

**Genetics Exercises**  
**M1 Genotype-Phenotype**  
**October 2022**

1. The term « gene » can have several meanings (Table 1).

Table 1. Definitions of the Term “Gene”

<b>A) Genes IX (Lewin, 2006, p. 845 and 852, Glossary)</b> A gene is the segment of DNA specifying a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer), as well as intervening sequences (introns) between individual coding segments (exons).
<b>B) Quantitative Genetics (Falconer &amp; Mackay, 1996, pp. 1-2)</b> A gene is a unit of inheritance that is transmitted from parents to offspring. Suppose for simplicity that we were concerned with a certain autosomal locus, A, and that two different alleles at this locus, A1 and A2. [...] Each A1A1 individual contains two A1 genes.

Choose which definition(s) have been implicitly used in the following sentences:

- a. Many of the **genes** not targeted by our library encode olfactory receptors that are unlikely to be cell-essential. (Blomen et al., Science 2015)
- b. These Polycomb-repressed domains harbour **genes** encoding key developmental transcription factors, whose misexpression can have detrimental consequences in differentiated cells. (Boettiger et al., Nature 2016)
- c. There has not yet been sufficient time for the corresponding resistance **genes** to spread into environmental reservoirs. (Versluis et al., Scientific Reports 2015)
- d. Parkinson Disease is generally considered a multifactorial disorder that arises owing to a combination of **genes** and environmental factors. (Hou et al., Nature Reviews Neurology 2015)
- e. ARID1B and ARID2 participate in widespread cooperation to repress hundreds of **genes**. (Raab et al., PLoS Genetics 2015)
- f. Simulations reveal that hybrid populations rapidly and frequently become isolated from parental species by fixing combinations of **genes** that hinder successful reproduction with parental species. (Schumer et al., PLoS Genetics 2015)
- g. Higher **gene** flow in sex-related chromosomes than in autosomes during fungal divergence. (Hartmann et al., Mol Biol Evol. 2019)

2. What are the following numbers?

- a. Number of telomeres in a cell in G1 phase if its karyotype is  $2n=16$
- b. Number of telomeres in a cell in G2 phase if its karyotype is  $2n=16$
- c. Size of the human genome in base pairs
- d. Number of recombination event per chromosome
- e. % identity between human and chimpanzee DNA
- f. Number of genes in the human mitochondrial genome
- g. Number of different amino acids in the genetic code table
- h. Total number of possible codons
- i. Average number of de novo mutations in a person (germline-mutations) compared to his parents

3. Draw a cross between two parents, each homozygote for different alleles (a1,a2 and b1,b2) at two loci, *a* and *b*. Which generation may present the first recombined alleles between the two loci?

What will be the possible genotypes of the second generation (F2) after a cross among F1s?

Calculate the frequency of the different genotypes of F2 individuals:

- 4.1 if *a* and *b* are not linked, and
- 4.2 if they are located 1 cM apart on the same linkage group.

4. How many alleles of a given gene can be found in a haploid individual? in a diploid individual? in a population of diploid organisms after a chemical mutagenesis? in a natural population of diploid organisms?

5. Two snapdragons, one red and one white, are crossed. Their progeny is pink. What do you conclude? How many genes are involved in the color difference between the two parents?

6. One albino pigeon is caught in the Luxembourg garden and another in Central Park. The albino phenotype is caused by a recessive allele. What can you do to determine whether the same gene is responsible for the albino phenotype of both pigeons?

Unfortunately both are males. What can you propose instead?

7. A mutant *Drosophila* strain has no eyes. An eyeless female is crossed with a male of a wild-type line and F1 flies all have eyes. The F1 males are then backcrossed to the eyeless mother. The F2 generation displays a total of 87 flies with no eyes and 92 flies with normal eyes. What can you conclude about the genetic basis for the loss of eye? What can you conclude about the number of genes necessary for eye formation?

8. A line of *Drosophila* flies without eyes obtained after mutagenesis is crossed to a wild-type line showing a mean of 108 (+/- 5) ommatidia per eye. The F1 generation displays a mean of 35 (+/- 18) ommatidia per eye. What can you conclude?

What can you expect in the F2 generation if a single locus is involved?

