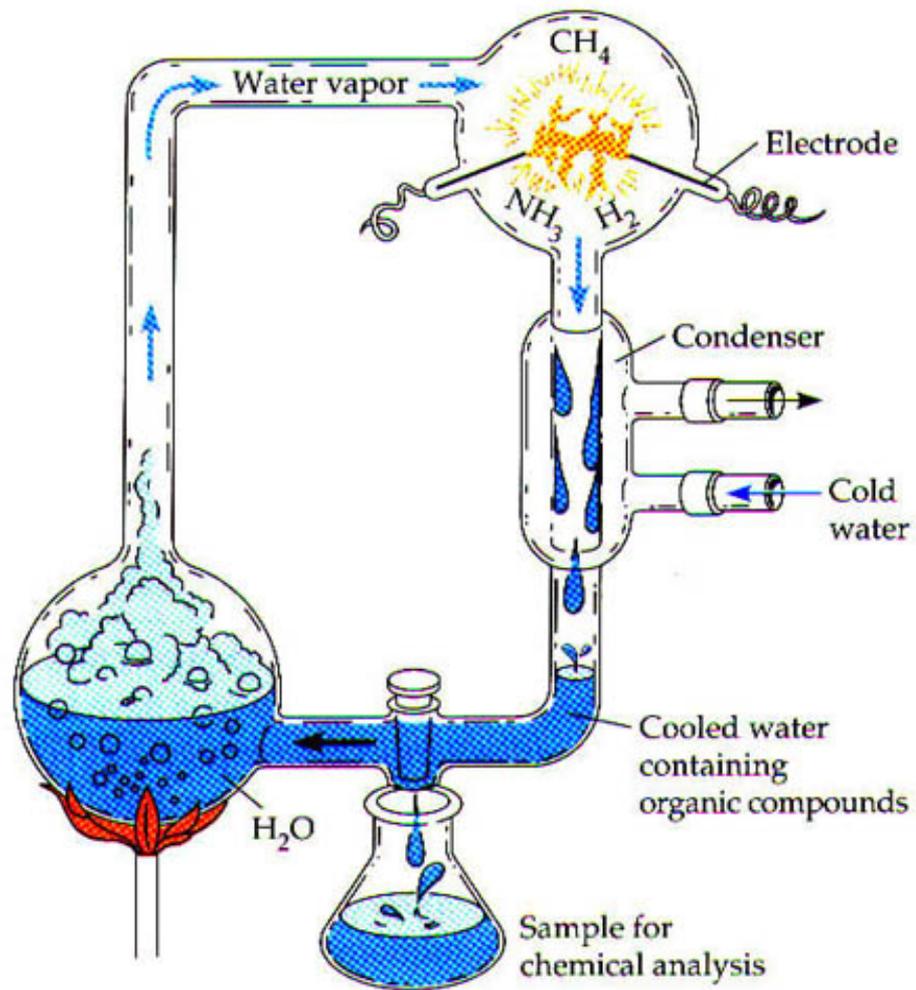
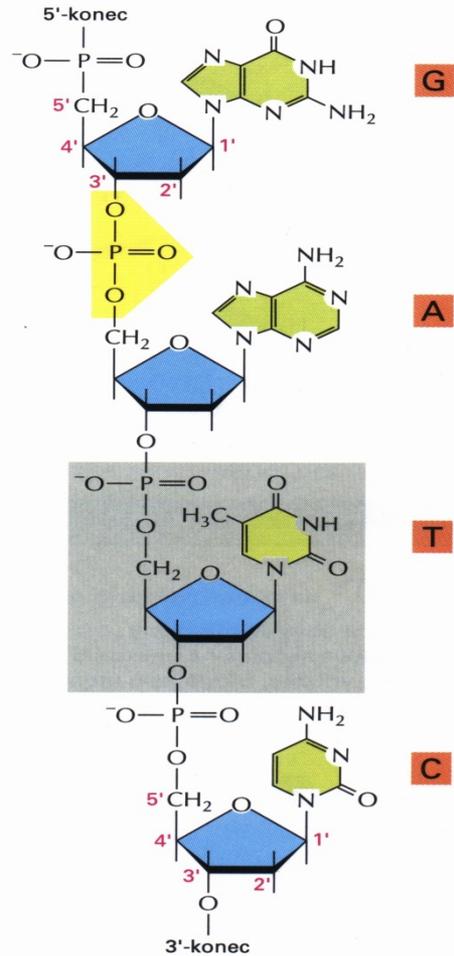


Od vzniku života po evoluci člověka

Václav Pačes

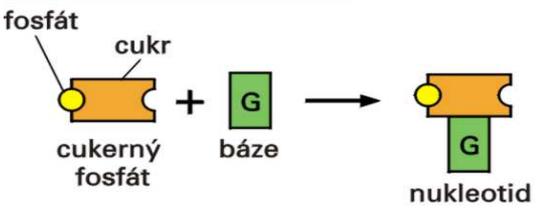
Ústav molekulární genetiky
Akademie věd České republiky



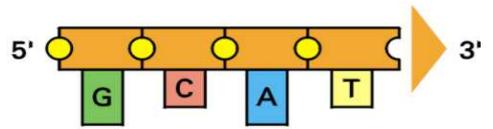


Otázka 2-7 Co se myslí „polaritou“ poly-peptidového řetězce a „polaritou“ chemické vazby? Jak se tyto dva významy liší?

