BB101

Tutorial 3 - Genetics 22/1/18

# **Tutorial**

	D3-T5
Gene ID	2645
Date of last update	
Gene symbol	
Gene description	
Locus tag	
Location	
Size of gene (bp)	
Organism	
Superkingdom	
Size of Chromosome (bps)	
# Genes on Chomosome	
Flanking gene to the left on the genome	
Flanking gene to the right on the genome	
EC#	

# **Tutorial**

Basic Local Alignment Search Tool (BLAST)		
Accession number	AAA98797.1	
Protein Name		
Organism Name		
Sequence Length		
Uniprot id		
No. Of BLAST hits		
PDB id		
No. Of BLAST hits		

Multiple Sequence Alignment (MSA)		
	a) AAA98797.1, b) AAA30988.1, c) AAA51411.1,	
Accession No.s	d) CAA59279.1, e) CAA76841.1	
Evolutionary related		

# **MENDEL'S LAW**

Mendel deduced the underlying principles of genetics from these patterns:-

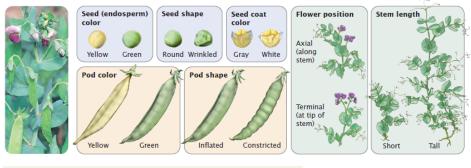
- 1. Dominance
- 2. Segregation (3:1 ratio)
- 3. Independent assortment (9:3:3:1 ratio)



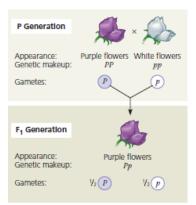
**Gregor Mendel** 

Refer to Campbell, 10th Edition

# **LAW OF DOMINANCE**







	Sperm from F <sub>1</sub> ( <i>Pp</i> ) plant	
F <sub>2</sub> Generation	(P) (p)	
Eggs from F <sub>1</sub> ( <i>Pp</i> ) plant	P PP PP	
	3 🧀 : 1 💫	

Law of segregation

Blood type	Genotype	
A	I <sup>A</sup> , I <sup>O</sup>	AO
	IA, IA	AA
В	I <sup>B</sup> , I <sup>O</sup>	ВО
	$I^B$ , $I^B$	ВВ
AB	I <sup>A</sup> , I <sup>B</sup>	AB
0	Io Io	00

Codominance





Codominant

Incomplete Dominance

.....

Law of independent assortment

P Generation

F<sub>1</sub> Generation

**Predictions** 

Predicted offspring of F<sub>2</sub> generation

YYRR

Hypothesis of /

Phenotypic ratio 3:1

Gametes (YR) ×

YyRr

dependent assortment independent assortment

Hypothesis of

YYrr

YyRr

Phenotypic ratio 9:3:3:1

YYRr

The following two genotypes are crossed: Aa Bb Cc dd Ee \*Aa bb Cc Dd Ee. What will the proportion of the following genotypes be among the progeny of this cross?

- a. Aa Bb Cc Dd Ee
- **b.** Aa bb Cc dd ee
- c. aa bb cc dd ee
- d. AA BB CC DD EE

Ans: a. 1/32

- b. 1/64
- c. 1/256
- d. 0

A white-eyed fly, both of whose parents had white eyes, was crossed with a red-eyed fly, and all of their offspring (both male and female) were red-eyed.

a. Is the gene for red eyes or that for white eyes dominant? Proof?

Ans – Red eye is dominant as all the offspring produced were red eyed.

b. What was the genotype of the white-eyed parents?

Ans - ww

c. What was (were) the genotype(s) of the red-eyed offspring?

Ans - Ww

d. If one of the red-eyed offspring was mated with the white-eyed parent, what would be the expected ratio of offspring, with respect to eye color?

Ans – Ww X ww = Ww, Ww, ww, ww = 1/2

e. If two of the red-eyed offspring are mated, how many genetically different kinds of zygotes, with respect to eye color, will be formed, and what will the proportions be?

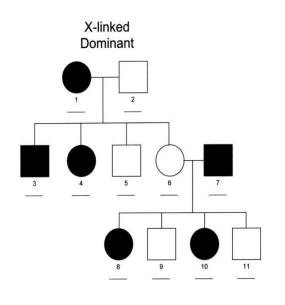
Ans - Ww X Ww = WW, Ww, Ww, ww = 1:2:1

In mice, black coat color (B) is dominant over brown (b), and a solid pattern (S) is dominant over white spotted (s). Color and spotting are controlled by genes that assort independently. A homozygous black, spotted mouse is crossed with a homozygous brown, solid mouse. All the F1 mice are black and solid. A testcross is then carried out by mating the F1 mice with brown, spotted mice.