9. A strain of flies with no hairs on part of the anterior legs is isolated from the Orsay orchard. It is crossed to a wild strain that was isolated on the Place Monge market, which shows a stable mean of 10.8 (+/- 0.5) hairs. The F1 generation displays a mean of 3.5 (+/- 1.8) hairs. What can you conclude?

What can you expect in the F2 generation?

10. A butterfly species exists in two forms, "normal" (N) and crenelated (C). Five butterfly pairs are mated:

cross	Parent phenotypes		F1	
	Males	Females	Males	Females
#1	N	N	100% N	100% N
#2	C	C	100% C	100% C
#3	C	N	50% N, 50% C	50% N, 50% C
#4	C	N	100% C	100% C
#5	N	C	100% C	100% N

Write the genotypes of the parents of each cross and the mode of inheritance and of phenotypic expression of the alleles. (NB: The chromosomal basis for sex determination is not the same in all organisms.)

11. In a black, diploid, beetle species, loss-of-function mutant lines in four genes, A, B, C, D, as well as double and triple mutant combinations are available. They show the following phenotypes:

A: black	A; D: albino	A; B; C: yellow
B: brown	C; D: yellow	A; B; D: albino
C: yellow	A; C: yellow	A; C; D: albino
D: black	B; C: yellow	B; C; D: yellow
	A; B: brown	

Draw the genetic and biochemical pathways for pigment synthesis.

Which pigment accumulates in:

- animals of genotype B; D?
- in the F1 progeny of A and D animals?

## I. Red and green aphids (Training for the exam)

Pea aphids can be green or red. Clones of green aphids (named Gxxx) and red aphids (named Rxx) are maintained via asexual reproduction in the laboratory.

Pea aphids carry several endosymbiont species, including *Buchnera aphidicola*, which is transmitted maternally.

### a. Present two possible trajectories for maternally transmitted alleles in pea aphids.

Crosses were performed to understand the genetic basis of the colour difference. Each line of the table represents the result of one cross.

Parental Clone 1	Parental Clone 2	Total # Progeny Clones	# Red	# Green
R 5A	G 8101	60	35	25
R 5A	G 2a	20	12	8
R 82b	G 2a	56	34	22
R 82b	G 921	12	9	3
R 82b	G 2a	8	4	4
G 721	G 921	10	0	10
G A2C	G 921	3	0	3
R 5A	R 5A	9	9	0

### b. If you assume that there is a single locus, is the red allele recessive or dominant? What is the genotype of clones R5A, G921 and GA2C?

The green and red colours are due to the presence of green and red carotenoids. Carotenoids are produced by plants, fungi and bacteria whereas animals are unable to produce carotenoids de novo. Accordingly, carotenoid biosynthetic enzymes genes are found in plants, fungi and bacterial, but usually not in animal genomes.

Let's see if the pea aphid genome contains such a carotenoid synthase cyclase gene!

### c. Retrieve a carotenoid synthase cyclase gene:

Go to NCBI Protein <https://www.ncbi.nlm.nih.gov/protein/>

Search for "carotenoid synthase cyclase"

"lycopene cyclase/phytoene synthase" is the type of gene we are looking for, let's copy this protein sequence: UniProtKB/Swiss-Prot: P37295.1.

### d. Search for possible carotenoid synthase genes in pea aphids:

Go to NCBI BLAST <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

Select the correct type of BLAST. BLASTP is only for annotated proteins.

Select the pea aphid sequence data: "Acyrtosiphon pisum (taxid:7029)"

Run BLAST.

### e. For comparison, search for possible carotenoid synthase genes in *Drosophila melanogaster* or *Anopheles gambiae* on two other browser tabs.

### f. Compare the results of the various BLAST searches.

Let's examine the hit sequences XM\_001943135.5 and XM\_016801018.2. On the right of the BLAST search results, click on page click on "Gene - associated gene details"

You can see that the sequence is found on Chromosome A1 – NC\_042494.1, so it is apparently not a contamination.

### g. What is the difference between hit sequences XM\_001943135.5 and XM\_016801018.2?

Carotenoid biosynthesis involves two types of enzymes: phytoene synthase/carotenoid cyclases and carotenoid desaturases. Table 1 and Fig S2A indicate all the carotenoid biosynthesis genes identified in pea aphids.

