A: 0.70	a: 0.30
A: 0.70	AA: 0.49	Aa: 0.21
a: 0.30	Aa: 0.21	aa: 0.09

AA 0.49 + Aa 0.42 + aa 0.09 = 1.00

Equal drawn boxes show outcomes, not equal probabilities.

Separate allele identity from equilibrium prediction

1. **Alleles.** At a two-allele locus $p + q = 1$, even when genotype proportions do not fit equilibrium.
2. **Random gametes.** AA p^2; Aa $pq + qp = 2pq$; aa q^2. For $p = 0.70$, $q = 0.30$: 0.49, 0.42, 0.09.
3. **Expected counts.** $N = 1000$ gives 490, 420, 90. Dominant phenotype frequency is 0.91, not $p = 0.70$; dominance does not mean commonness.

Breeding need not change the survivors' allele frequencies again

1. **Survivor pool.** A $= 5/7$; a $= 2/7$.
2. **Random combinations.** AA $= 25/49$; Aa $= 20/49$; aa $= 4/49$ before further selection.
3. **Distinction.** Genotype proportions can change while the allele frequencies remain $5/7$ and $2/7$. Square-root inference from recessive phenotype requires the model assumptions.

State ideal conditions before interpreting a fit

Condition	Reason and boundary
Random mating	Supports expected gamete combinations
No relevant selection	Genotypes contribute equally in the ideal model
No mutation or gene flow	No new or imported allele-frequency change
Very large population	Drift negligible; finite observed counts can fluctuate

Count directly before testing expected proportions

1. **Observed genotypes.** AA 40, Aa 20, aa 40; N = 100. A = (80 + 20)/200 = 0.50; a = 0.50.
2. **Expected.** Random-combination products give 0.25, 0.50, 0.25, not observed 0.40, 0.20, 0.40.
3. **Evaluate.** Inbreeding or subdivision may explain heterozygote deficit. Selection is not uniquely proven; model agreement also cannot prove every assumption true.

Human influence is broader than deliberate parent selection

Distinguish chosen breeding from an altered environment

Artificial selection chooses breeding parents with desired heritable features, such as crop yield or an animal characteristic, over generations.

Antibiotic exposure unintentionally selects resistant bacteria. It alters the environment rather than deliberately choosing and mating resistant parents.

Reduced diversity, harmful recessives, correlated costs and environmental dependence can limit breeding outcomes. Desired traits are not universally beneficial.

Work through the complete handout questions

Build a chain, compute a comparison, evaluate the evidence

Shared questions connect mutation, competition, pressure, fitness, heritability, sexual selection and population copy counts.

Practice fitness: ten parents per group leave 50 versus 30 offspring at the defined stage. Compute contribution and relative fitness.

AHL: use the real database denominator; contrast selection patterns; infer frequencies under Hardy–Weinberg and explain a genotype-model mismatch.

Check the shared numerical comparisons

1. **Fitness.** $50/10 = 5$; $30/10 = 3$. Relative fitness 1 and $3/5 = 0.60$.
2. **Frequency.** $90/200 = 45\%$; $120/200 = 60\%$; $140/200 = 70\%$. Changes $+15$ and $+10$ percentage points; first relative rise 33.3%.
3. **Survivors.** A $120/168 \approx 0.714$; a $48/168 \approx 0.286$. Individual genotypes remain unchanged.

AHL practice: recessive phenotype and expected genotype counts

1. **Model assumption.** Recessive phenotype 9% gives $q^2 = 0.09$ only under the stated model; $q = 0.30$, $p = 0.70$.
2. **Predictions.** AA 0.49, Aa 0.42, aa 0.09; $N = 1000$ gives 490, 420, 90; dominant phenotype 910.
3. **Direct counts.** Known genotypes give allele frequencies directly without equilibrium. A heterozygote deficit alone does not name its cause.

Check yourself

Use the population, denominator and assumptions named by the question

Link heritable variation, pressure, reproductive contribution and transmission. Separate individual acclimatization from population evolution.

Distinguish percentage points from relative change, a survival benefit from total fitness, and a descriptive pattern from a unique causal demonstration.

AHL: keep gene pools, allele frequencies, genotype proportions and phenotypes distinct; state assumptions before square-root calculations.