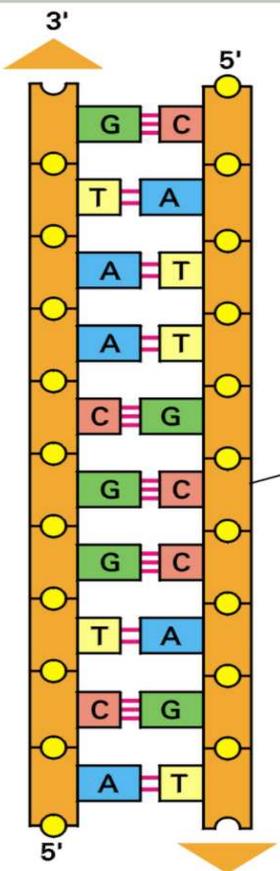
stavební kameny DNA



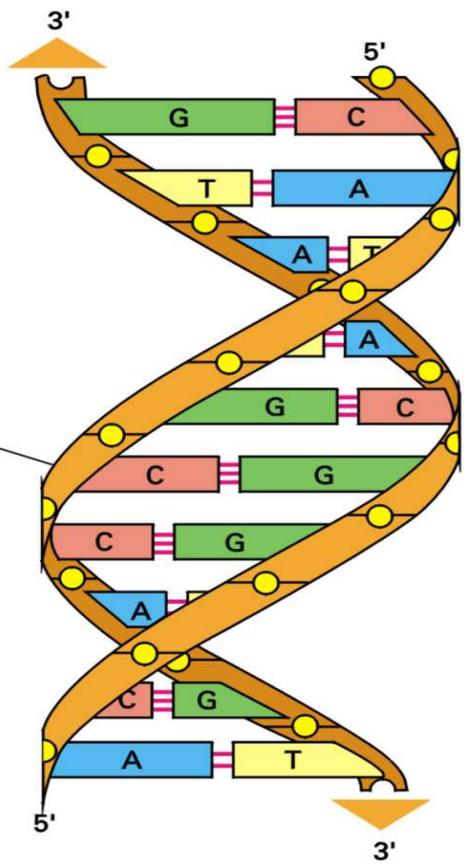
řetězec DNA



dvouřetězcová DNA



dvojšroubovice DNA

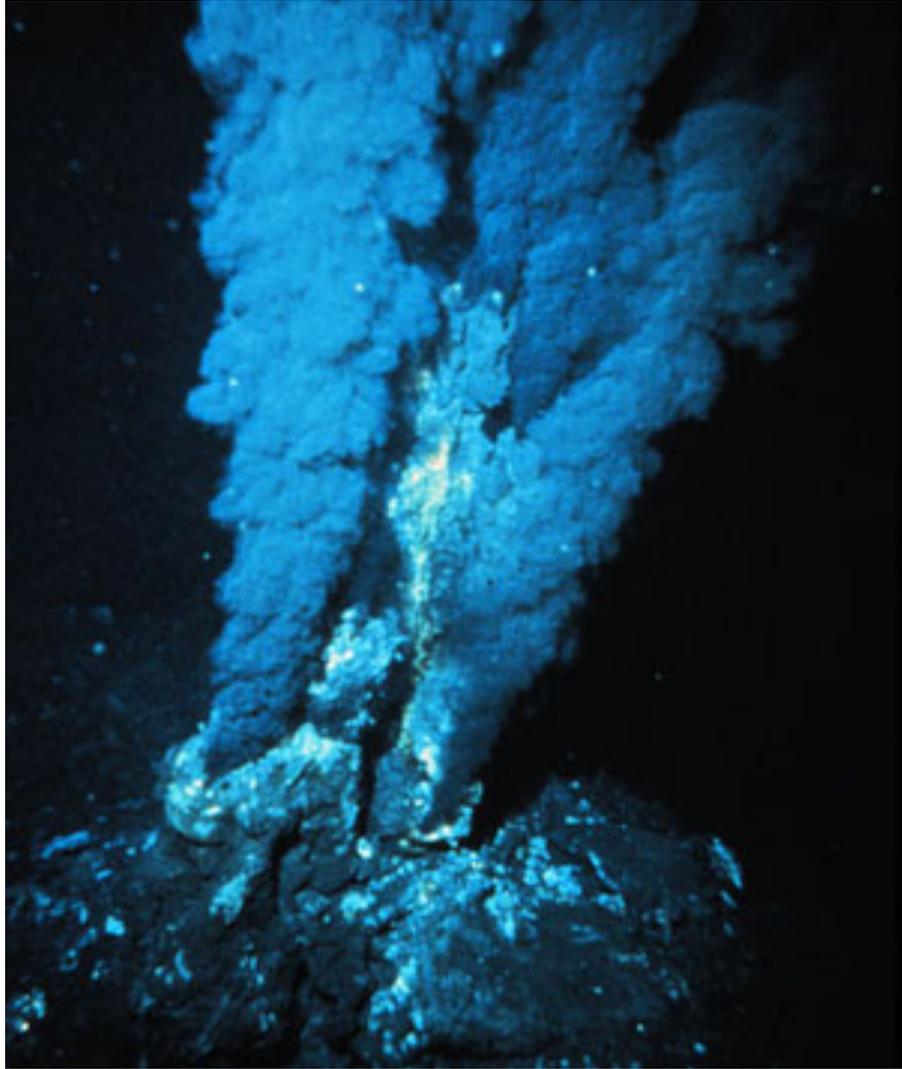


kostra cukerného fosfátu

páry bází vázaných vodíkovými můstky

Life Without the Double Helix

DNA replication.
Coloured Transmission Electron Micrograph (TEM) of human DNA from a HeLa cancer cell, showing a stage of DNA replication. The strand of DNA is coloured yellow; it has formed into a Y-shaped molecule termed a replication fork, where the DNA has unwound into two single strands. Normally, DNA consists of two tightly wound spiral strands. During replication, a "bubble" region forms which enlarges to form a replication fork. It is here that daughter strands form as the parent DNA acts as a template for the construction of a new matching strand. In this way the sequence of bases (or genetic information) along the DNA molecule is replicated.



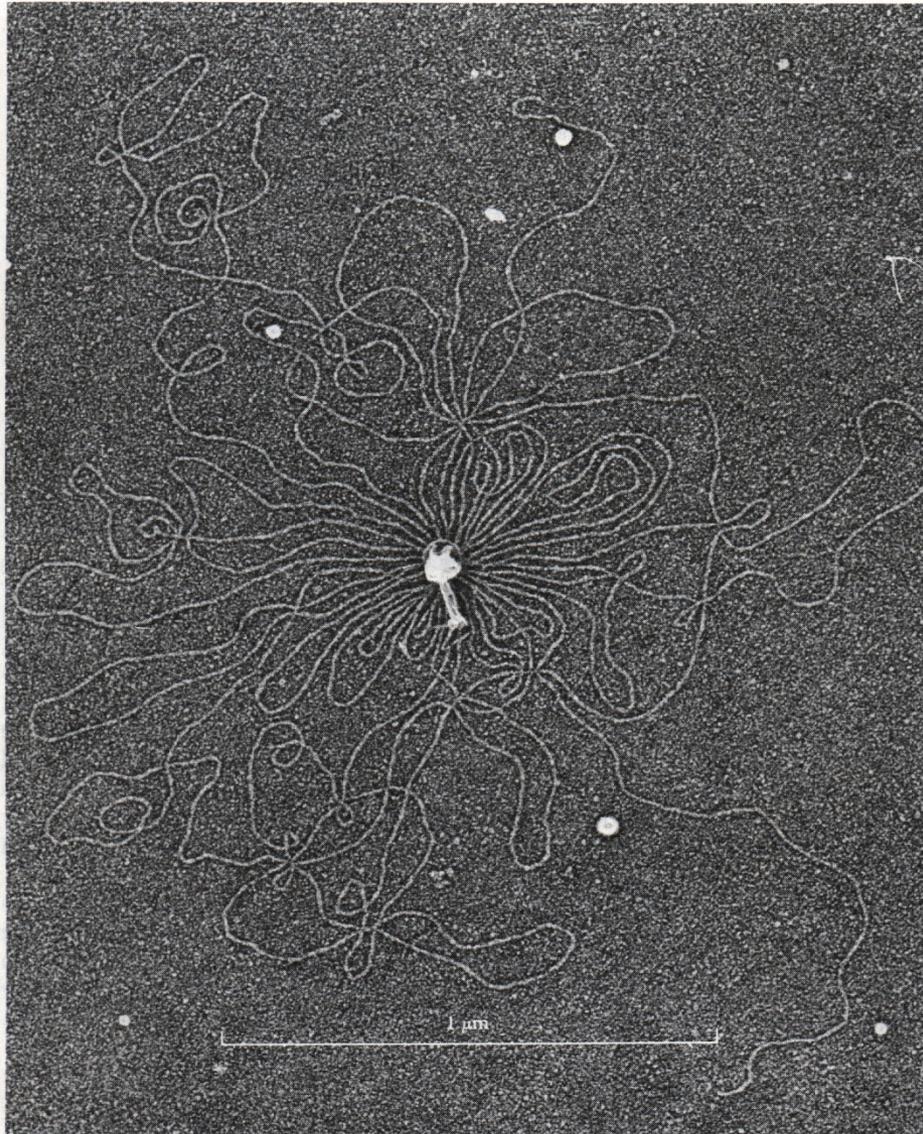
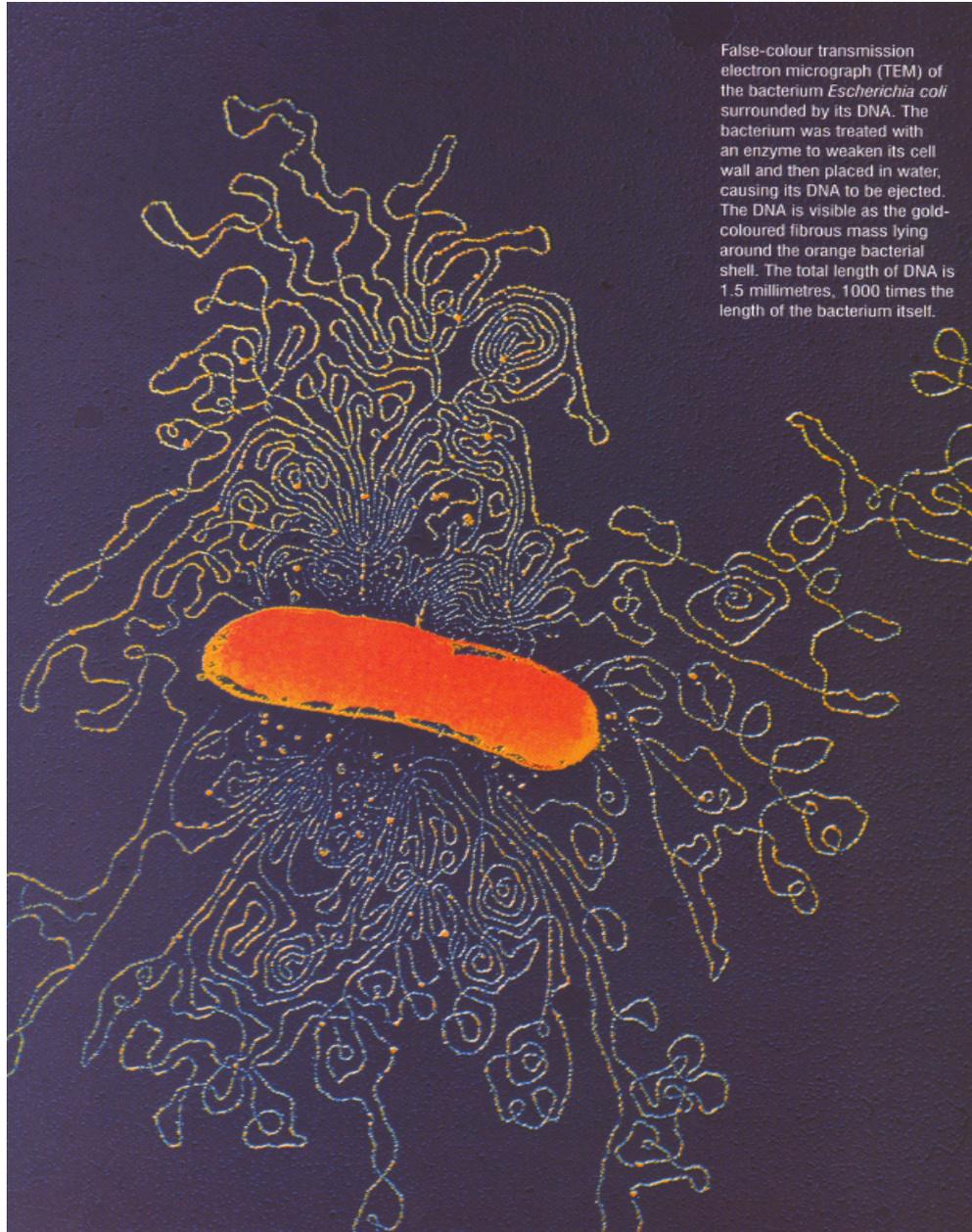
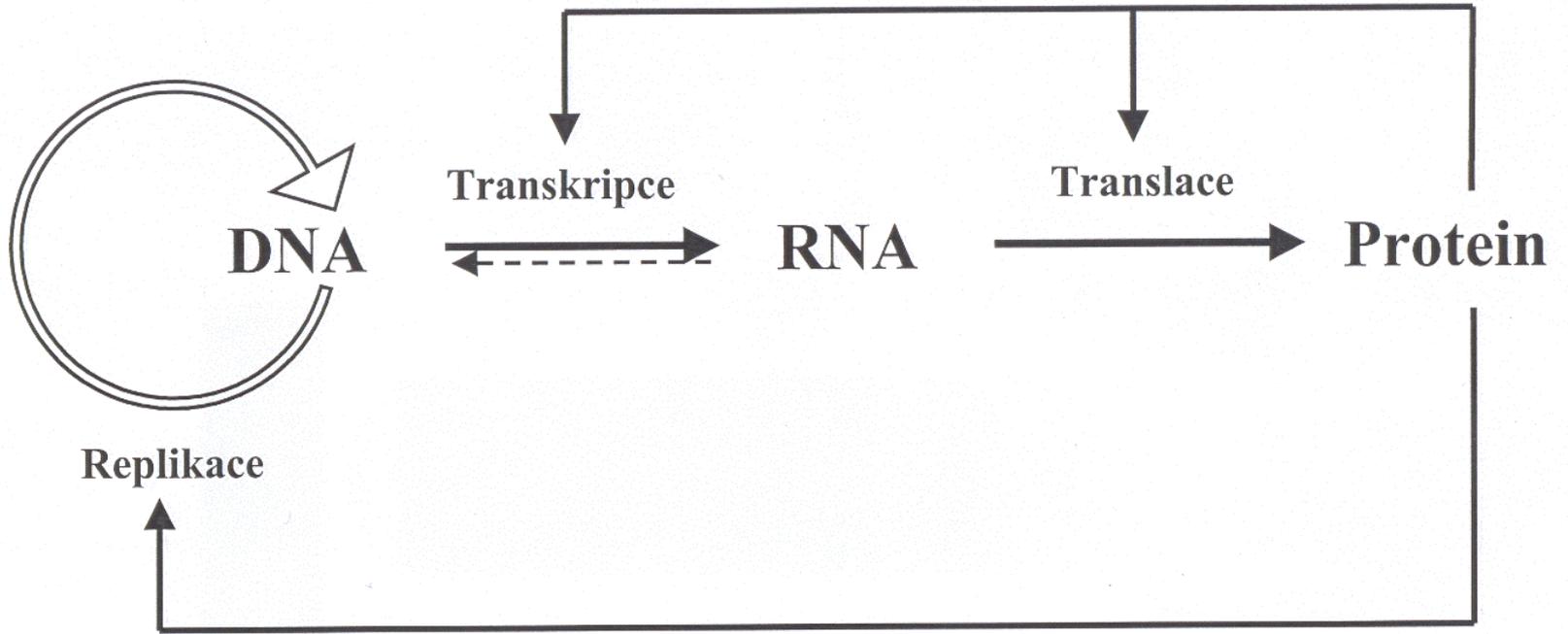