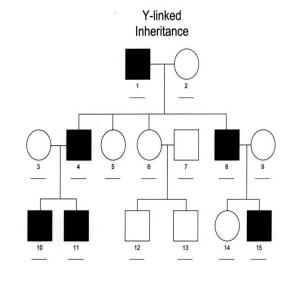
- **a.** Give the genotypes of the parents and the F1 mice.
- **b.** Give the genotypes and phenotypes, along with their expected ratios, of the progeny expected from the testcross.
- Ans: a. Parents BBss, bbSS; F1 BbSs
- b. Genotype Bbss, BbSs, bbSs, bbSs; Ratio 1:1:1:1
- Phenotype Black Spotted, Black Solid, Brown Spotted, Brown Solid

- In *Drosophila melanogaster*, forked bristles are caused by an allele (Xf) that is X linked and recessive to an allele for normal bristles (X+). Brown eyes are caused by an allele (b) that is autosomal and recessive to an allele for red eyes (b+). A female fly that is homozygous for normal bristles and red eyes mates with a male fly that has forked bristles and brown eyes. The F1 are intercrossed to produce the F2. What will the phenotypes and proportions of the F2 flies be from this cross?
- Ans: Red normal female 6/16
- Red normal male 3/16
- Red forked-bristle male 3/16
- Brown normal female 2/16
- Brown normal male 1/16
- Brown forked-bristle male 1/16

# PEDIGREE ANALYSIS OF SEX LINKED DISORDERS



X-linked
Recessive

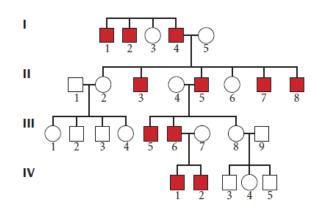


X-linked dominant

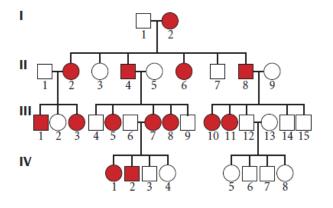
X-linked recessive

Y-linked

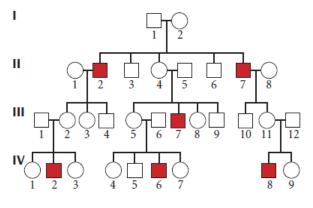
#### Guess the mode of inheritance.



Y-linked inheritance



X-linked dominant



X-linked recessive

Betty has normal vision, but her mother is color blind. Bill is color blind. If Bill and Betty marry and have a child together, what is the probability that the child will be color blind?

Ans: Mother – XCXC

Betty – X<sup>c</sup>X, Bill –XY

Progeny – Half – X<sup>C</sup>X<sup>C</sup>, X<sup>C</sup>Y

Haemophilia (reduced blood clotting) is an X-linked recessive disease in humans. A woman with haemophilia mates with a man who exhibits normal blood clotting. What is the probability that their child will have haemophilia?

Ans: ½. All the male progenies will be affected.

Joe has classic hemophilia, an X-linked recessive disease. Could Joe have inherited the gene for this disease from the following persons?

#### Yes / No

- a. His mother's mother \_\_\_\_\_
- b. His mother's father \_\_\_\_\_
- c. His father's mother \_\_\_\_\_
- d. His father's father \_\_\_\_\_

Ans: Yes, Yes, No, No

A chromosome has the following segments, where • represents the centromere.

ABCDE • FG

What types of chromosome mutations are required to change this chromosome into each of the following chromosomes? (In some cases, more than one chromosome mutation may be required.)

- a. ABE•FG
- **b.** A E D C B F G
- c. ABABCDE FG
- d. AF EDCBG
- e. A B C D E E D C F G

Ans: a. Deletion

- b. Paracentric Inversion
- c. Duplication
- d. Pericentric inversion
- e. Duplication and inversion

# **APPLICATIONS OF GENETICS**



Graf Eberhard von Hohen Esp. 1900 - 1910



Wild ... n .... 1020



Tell von der Kriminalpolizei. 1910



ngo v. Piastendamm. 1940



lodo vom Boxberg. 1920



⑥ OPEN ACCESS
Ø PEER-REVIEWED

RESEARCHARTICLE

Genetic Panel Screening of Nearly 100 Mutations Reveals New Insights into the Breed Distribution of Risk Variants for Canine Hereditary Disorders

Jonas Donner ☑, Maria Kaukonen ☑, Heidi Anderson ☑, Fredrik Möller, Kaisa Kyöstilä, Satu Sankari, Marjo Hytönen, Urs Giger, Hannes Lohi

Published: August 15, 2016 • https://doi.org/10.1371/journal.pone.0161005

15	5
Save	Citation
12,893	16
View	Share