

## **Contents**

<b>Transmission Genetics</b>	<b>2</b>
<b>Single-Gene Traits</b>	<b>5</b>
<b>Population Genetics</b>	<b>6</b>
<b>Quantitative Genetics</b>	<b>9</b>
<b>Cytogenetics</b>	<b>10</b>
<b>Molecular Genetics</b>	<b>14</b>
<b>Plant Breeding</b>	<b>16</b>
<b>Animal Breeding and Biotechnology</b>	<b>17</b>
<b>Wildlife</b>	<b>19</b>

# Transmission Genetics

## Alleles

- **Lethal** – homozygous recessive die in utero or after birth
- **Multiple** – dominance indicated by > or =

“Pairs of alleles separate cleanly in gamete formation, and have equal chance of being transmitted to any one gamete”

## Dominance

- **Backcross** –  $F_1 \times$  parent
- **Testcross**
  - ❖ Crossed with a homozygous recessive
  - ❖ Progeny's phenotypic ratio = other parent's genotypic ratio

	Heterozygote Appears...	F <sub>2</sub> Phenotypes	Example
Complete	AA	3:1	Polled cattle
Co	Intermediate	1:2:1	Roan cattle
Incomplete	Blend	1:2:1	Long legs: short legs: 'bulldog' calf

## Characteristics

- Pedigrees represent the inheritance of a characteristic
- Referencing
  - ❖ Roman numeral = generation
  - ❖ Number = individual

## Autosomal

### Dominant

- Doesn't skip generations
- Affected have affected parent(s)
- Affected parents can produce normal offspring
- Equal number of M and F are affected

### Recessive

- Can skip generations
- Often appears when unaffected relatives mate
- Affected parents produce affected offspring
- Carrier parents can produce affected offspring
- Equal number of M and F are affected

## X-Linked

### Dominant

- Affected have affected parent(s)
- Affected M transmits to:
  - ❖ All daughters
  - ❖ No sons
- More F affected

### Recessive

- More M affected:
  - ❖ Affected F X Normal M = all affected sons
  - ❖ Carrier F X Normal M =  $\frac{1}{2}$  affected sons
- F are often carriers
- Affected parents produce affected offspring

## Independent Assortment

“The segregation of one pair of alleles is independent to the segregation of other pairs of alleles at other loci”

### Double Heterozygotes (AaBb)

- **9:3:3:1** dihybrid ratio
- Testcross – 1:1:1:1 (AB: Ab: aB: ab) gamete ratio
- **Three Events**
  - ❖ Gene 1 segregates 3:1
  - ❖ Gene 2 segregates 3:1
  - ❖ Independent assortment

$$\chi^2_{\text{Classes}-1} = \sum \frac{(O - E)^2}{E}$$

	YR	Yr	yR	yr	Total
<b>Observed</b>	315	101	108	32	556
<b>Expected (9:3:3:1)</b>	312.75	104.25	104.25	34.75	556

$$\begin{aligned} \chi^2_1(\text{Independence}) &= \chi^2_3(9:3:3:1) - \chi^2_1(Y:y \ 3:1) - \chi^2_1(R:r \ 3:1) \\ &= 0.470 - 0.0096 - 0.346 \\ &= 0.1144 \\ P &= 0.7 - 0.8 \end{aligned}$$

### Epistasis

- **Epistasis** – the genotype at one locus inhibits the phenotype produced by the genotype at a separate locus
- Occurs when both genes control the same phenotypic trait

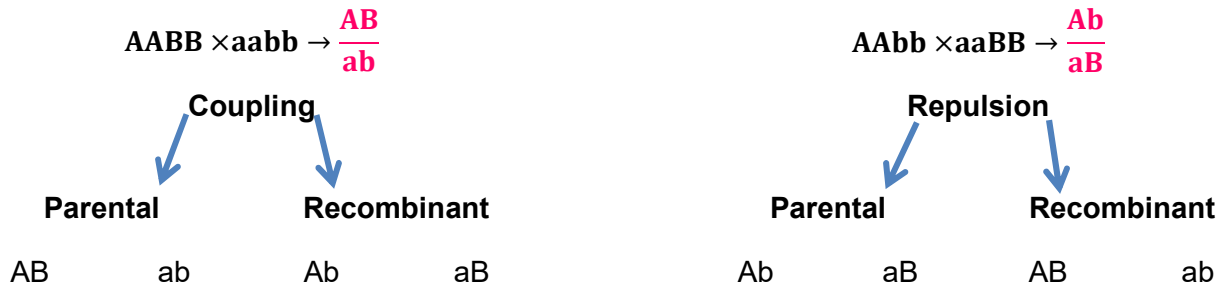
	Definition	A_B_	A_bb	aaB_	aabb
<b>Dominant Complementary</b>	A & B are both needed for expression	9	7		
<b>Recessive Complementary</b>	a and b are both needed for expression Also known as <u>duplicate dominant</u>	15			1
<b>Dominant Epistasis</b>	A inhibits the expression of B– /bb genotype	12		3	1
<b>Recessive Epistasis</b>	aa inhibits the expression of B– /bb genotype	9	3	4	
<b>Epistasis with Dominant Inhibitor</b>	A inhibits the expression of B (appear bb)			3	
<b>Cumulative</b>	A & B are additive	9	6		1

## Linkage

- The segregation of alleles at one gene affects the segregation of alleles at another
- Types
  - ❖ **Complete** –  $r = 0$ : no recombinants
  - ❖ **None** –  $r = 0.5$ : independent assortment
  - ❖ **Partial** –  $r = 0 - 0.5$

## Double Heterozygotes

- Parental** ( $1 - r/2$ ) – gametes could have been produced by the grandparents
- Recombinant** ( $r/2$ ) – ‘new’



## Detecting Linkage

$F_1$  testcross **doesn't** produce 1:1:1:1 gamete ratio

$$R = \frac{\text{Recombinant Gametes}}{\text{Total Gametes}}$$

% Recombinants

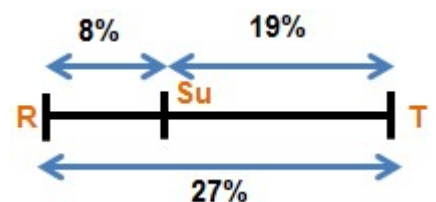
$$S.E. (R) = \sqrt{\frac{r(1-r)}{N}}$$

Standard Error

## Three Point Testcrosses

### Steps

- Determine parental (largest two) and double recombinants (smallest two)
- Determine gene order
  - ❖ Parental and double recombinant have identical ‘end’ genes
  - ❖ “Different gene” is in the middle
- Calculate recombination values ( $R$ )
  - ❖ A-B, B-C and A-C
  - ❖ For A-C, multiply the double recombinants by two
- Gene map



## Map Distance (cM)

- Double recombinants are only detected if there's a middle gene ‘marker’
- Result
  - ❖  $R < 10\%$ 
    - Few recombinants
    - % = true map distance
  - ❖  $R > 10\%$ 
    - Frequent recombinants
    - % < true map distance

## Linkage Groups

- Linkage group** – genes that are linked
- Well studied species have one linkage group per haploid chromosome