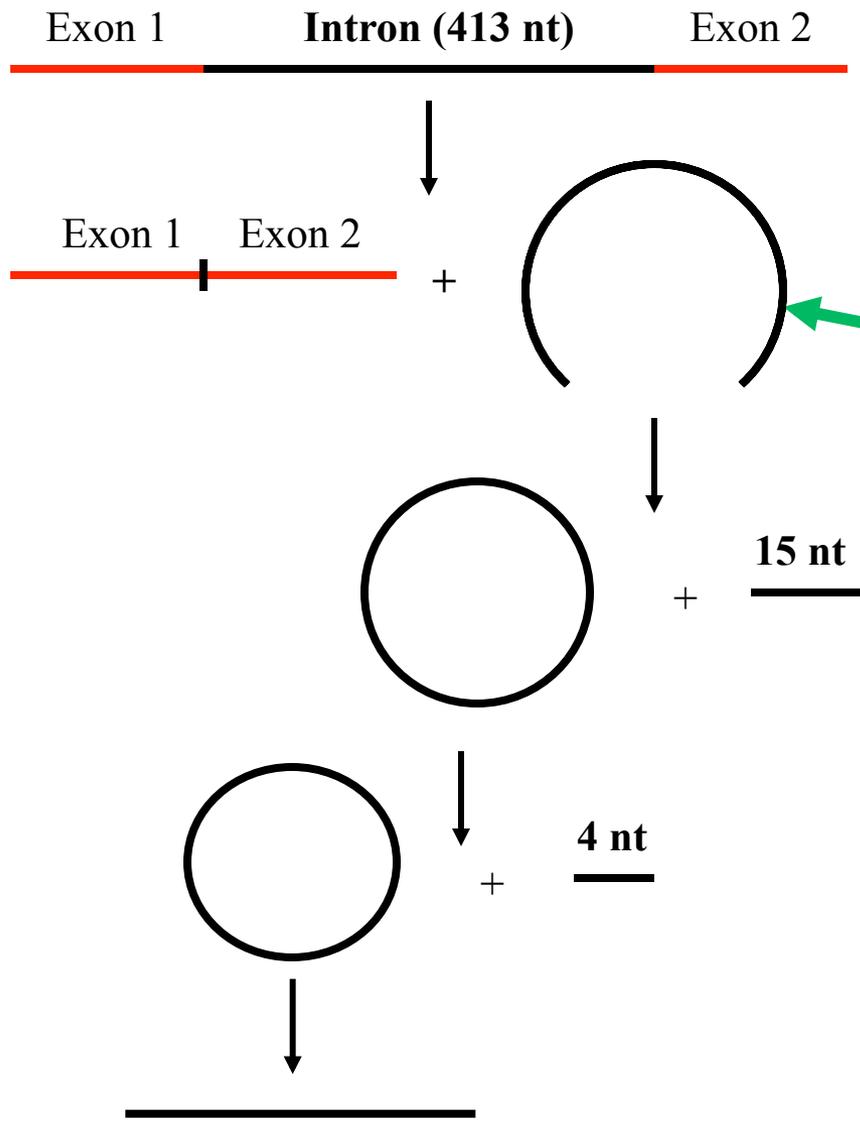
FIGURE 10-6

Electron micrograph of the DNA molecule of T-even phage released from the phage head by osmotic shock. Center: The phage ghost. Bottom right and top center: The two ends of the DNA molecule. [From A. K. Kleinschmidt, D. Lang, D. Jacherts, and R. K. Zahn, *Biochim. Biophys. Acta* **61**, 857 (1962).]



False-colour transmission electron micrograph (TEM) of the bacterium *Escherichia coli* surrounded by its DNA. The bacterium was treated with an enzyme to weaken its cell wall and then placed in water, causing its DNA to be ejected. The DNA is visible as the gold-coloured fibrous mass lying around the orange bacterial shell. The total length of DNA is 1.5 millimetres, 1000 times the length of the bacterium itself.

