

Non-Mendelian inheritance

- 1) Multiple alleles: more than two phenotypes due to more than two alleles being present
- 2) Incomplete dominance: both phenotypes may be dominant, resulting in an intermediate phenotype.
- 3) Codominance: both dominant traits are present in offspring, resulting in both alleles being expressed together.
- 3) Codominance: both dominant traits are present in offspring, resulting in both alleles being expressed together.
- 4) Pleiotropy: mutations have more than one phenotypic effect.
- 5) Epistasis: interaction of more than one gene masks the phenotypic effect of one of them.

Sex linkage

This is because the recessive allele on the X chromosome will show in the phenotype in males, as they have XY, so there is no dominant allele to override it (whereas females have XX, so will always have the dominant allele).

X chromosomes – 1,000 to 2,000 genes
Y chromosomes – 70 genes

Males and females carry a different dose of X, so males have dosage compensation – they produce double the amount of gene product (upregulation of X in males)

Linkage

Genes are physically linked when they are on the same chromosome.

Genes on separate chromosomes are never linked

Genes that are farther away from each other are more likely to be separated during a process called homologous recombination, and are practically unlinked

Breaking linkage

Two parental chromosomes, two recombinant chromosomes

Crossing over always occurs and is regulated

The probability of crossing over between two genes depends on their distance from each other on the chromosome.

Double crossing over undoes the effect of one crossing over, therefore, the parental and recombinant genes stay the same.

Double crossing overs close to each other are rare, due to crossing over interference: one crossing over reduces the possibility of a second.

Genetic mapping

The percentage of recombinant offspring (recombination frequency) = distance between genes on a chromosome

1% frequency = 1 map unit (centimorgan, cM)

How to plot a gene map

1. the lowest frequency is the double crossing over
2. the highest is the parental genes
3. find the pairs of the other crossing over/s
4. to determine the gene in the middle, look at which allele has swapped between the parental gene and the double cross.
5. to calculate the distance between alleles, remember that it is the recombination frequency between one cross and the recombination frequency of another cross. This is calculated by adding together the frequency of both alleles in the pair, and the alleles in the double cross.

Linkage group

Linkage can only be detected when recombination frequency is less than 50%

When genes are far apart on the chromosome, crossing over will always occur, so genes appear unlinked.

There is a difference between 'physically linked' and 'genetically linked' – if asked how many linkage groups there are in an organism with x chromosomes, you cannot tell.

Genetic mapping can only establish linkage groups.



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