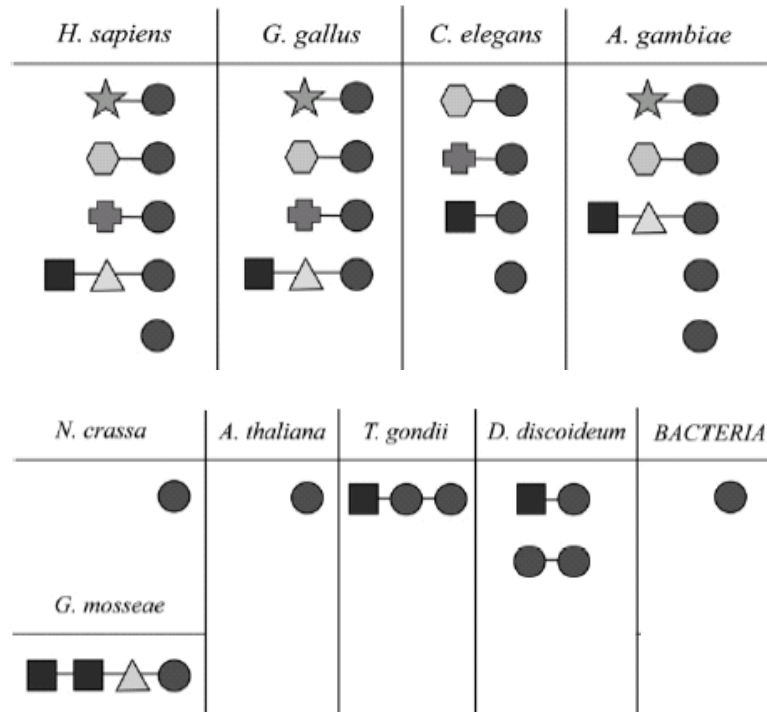


BIO 3102 Practice set #3

Question 1

$T_D = 30$ million years

Question 2



Types of evolutionary events?

Gene duplication

Domain duplication

Domain acquisitions

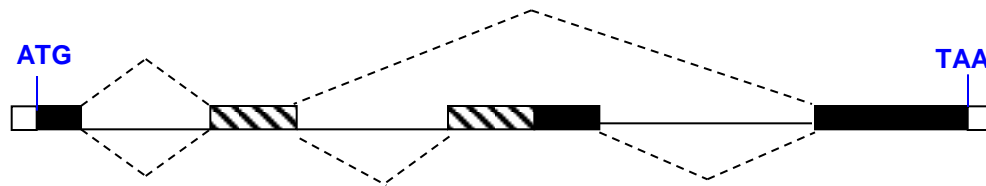
*(eg. intron-mediated
exon shuffling)*

Timing of certain events?

Status in archaea?

Question 3

Alternative splicing



1 cm = 400 bp

Expected nature of proteins?

Upper pathway: coding region = 1 kb so protein length = 333 aa

Lower pathway: coding region = 1.6 kb 533 aa

Length of mRNAs? coding + UTRs + polyA tail (~ 200 nt)

Different evolutionary strategy to achieve same biological outcome?

Gene duplication

Different example of acquiring new function without gene duplication?