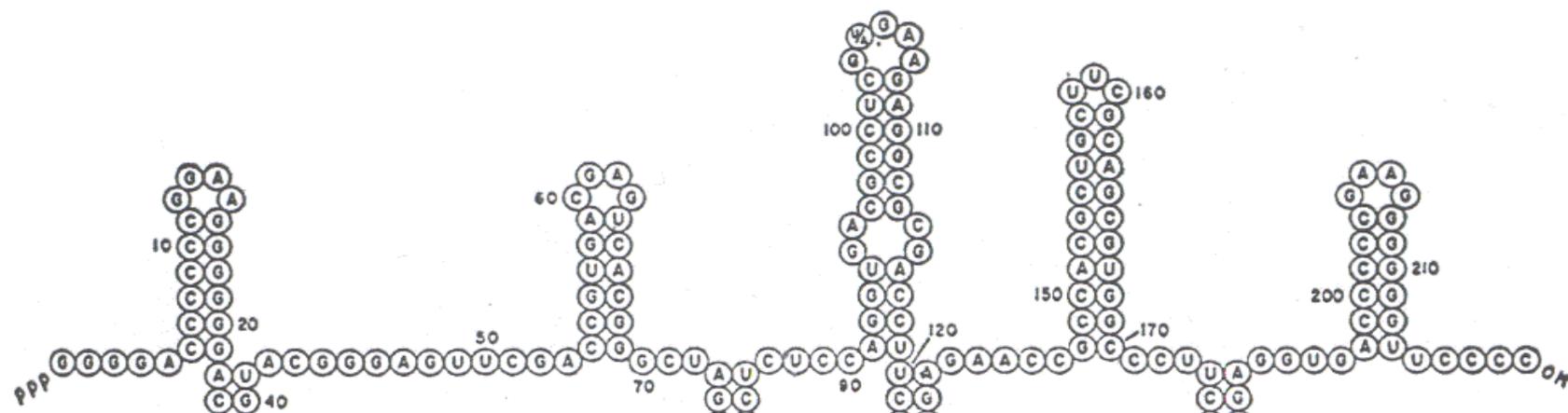




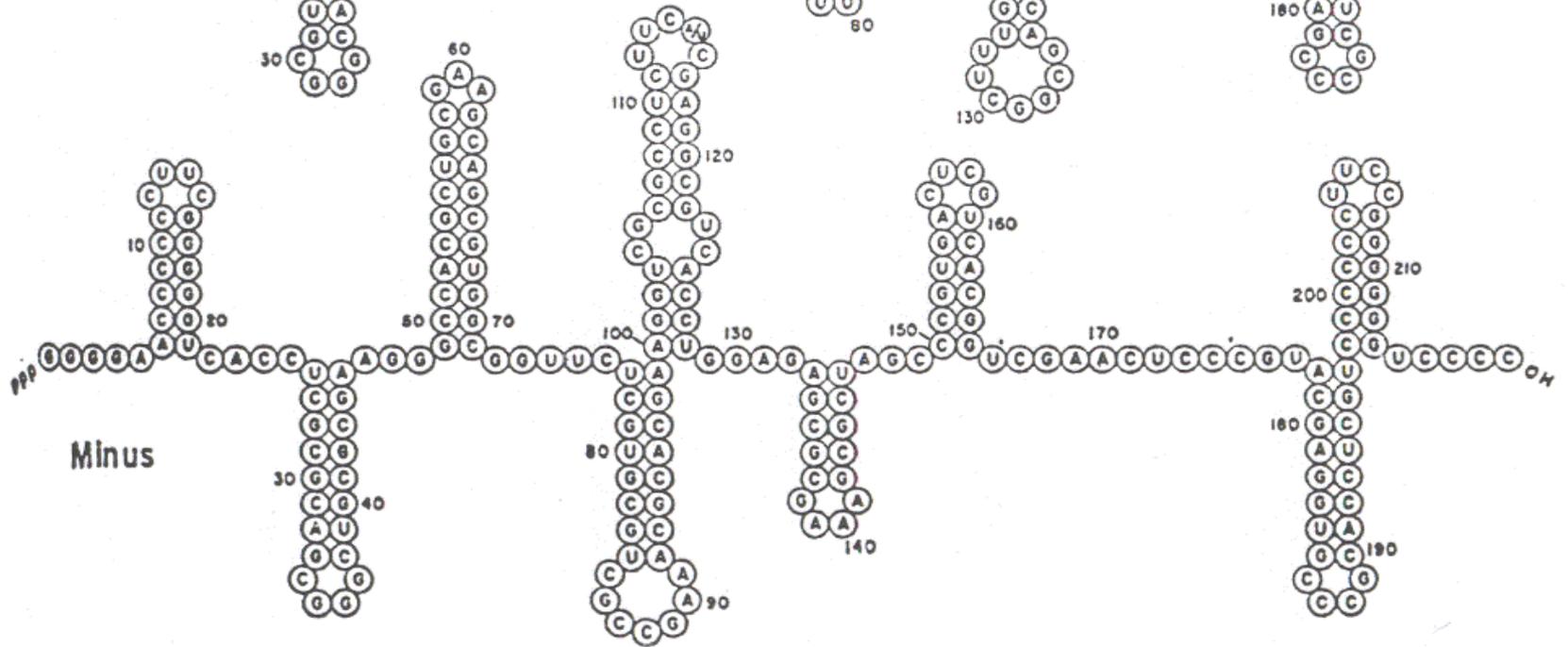
Genome of RNA-bacteriophage Q β



Plus



Minus



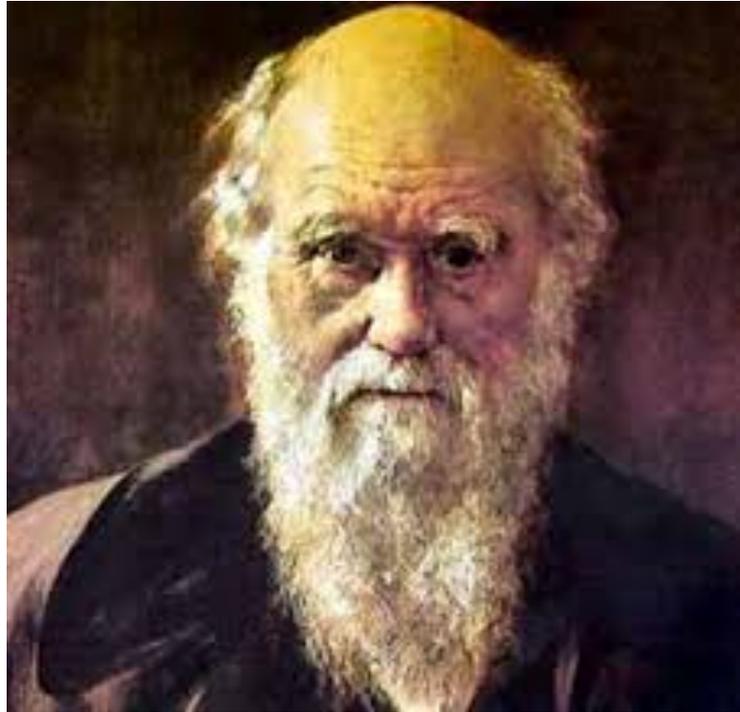
Selected Genome Projects

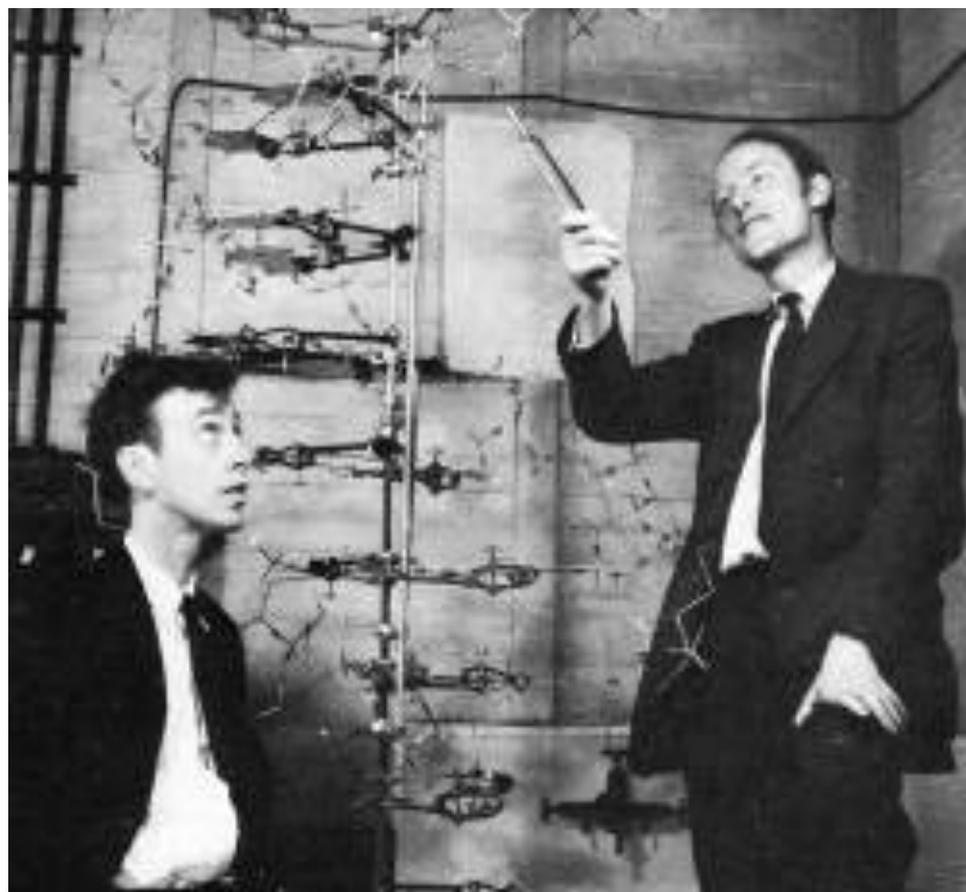
Category	Species	Genome size (Mb)		Genes
PROKARYOTES				
Actinobacteria	<i>Mycobacterium tuberculosis</i>	4,4		4397
Chlamydia	<i>Chlamydia pneumoniae</i>	1,1		1000
Cyanobacteria	<i>Synechocystis species</i>	3,6		3215
Gram-positive bacteria	<i>Bacillus subtilis</i>	4,2		4221
	<i>Mycoplasma genitalium</i>	0,5		503
Oxygen-reducing bacteria	<i>Aquifex aeolicus</i>	1,5		1572
Proteobacteria	<i>Escherichia coli</i>	4,6		4397
	<i>Haemophilus influenzae</i>	1,8		1791
	<i>Helicobacter pylori</i>	1,7		1609
	<i>Rickettsia prowazekii</i>	1,1		834
	<i>Deinococcus radiodurans</i>	3,2		3000
Radioresistent bacteria				
Spirochete	<i>Borrelia burgdorferi</i>	0,9		1279
	<i>Treptonema pallidum</i>	1,1		1082
Archea	<i>methanococcus jannaschii</i>	1,6		1813
EUKARYOTES		Chromosomes		
Fungi	<i>Saccharomyces cerevisiae</i>	16	12	6548
Nematode	<i>Caenorhabditis elegans</i>	6	97	19000
Insect	<i>Drosophila melanogaster</i>	6	137	13500
Plants	<i>Arabidopsis thaliana</i>	5	116	25545
Fish	<i>Fugu rubripes</i>	22	400	25000
Human	<i>Homo sapiens</i>	23	3000	25000