**h. What is represented by blue boxes on Fig. S2?**

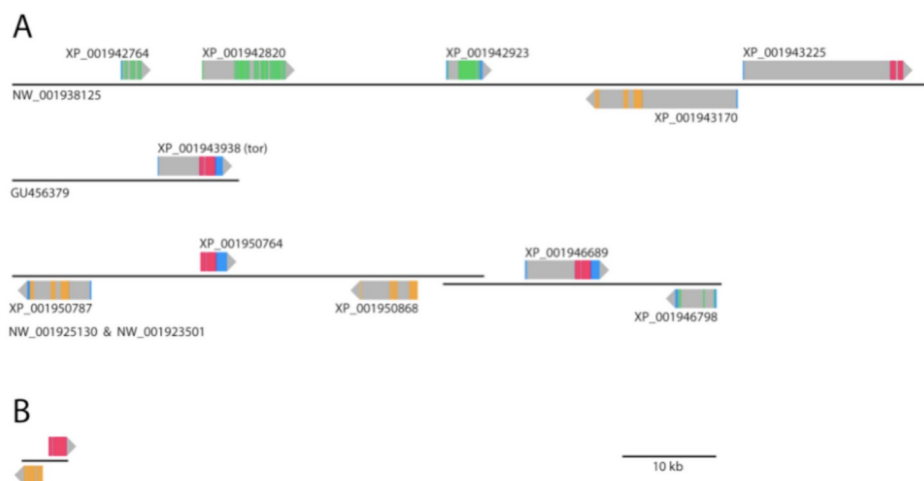
**i. What is special about the location of the phytoene synthase/carotenoid cyclase genes and carotenoid desaturase genes in the pea aphid genome?**

**Table 1.** Genes in the *A. pisum* genome with closest homology to carotenoid biosynthetic enzymes, including scaffold of origin and matching EST sequences. Similar color indicates that the gene is on the same scaffold. The 3' end of scaffold NW\_001925130 overlaps with the 5' end

of NW\_001923501 for 5400 base pairs, and PCR demonstrated continuity of these scaffolds. Pink row is the gene corresponding to *tor<sup>R</sup>* and conferring red color (see text). Protein length, amino acids; ESTs are those present in GenBank, mostly from clone LSR1.

Enzyme type	Protein		mRNA		ESTs (n)	LOC_ID/ACYPI_ID	Scaffold		Gene		
	Accession	Length (aa)	Accession	Length (bp)			Accessions	Length (bp)	Start	End	Length (bp)
Carotenoid synthase/cyclase	XP_001943170	608	XM_001943135	1,981	4	LOC100161104/ACYPI002354	NW_001938125/SCAFFOLD9039	96,434	60,929	75,839	14,910
Carotenoid synthase/cyclase	XP_001950787	588	XM_001950729	2,223	9	LOC100159332/ACYPI000715	NW_001925130/SCAFFOLD17863	49,317	1,564	8,266	6,702
Carotenoid synthase/cyclase	XP_001950868	589	XM_001950833	1,770	8	LOC100164140/ACYPI005179	NW_001925130/SCAFFOLD17863	49,317	36,365	42,379	6,014
Carotenoid desaturase	XP_001943225	373	XM_001943190	1,247	3	LOC100159050/ACYPI000460	NW_001938125/SCAFFOLD9039	96,434	76,368	93,106	16,738
Carotenoid desaturase	XP_001950764	528	XM_001950729	2,718	7	LOC100161380/ACYPI002604	NW_001925130/SCAFFOLD17863	49,317	19,665	22,451	2,786
Carotenoid desaturase	XP_001946689	526	XM_001946654	2,693	25	LOC100169110/ACYPI009757	NW_001923501/SCAFFOLD16397	29,128	8,574	16,388	7,814
Carotenoid desaturase	XP_001943938	510	XM_001943903	2,410	57	LOC100169245/ACYPI009883	NW_001918682/SCAFFOLD12059	31,283	1,415	8,641	7,226

