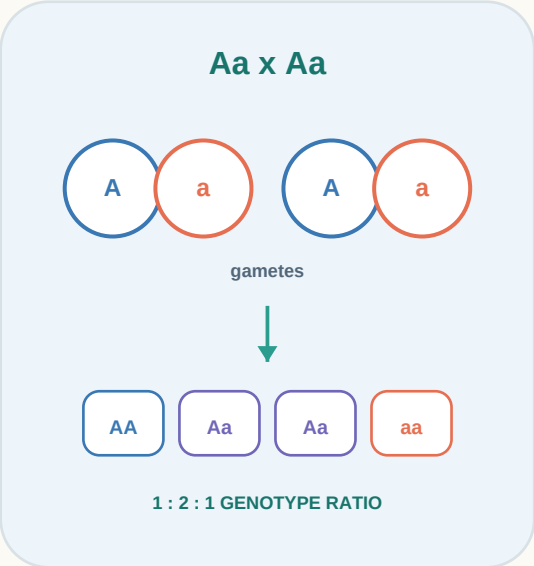
AP BIOLOGY | UNIT 5

TOPIC 5.3

Mendelian Genetics

Mendelian genetics connects allele separation during meiosis with predictable genotype and phenotype probabilities in offspring.



THE CORE CAUSAL CHAIN

ALLELE PAIR
one copy from each parent

→

SEGREGATION
alleles separate

→

GAMETES
one allele per gene

→

FERTILIZATION
pairs restored

BY THE END, YOU SHOULD BE ABLE TO...

1. Apply segregation and independent assortment.
2. Predict genotype and phenotype probabilities.
3. Evaluate inheritance models using evidence.

CENTRAL IDEA

Inheritance ratios are probabilities, not guarantees. They arise because alleles segregate into gametes and reunite randomly at fertilization.

1 Mendel's laws connect meiosis to inheritance

Segregation explains one gene at a time; independent assortment applies to unlinked genes and generates multiple gamete combinations.

TWO FOUNDATIONAL LAWS

LAW OF SEGREGATION

Aa produces which gametes?

The two alleles for one gene separate during gamete formation.

A | a

INDEPENDENT ASSORTMENT

AaBb produces which gametes?

When genes are unlinked, allele pairs assort independently.

AB | Ab | aB | ab

MONOHYBRID CROSS: Aa x Aa

	A	a
A	AA	Aa
a	Aa	aa

GENOTYPE RATIO 1 : 2 : 1

1 AA : 2 Aa : 1 aa

PHENOTYPE RATIO 3 : 1

3 dominant phenotype : 1 recessive phenotype

COMMON ERROR

A dominant allele is not necessarily common, stronger, or better. Dominance describes the heterozygote phenotype, not an allele's frequency or value.

2 Models and data test inheritance hypotheses

Probability predicts expected outcomes; test crosses, pedigrees, and chi-square analysis compare those predictions with evidence.

PROBABILITY RULES

PRODUCT RULE

AND -> multiply

Use when independent events must both occur.

SUM RULE

OR -> add

Use when mutually exclusive outcomes can each satisfy the event.

THREE WAYS TO EVALUATE A MODEL

TEST CROSS

Cross A_ with aa. A 1:1 phenotype ratio supports Aa; all dominant offspring supports AA.

PEDIGREE

Track a phenotype across generations to infer likely genotypes and inheritance patterns.

CHI-SQUARE

Compare observed and expected counts to test whether deviations may be due to chance.

CHI-SQUARE WORKFLOW

OBSERVED COUNTS -> EXPECTED COUNTS -> sum (O - E)^2 / E

COMPARE THE RESULT WITH A CRITICAL VALUE USING df = categories - 1

INTERPRETATION

A small difference between observed and expected data may result from sampling chance. A sufficiently large chi-square value leads you to reject the proposed inheritance model; it does not prove a particular alternative model.