Key steps (jumps) in evolution

- How life started? (pre-biotic to biotic)
- The first cell (compartmentation)
- Multicellular organisms (cooperation)
- Tissues and organs (specialization)
- Brain (networking)
- Sexual reproduction (combination)
- Vertebrates (structure)
- Mammals (progeny)
- Humans (communication)

Haploid genomes:

	Chromosome # (2N)	Chromosome length (average)	DNA per cell	Megabases per genome	# of genes per genome
Amphioxus	38	3 μm	0.9 pg	520	22,000
Human	46	15 μm	3.5 pg	3,000	25,000

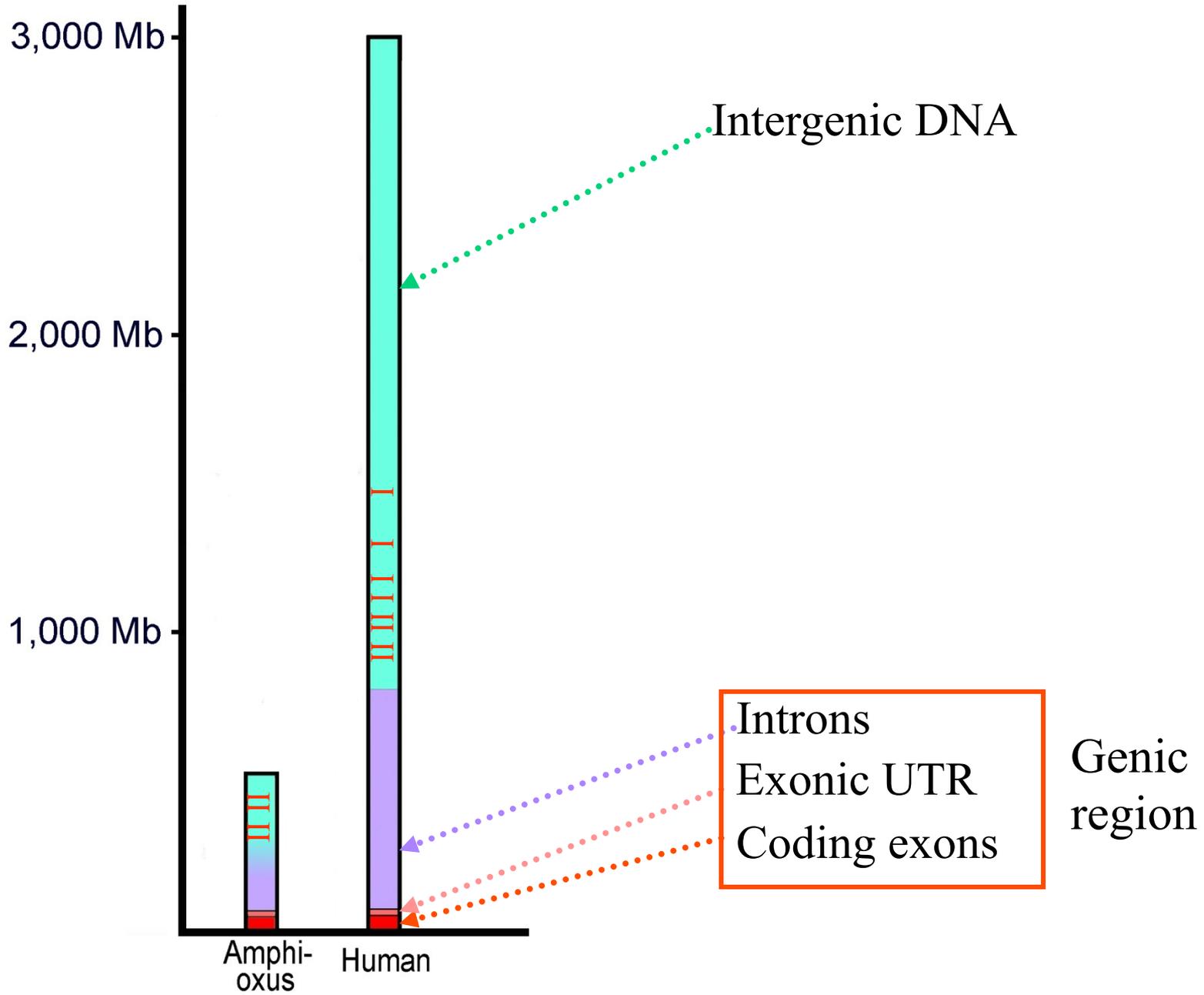
In spite of their much larger DNA content vertebrates have only 25% more genes than amphioxus

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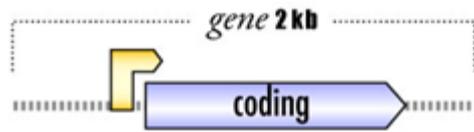
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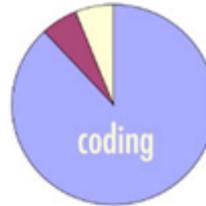
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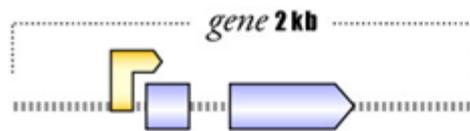
Genome complexity



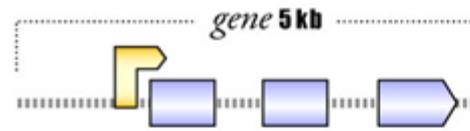
S. cerevisiae
14 Mb
~6,000 genes (16 chr.)



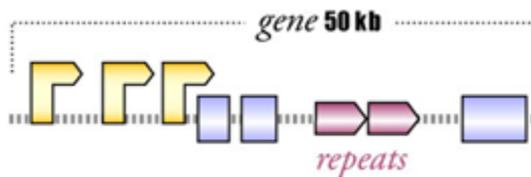
S. pombe
13.8 Mb
~5,000 genes (3 chr.)



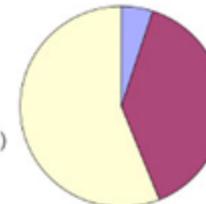
A. thaliana
125 Mb
>25,000 genes (5 chr.)



D. melanogaster
180 Mb
>14,000 genes (4 chr.)



M. musculus
2.4 Gb
>25,000 genes (20 chr.)



H. sapiens
3.2 Gb
>25,000 genes (23 chr.)



Major events in genome evolution

- Mutations (SNP)
- Duplications
 - genome-wide duplications
 - tandem duplications - amplifications
- Rearrangements
- Horizontal transfer
- Parasitic DNA

Some Data on Human Genome

- **3.1647 Bbp**
- **Average gene is three thousand bp long**
- **The longest gene (for dystrophin) is 2.4 Mbp long**
- **Total number of genes is estimated to be 25 000**
- **Less than 2% of DNA encode proteins**
- **Over 50% of identified genes have unknown functions**
- **Over 50% of junk DNA are repetitive elements**
- **Around 20% of our genome is transcribed**

Importance of chimp genome

Medical Condition

Definite

HIV progression to AIDS

Influenza A symptomatology

Hepatitis B/C late complications

Malaria

Menopause

Likely

E. coli K99 gastroenteritis

Alzheimer's disease pathology

Coronary atherosclerosis

Epithelial cancers

Speculative

Menstrual blood loss

Early fetal wastage

Human

Common

Moderate to severe

Moderate to severe

Susceptible

Universal

Resistant

Complete

Common

Common

Variable

High

Great Apes

Very rare

Mild

Mild

Resistant

Rare

Sensitive?

Incomplete

Uncommon

Rare

Lower amount?