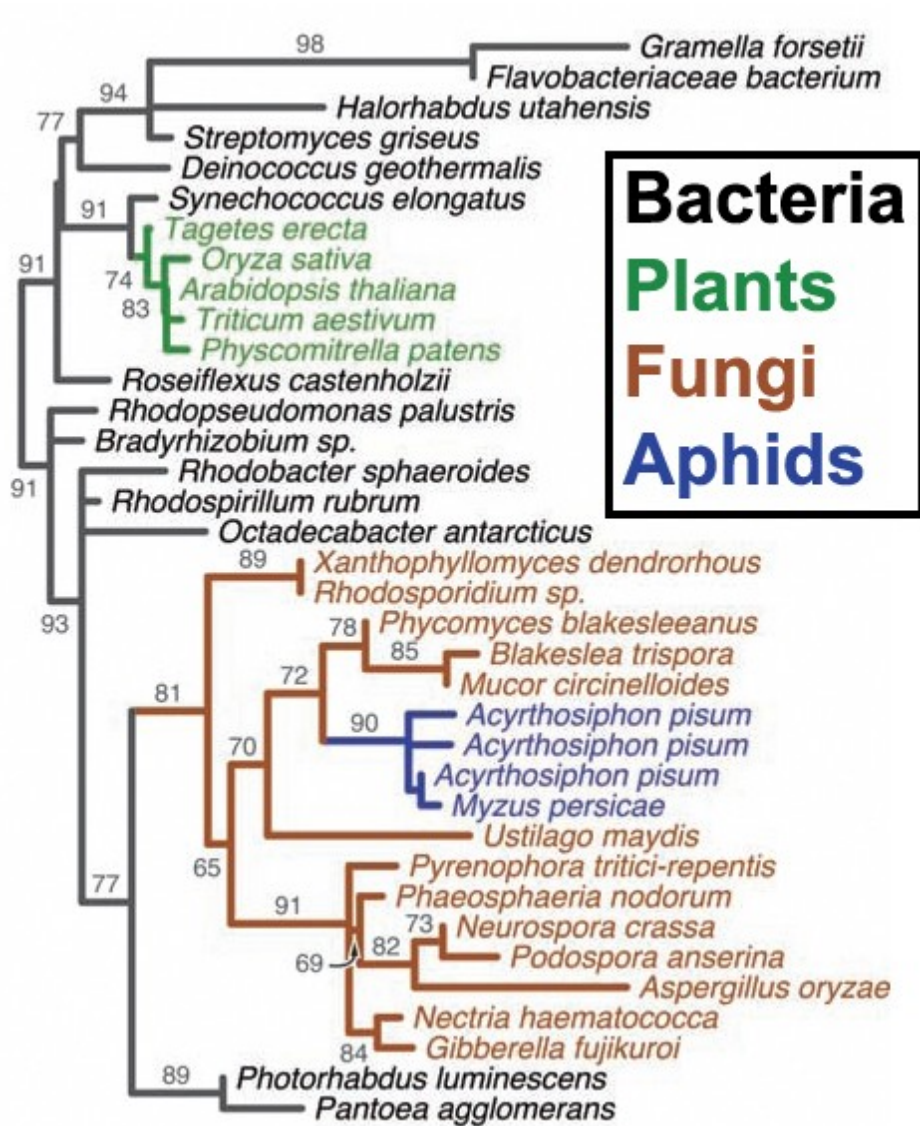
**Fig. S2.** Arrangement of the carotenoid biosynthetic genes (A) in the *A. pisum* genome and (B) in the genome of the fungus *Blakeslea trispora* (S12). Black lines represent genomic sequence. Genes are represented by block arrows with blue for UTR, grey for introns. Exons of carotenoid desaturase genes are red, exons of phytoene synthase/carotenoid cyclase genes are orange, and exons of other genes are green. Scaffold numbers from the *A. pisum* genome project are given, except for the region corresponding to the *tor* locus for which our sequence accession number is given.



To obtain a broader comparison of taxa, let's take one of the pea aphid sequences (one of the largest ones: ACCESSION XM\_001943135) and search across all aphid species.

**g. Run a TBLASTX search with ACCESSION XM\_001943135 as a query across all aphids ("Aphidomorpha") and analyse the results. This search can take a while...**

All the sequences aligning to carotenoid synthase cyclase genes were retrieved and a phylogenetic tree was made:



**Bacteria**  
**Plants**  
**Fungi**  
**Aphids**

h. Interpret the results.

i. Search NCBI Taxonomy (<https://www.ncbi.nlm.nih.gov/taxonomy/>) to check what *Myzus persicae* is.

j. Use time tree (<http://www.timetree.org/>) to estimate the time when the exchange occurred between fungi and aphids.

k. Is this an upper bound or a lower bound of the time point? What would you do to get the other bound of the time estimate?