

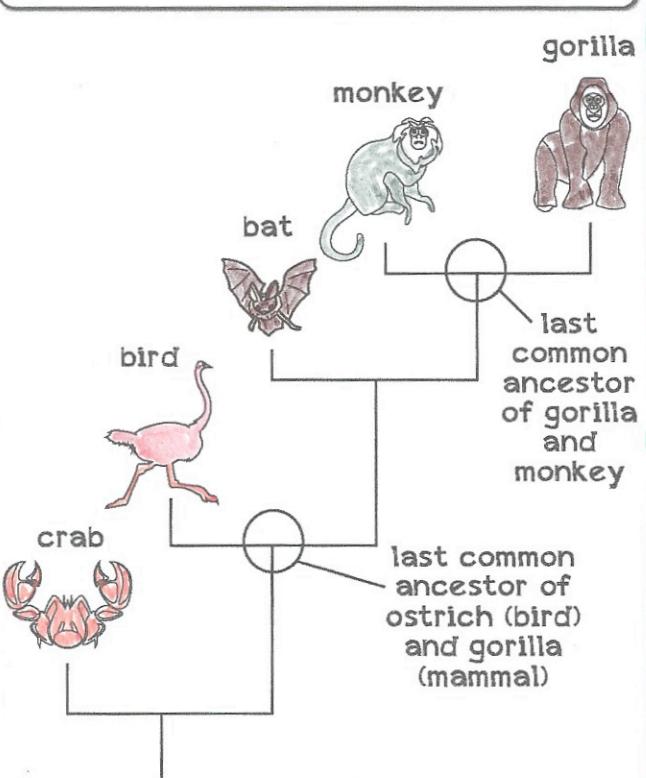
	U	C	A	G	
U	UUU Phe	UCU	UAU Tyr	UGU Cys	U
	UUC	UCC	UAC	UGC	C
	UUA Leu	UCA	UAA STOP	UGA STOP	A
	UUG	UCG	UAG STOP	UGG Trp	G
C	CUU	CCU	CAU His	CGU	U
	CUC	CCC	CAC	CGC	C
	CUA	CCA	CAA Gln	CGA Arg	A
	CUG	CCG	CAG	CGG	G
A	AUU	ACU	AAU Asn	AGU Ser	U
	AUC Ile	ACC	AAC	AGC	C
	AUA	ACA	AAA Lys	AGA Arg	A
	AUG Met	ACG	AAG	AGG	G
G	GUU	GCU	GAU Asp	GGU	U
	GUC Val	GCC	GAC	GGC	C
	GUA	GCA	GAA Glu	GGA Gly	A
	GUG	GCG	GAG	GGG	G

Universal Genetic Code

- In almost all organisms on earth, the same codons are used to code for the same amino acids!
- This is evidence that there is a Last Universal Common Ancestor that used this coding system in its RNA or DNA to produce its proteins and ribosomes to do the translation process.
- It is thought that organisms that try to deviate from this universal code must have a big disadvantage, which is why very few species today are known to deviate from this code. Scientists don't yet understand why species haven't evolved away from using this code.

Similarity of Genomes

- As scientists sequence more and more genomes of organisms, they find that all organisms on earth share a certain degree of genetic similarity, suggesting they have a universal common ancestor.
- One of the genes that is highly conserved is the sequence of the ribosome. The ribosome seems to be a necessity for life.
- Scientists often take the genetic sequence of the ribosome in different organisms and compare how similar they are to each other.
- The similarity of the gene sequences in two species can be defined in a calculated value called genetic distance. The larger the genetic distance, the further back in time was the split in their ancestry that eventually produced the two species.
- Scientists can use phylogenetic tree diagrams to display their findings in their studies of genetic distance between different organisms.

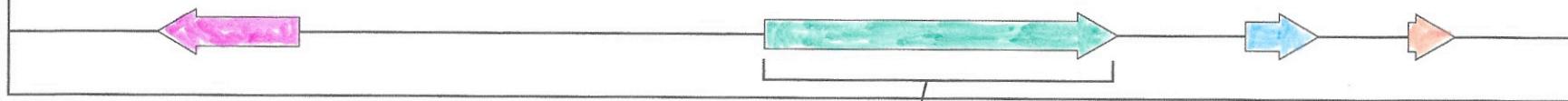


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Comparative Genomics

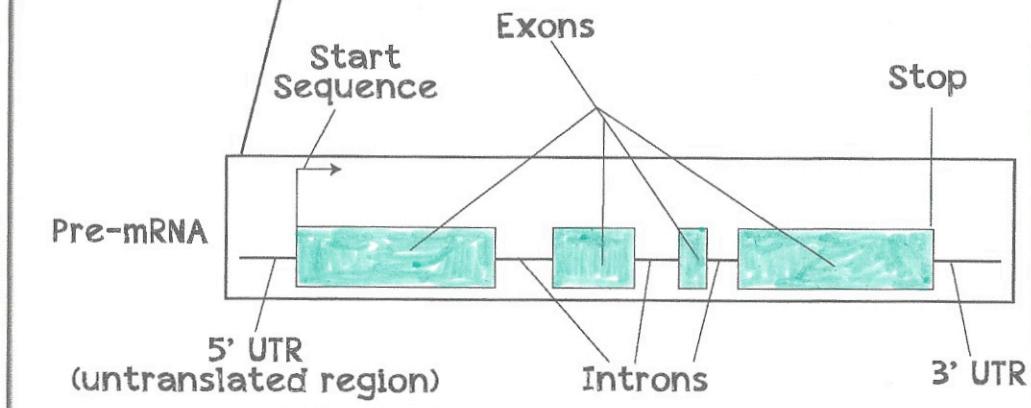
GENOME

- Coding Regions** • Coding regions in the genome are symbolized by arrows. These are the regions in the genome that are transcribed into RNA and those RNAs are in turn translated into a protein. Coding regions are often conserved between different related species.
- In less complex organisms, a high percentage of the genome is made of coding regions. In more complex organisms, a low percentage of the genome is made of coding regions.
 - In humans, coding regions are estimated to take up only 2% of the human genome.