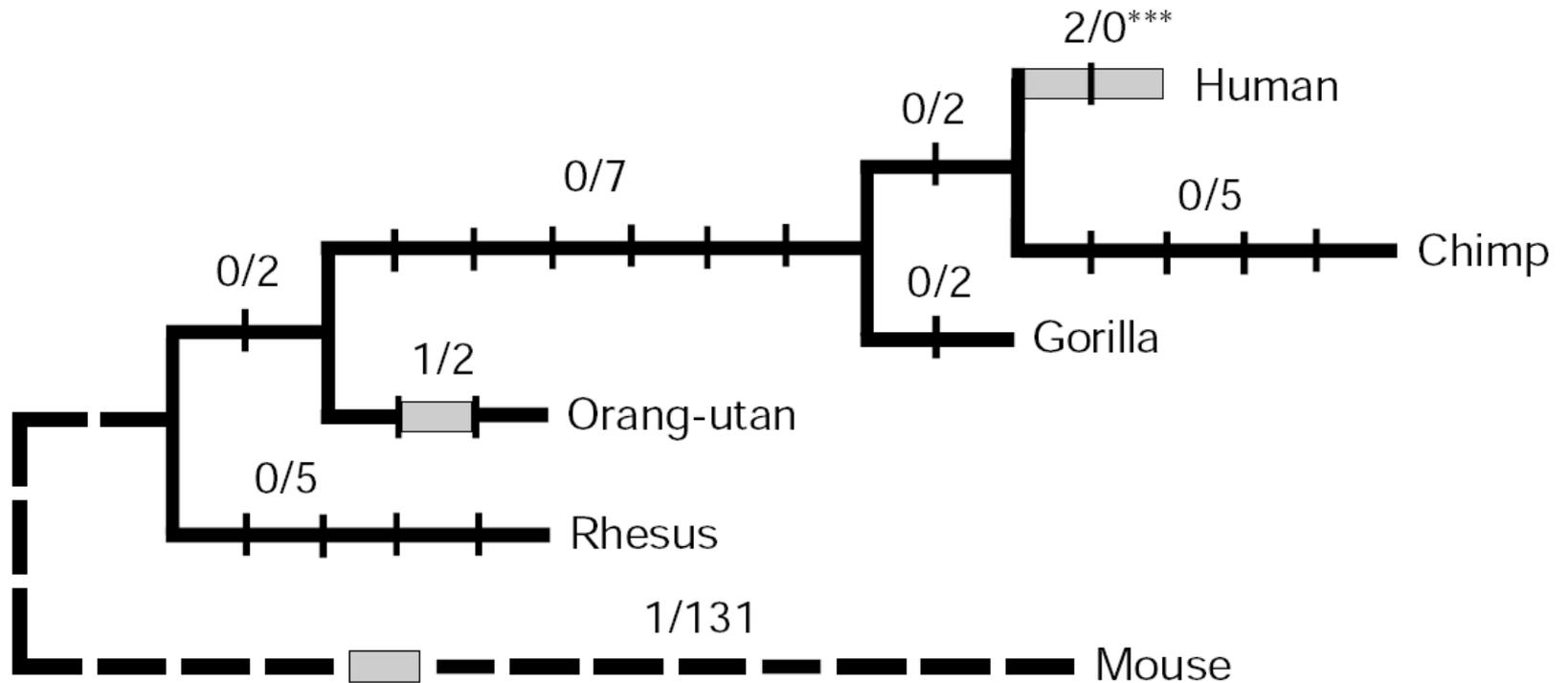
Low?



FOXP2

- **Mutations lead to articulation impairment (KE family).**
- **Only three aa changes between human and mouse.**
- **Two specific changes [thr -> asp (233) and asp -> ser (325)] appeared 100 000 – 200 000 years ago when *Homo sapiens* appeared.**

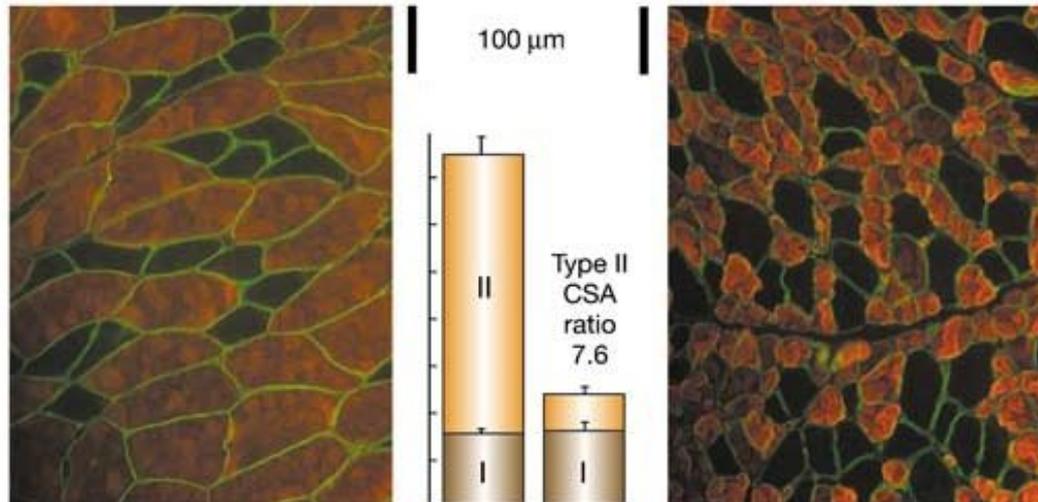
Evolution of FOXP2

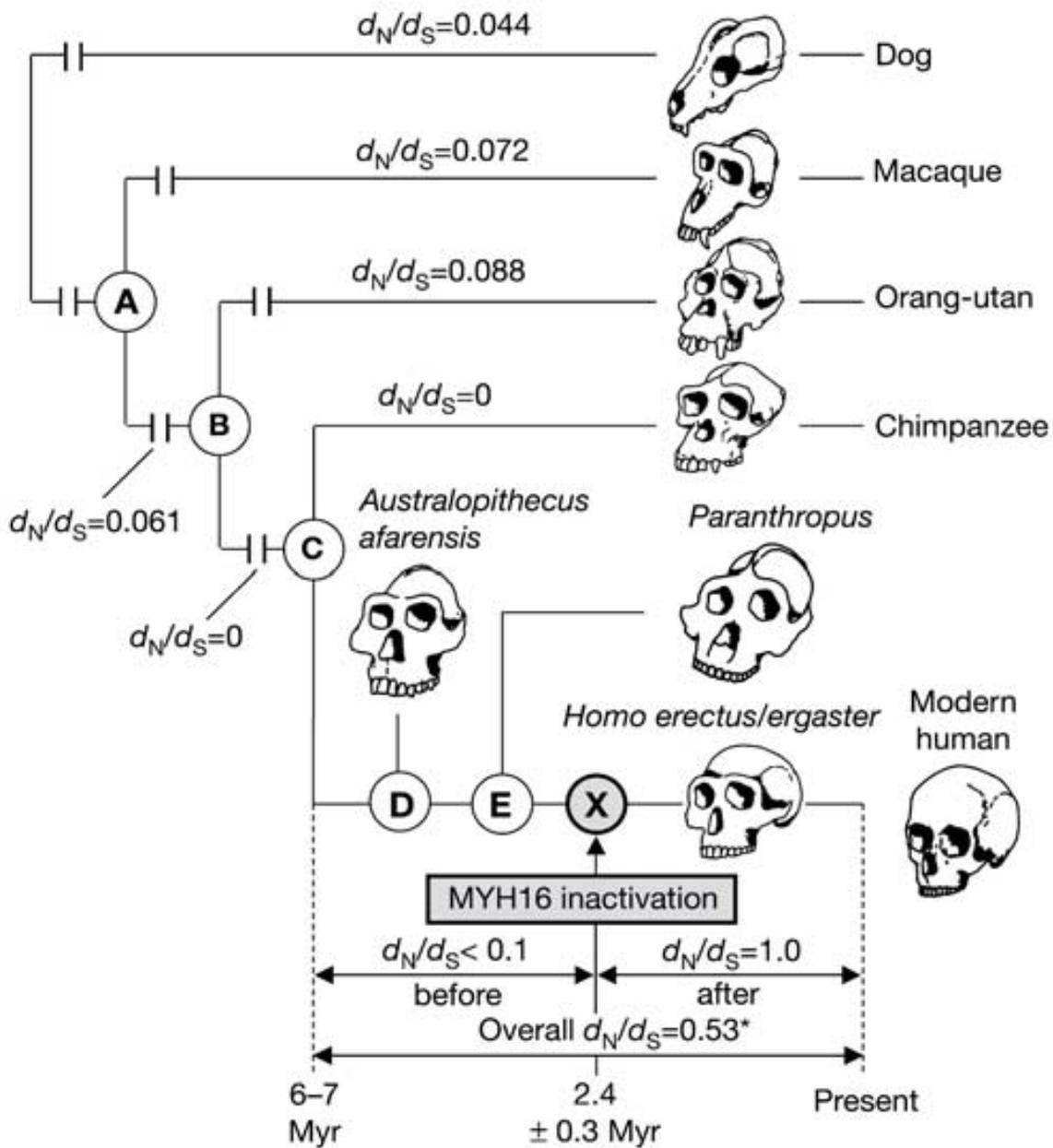


— Base substitution

■ Amino acid substitution

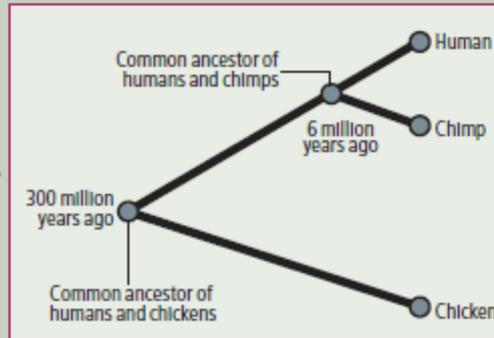
MYH16 inactivation





SCANNING THE GENOME

To find the parts of our genome that make us human, the author wrote a computer program that searched for the DNA sequences that have changed the most since humans and chimpanzees diverged from their last common ancestor. Topping the list was a 118-letter snippet of code known as human accelerated region 1 (HAR1). This region of the genome changed very little for most of vertebrate evolution, with chimp and chicken sequences differing by just two letters. Human and chimp HAR1s, however, differ by 18 letters, suggesting that HAR1 acquired an important new function in humans.



