Origin and Diversity of Life 2014-2015
Lecture 15
Inheritance of Single Genes

You will be able to find information on the topics covered in this lecture from the following text books.

Raven, Johnson, Losos and Singer 'Biology' 7th ed. Chapters 13
Purves *et al.* 'Life' 7th ed. Chapter 10
Campbell and Reece 'Biology' 7th ed. Chapters 14
Starr and Taggert, 'Biology' 11th ed. Chapters 10 and 11
Solomon, Berg and Martin 7th ed. Chapter 10

and any other genetics text book by looking up any of the key words below in the index.

As a result of this lecture
You should understand that genes can only be studied if we have two or more variants (alleles) the inheritance of which can be followed in genetic crosses, know the difference between genotype and phenotype and how to work out the frequency of different genotypes and phenotypes resulting from crosses in which two alleles of a single gene are segregating.

You should also be able to explain what is meant by each of the following

Allele
Co-dominant – results in intermediate pheno in hete
Conditional mutation
Dominant
Expressivity
Gene
Genotype – alleles of all genes that individual has
Heterozygote
Homozygote
Mutation
Pleiotropy
Phenotype
Penetrance – degree to which pheno effect is manifest
Recessive
Test cross = unknown (FF or ff) x ff
Wild-type

There will be a brief self assessment exercise on Learn after the lecture (Self-Assessment>Lecture 15). This is for your benefit and does not contribute towards the mark for the course.

To work out genetics need phenotypes, Pedigree chart and inheritance

Dominant trait – ex Brachydactyly
- pheno in every generation
- every affected has affected parent
- 1:1 ratio
- 1 allele is enough

Recessive trait – ex. Albinism
- not in all generations
- affected ♂ has unaffected parents
- affected parent not necessarily has all children
- only homozygotes affected

Recombination due to meiosis

Independent Assortment

If genes are on different chromo
(A ≠ B on different genes, A ≠ A on different chro.)

2 Point cross: A/a B/b × a/a b/b

Ratio 1 1 1 1
- 1 1: parental pheno
- 1 1: recombinants

Crossing Over

If genes are on the same chromo
(just different sister chromatids)

2 point cross: AB/ab × ab/ab

Ratio: 1:1 if no crossing over
- 1: both parental

Ratio: 10 : 10 : small small if crossing!
- 10 : 10: parental
- small small: recombinants unequal

Repulsion (trans)

- if recessive and dominant on the same copy

A b / A b × a B / a B

Recombinants: A B / a b
a b / a b

Coupling (cis)

- if dominant alleles on the same chromo

A B / A B × a b / a b

Recombinants A b / a b
a B / a b

Genetic Map – created due to crossing over – it depends on a distance between 2 genes on a chromo
the bigger the more crossing over

$$\text{Recombination frequency} = \frac{\text{recombinants}}{\text{total}} = \ldots [\text{cM}] = \ldots [\text{map units}]$$

Three Point test cross – 3 genes – allow to state the relationship between them

ex. P R J / P R J × p j / p j

- recombinants: pRJ, Prj, pRj, PRj, prJ, PrJ
- find recombination between P–R: Prj, pRJ, pRj, Prj
  —" — R–J & P–J, pRJ, pRj, Prj
- P–R = 28.4 → J in the middle
  P–J = 21.2
  R–J = 10
  } 21.2 + 10 = 31.2 ≠ 28.4 ↖ due to double crossovers (no crossing over that gives rise to parental combination observed)

Gene linkage: recombination < 50%

↳ sex linkage 1 ♀ AA 1 ♀ Aa · 1 ♂ A 1 ♂ a
Pheno 2 ♀ 1 ♂ 1 ♂

ex. haemophilia: sex l., recessive. ♂ affected more frequently, ♀ hetero
ex congenital hypertrichosis if ♀ affected: ♂ affected, if ♂ affected unaffected ♂ but all daughters affected!
sex l. dominant