Noncoding regions

- Noncoding regions are shown on genome diagrams as lines in between the arrows.
- Some noncoding DNA is transcribed into functional RNA molecules (like transfer RNA, ribosomal RNA, and regulatory RNAs)
- In the human genome, 98% of DNA is noncoding. Scientists don't know how much of that 98% is useful or "junk DNA".
- Pseudogenes are also present in noncoding DNA. These are the nonfunctional remnants of genes that scientists think used to function in our ancestors.
- Introns are noncoding regions that are found inside of genes and are cut out (spliced) at the mRNA modification stage.
- Noncoding regions tend to be less conserved between different species.



Name:

Parts of a Genome

Hox Genes

- One set of genes that is highly conserved are the Hox genes.
- The Hox genes are a set of genes that contain the code for several DNA-binding proteins, transcription factors that turn on body plan segments.
- In all animals with bilateral body structures, there seems to be a Hox gene set (or more than one set) that regulates how body structures develop.
- The genes are so conserved that if you replace a fruit fly Hox gene with a chicken Hox gene, you still get a functional fruit fly!

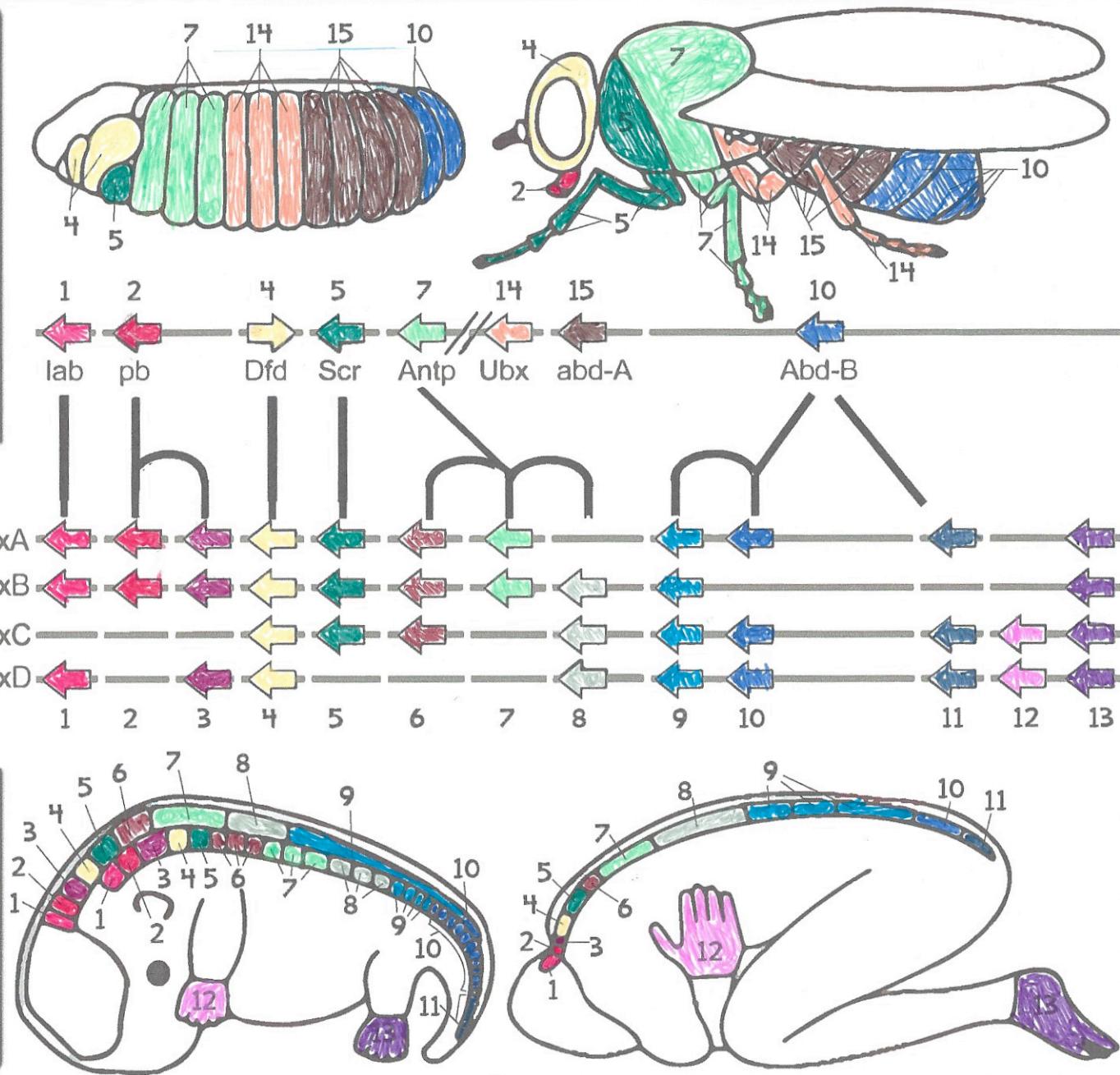


Diagram adapted (and simplified) from:
Improving Hox Protein Classification across the Major Model Organisms, PLOS ONE, 2010.
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