T	G	A	A	A	C	G	G	A	G	G	A	G	A	C	G	T	T	A	C
A	G	C	A	A	C	G	T	G	T	C	A	G	C	T	G	A	A	A	T
G	A	T	G	G	C	G	T	A	G	A	C	G	C	A	C	G	T	C	
A	G	C	G	G	C	G	G	A	A	A	T	G	G	T	T	T	C	T	A
T	C	A	A	A	T	G	A	A	A	G	T	G	T	T	T	A	G	A	
G	A	T	T	T	C	C	T	C	A	A	G	T	T	T	C	A			

Changes in human sequence relative to that of the chimp



T	G	A	A	A	T	G	G	A	G	G	A	G	A	A	A	T	T	A	C
A	G	C	A	A	T	T	A	T	C	A	A	C	T	G	A	A	A	T	
T	A	T	A	G	G	T	G	T	A	G	A	C	A	C	A	T	G	T	C
A	G	C	A	G	T	G	G	A	A	A	T	A	G	T	T	T	C	T	A
T	C	A	A	A	A	T	T	A	A	A	G	T	A	T	T	T	A	G	A
G	A	T	T	T	C	C	T	C	A	A	A	T	T	T	C	A			

Changes in chimp sequence relative to that of the chicken



T	G	A	A	A	T	G	G	A	G	G	A	G	A	A	A	T	T	A	C
A	G	C	A	A	T	T	A	T	C	A	A	C	T	G	A	A	A	T	
T	A	T	A	G	G	T	G	T	A	G	A	C	A	C	A	T	G	T	C
A	G	C	A	G	T	A	G	A	A	A	C	A	G	T	T	T	C	T	A
T	C	A	A	A	A	T	T	A	A	A	G	T	A	T	T	T	A	G	A
G	A	T	T	T	C	C	T	C	A	A	A	T	T	T	C	A			

ASPM and HAR1 involvement in brain formation

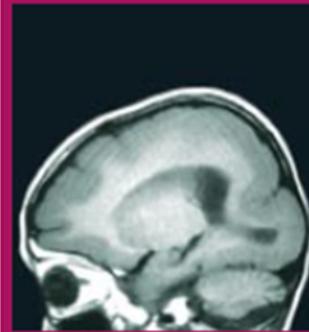
Normal brain



Mutated ASPM



HAR1 malfunction



BRAIN SHAPERS: Changes to certain genome sequences can have dramatic effects on the brain. Mutation of the *ASPM* gene, for example, leads to markedly reduced brain size (*middle*) compared with a normal brain (*top*), suggesting that this gene played a key role in the evolution of large brain size in humans. Malfunctions in the neurons in which *HAR1* is active during development, meanwhile, can lead to a severe disorder in which the brain's cerebral cortex fails to fold properly (*bottom*), hinting that *HAR1* is essential for the formation of a healthy cortex.

DISTINCTIVE DNA

Efforts to uncover uniquely human DNA have yielded a number of sequences that are distinctive in humans as compared with chimpanzees. A partial list of these sequences—and some of their functions—follows below.

SEQUENCE: *HAR1*

What it does: Active in the brain; may be necessary for development of the cerebral cortex, which is especially large in humans. Possibly also involved in sperm production.

SEQUENCE: *FOXP2*

What it does: Facilitates formation of words by the mouth, enabling modern human speech.

SEQUENCE: *AMY1*

What it does: Facilitates digestion of starch, which may have enabled early humans to exploit novel foods.

SEQUENCE: *ASPM*

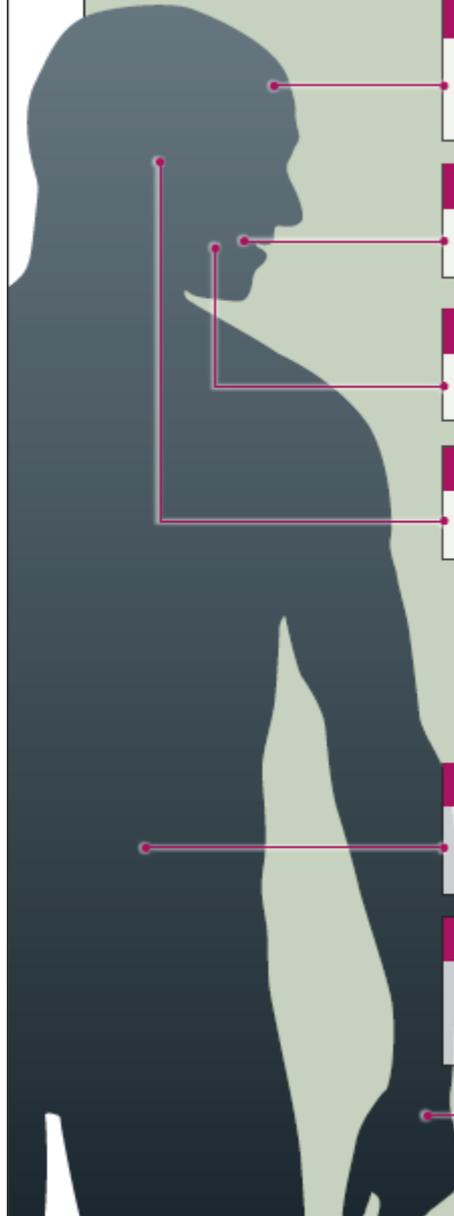
What it does: Controls brain size, which has more than tripled over the course of human evolution.

SEQUENCE: *LCT*

What it does: Permits digestion of milk sugar in adulthood, allowing people to make milk from domesticated animals a dietary staple.

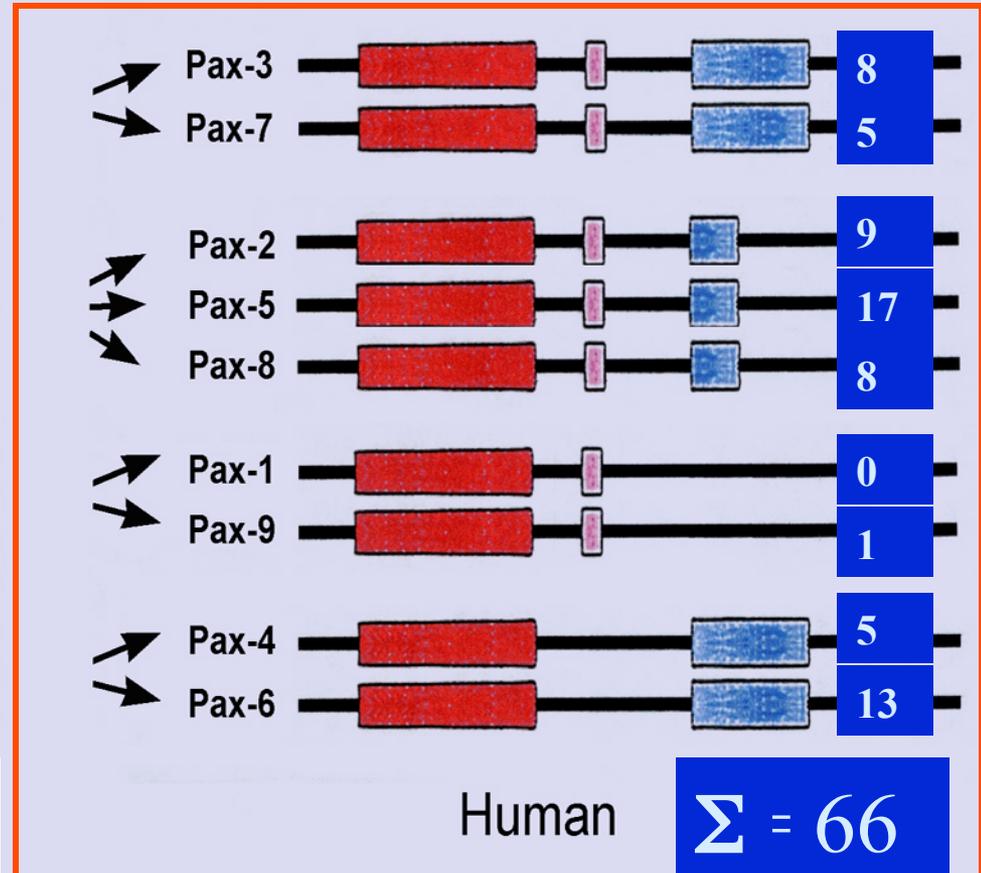
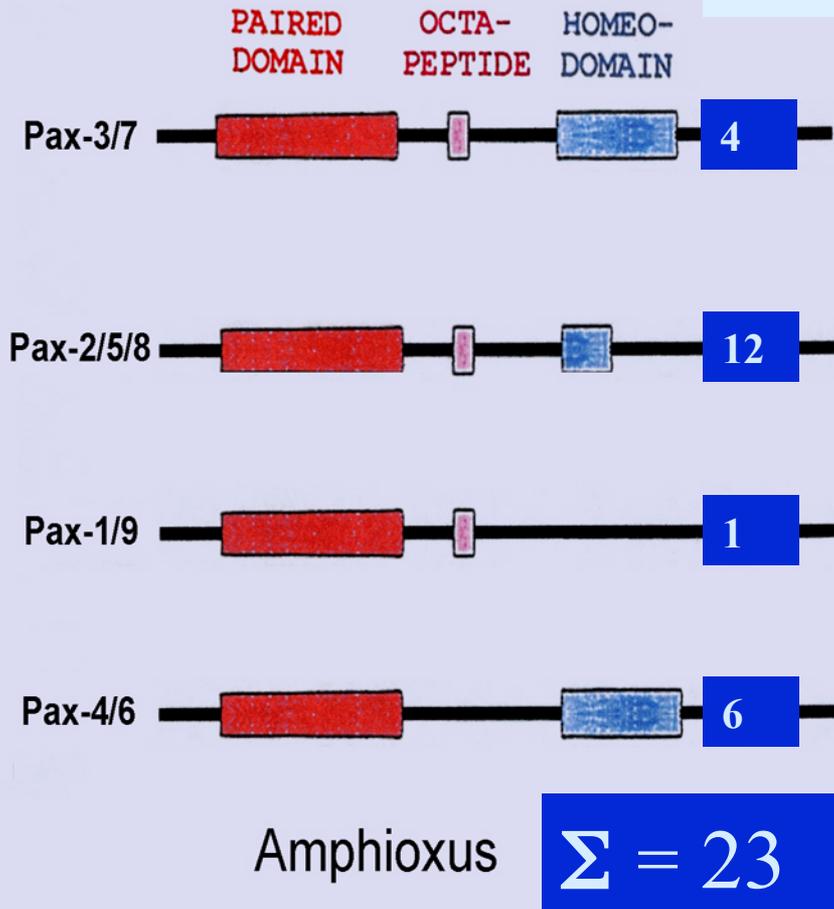
SEQUENCE: *HAR2*