Gene sharing

Note: resolution of adaptive conflict may later be by gene duplication

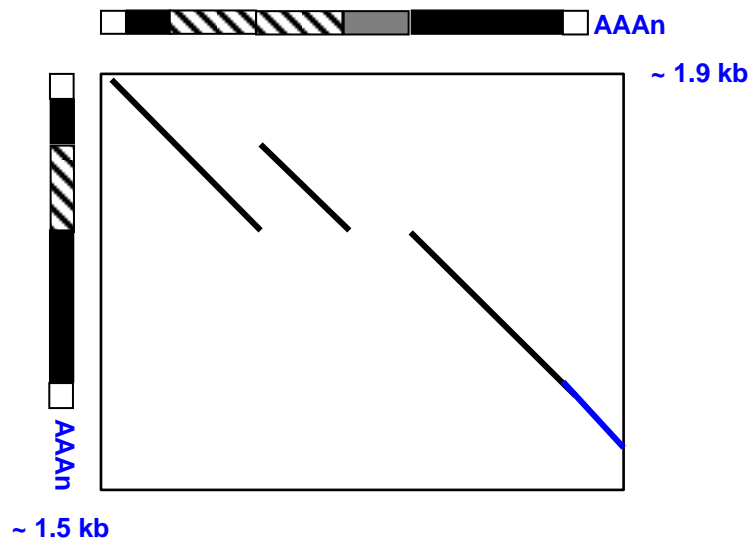
Pathway 1

ATG

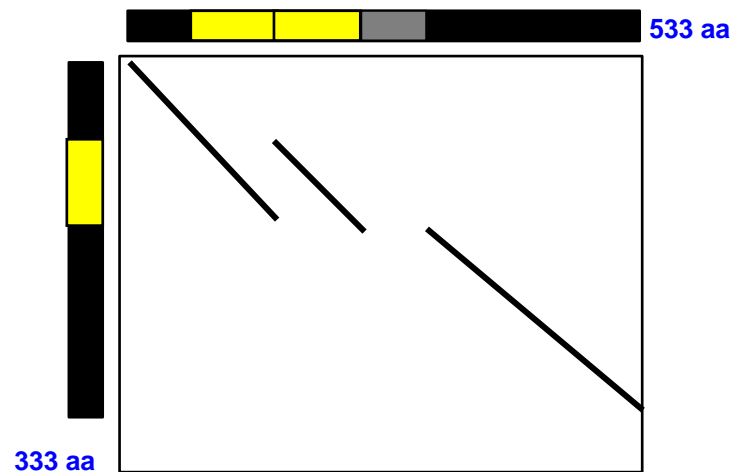
TAA

Pathway 2

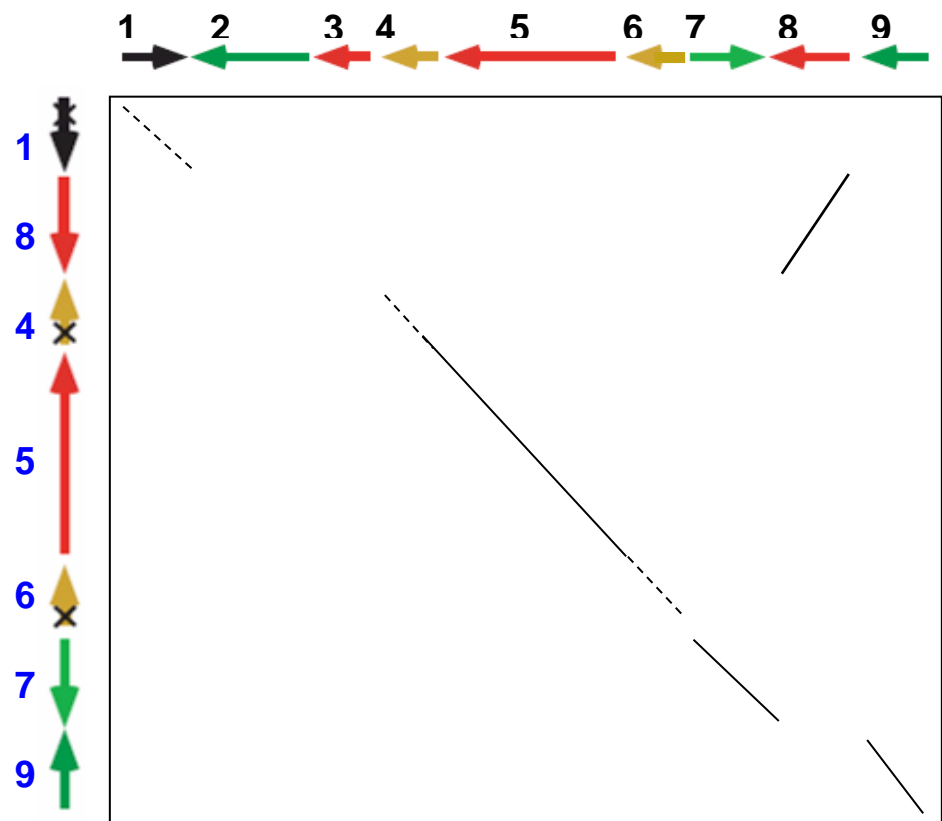
Comparison of mRNAs



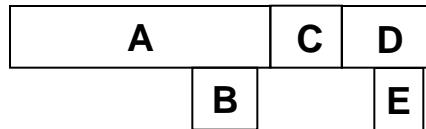
Comparison of proteins



Question 5



Question 6



A & C: DNA replication proteins
 B & D: capsid morphogenesis proteins
 E: host cell lysis protein

Gene region	K_s	K_n	K_n / K_s
A (non-overlapping)	2.07	0.33	0.16
A (overlapping gene B)	1.25	0.41	0.33
B (overlapping gene A)	0.45	0.56	1.24
D (non-overlapping)	1.64	0.29	0.18
D (overlapping gene E)	0.81	0.13	0.16
E (overlapping gene D)	0.19	0.27	1.42
C (non-overlapping)			

Overlapping genes in compact phage genome

Syn substitution in one reading frame is likely non-syn in another frame
 ...so overlapping reading frames are subject to additional constraint

Comparison of K_s vs. K_n

Positive selection for genes E and B? (Maybe recent origin...?)

or might K_s be exceptionally low because constrained in other frame?

Other possible reasons why a “silent” codon site might be under constraint?

Contains translational (or transcriptional) signals for overlapping gene? RNA folding?

Question 7 "Horizontal transfer and death of a fungal secondary metabolic gene cluster"

bik6 gene tree (bikaverin cluster in blue)

Dispersal of *bik* cluster genes, most lost but several retained (with new functions)?

EF1-α, housekeeping gene (used as "species tree")

Strong bootstrap values

Inversion

Cluster lacks "gene 1", so maybe others become pseudogenes (eg. gene 5)?

or maybe certain ones retained if provide novel functions?

High % identity suggests lateral transfer & that *F. species* was donor

Trees have different topologies

Close relatives of *B. cinerea* (ie. *S. scler* & *S. nod*) lack bikaverin genes

- acquired by lateral transfer (vs. independent loss in other lineages)?

- *bik* cluster flanking sequences differ between the clades (green vs. brown)

- independent acquisition at different genomic sites (vs. later DNA translocation)

- also rearrangements within flanking sequences (brown) between species