What it does: Drives gene activity in the wrist and thumb during development, an activity that may have given the hand enough dexterity to make and use complex tools.



Pax genes: the vertebrate proteome is markedly larger than the amphioxus proteome:

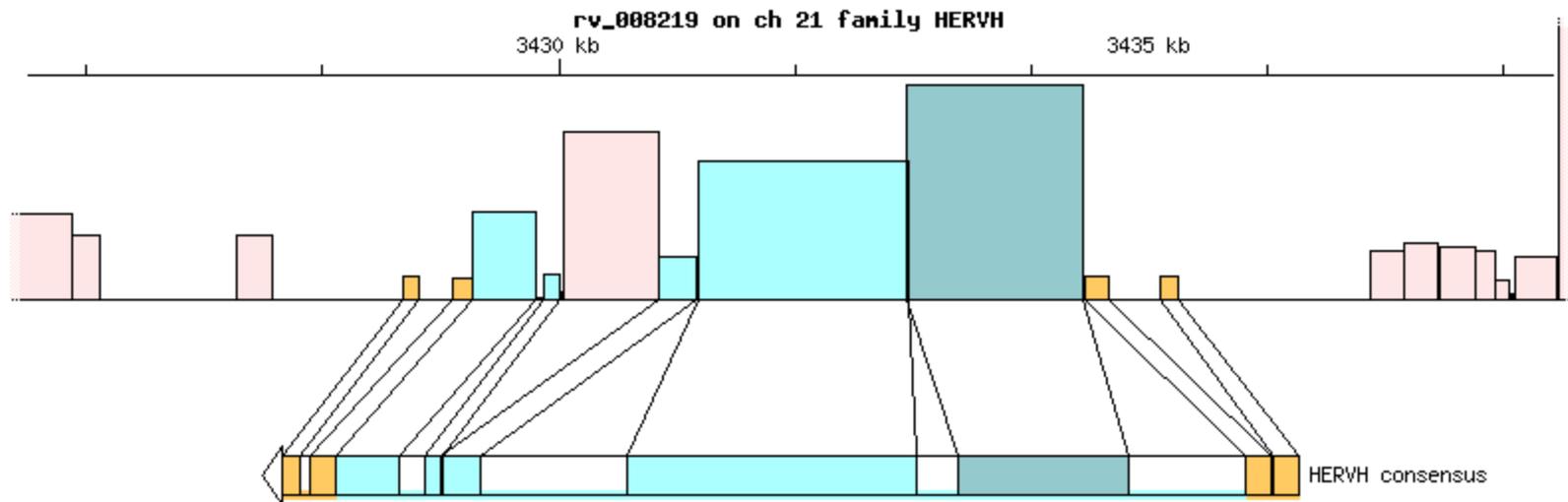
Protein isoforms



Importance of “junk” DNA

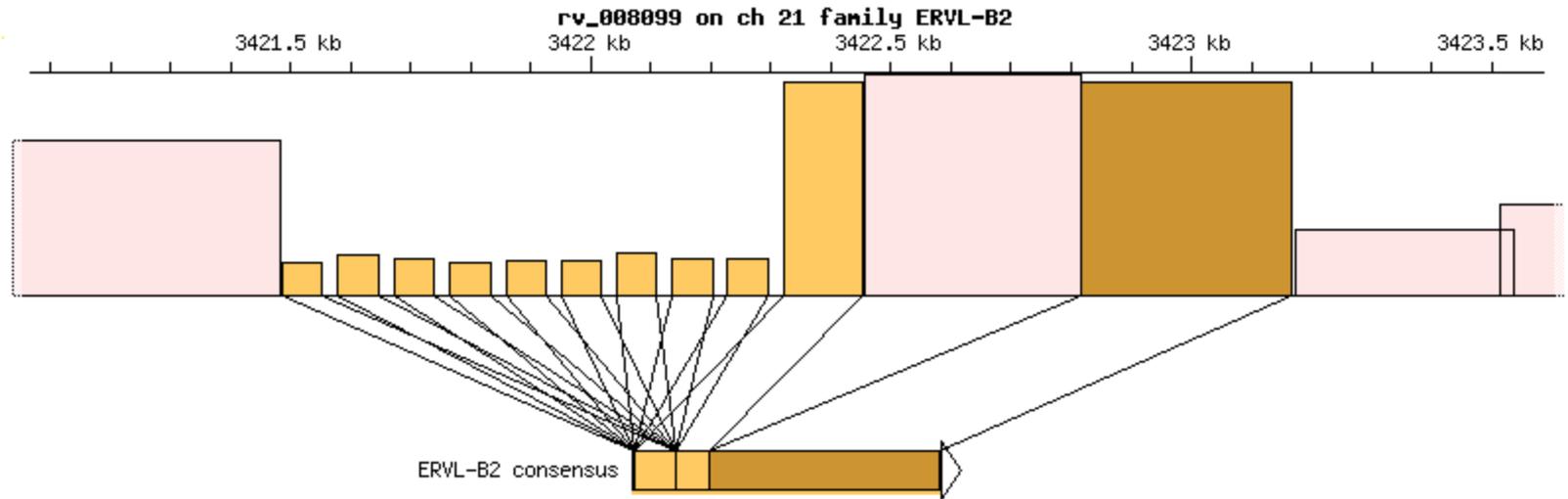
- ▶ Syncytin (adapted ancestral *env* polyprotein of HERV-W family)
- ▶ Social behavior in rodents (and possibly humans).
Microsatellite instability generates diversity in brain and sociobehavioral traits
- ▶ Regulation of gene expression and promotion of genetic diversity. Retrotransposons regulate host genes in mouse oocytes and preimplantation embryos
- ▶ Antifreeze-protein gene in fish
- ▶ Source of microRNAs. Highly conserved non-coding sequences are associated with vertebrate development
- ▶ LINE-1 retrotransposition is involved in repair of broken DNA strands

Human Endogenous Retroviruses (Example of HERV H)

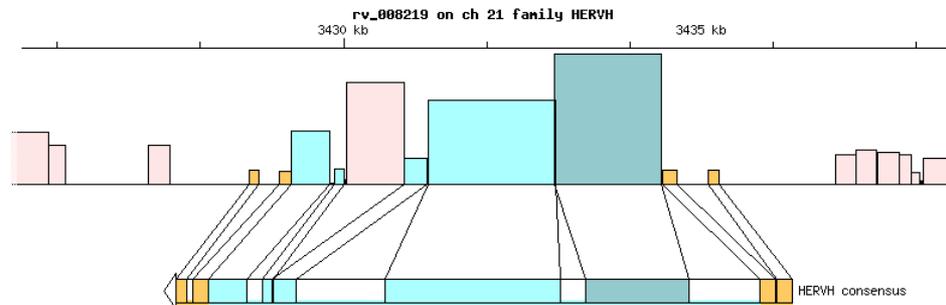


Color coding: Internal Internal used for classification LTR LTR used for classification Other HERV Other exo

Human Endogenous Retroviruses (Example of HERV L)



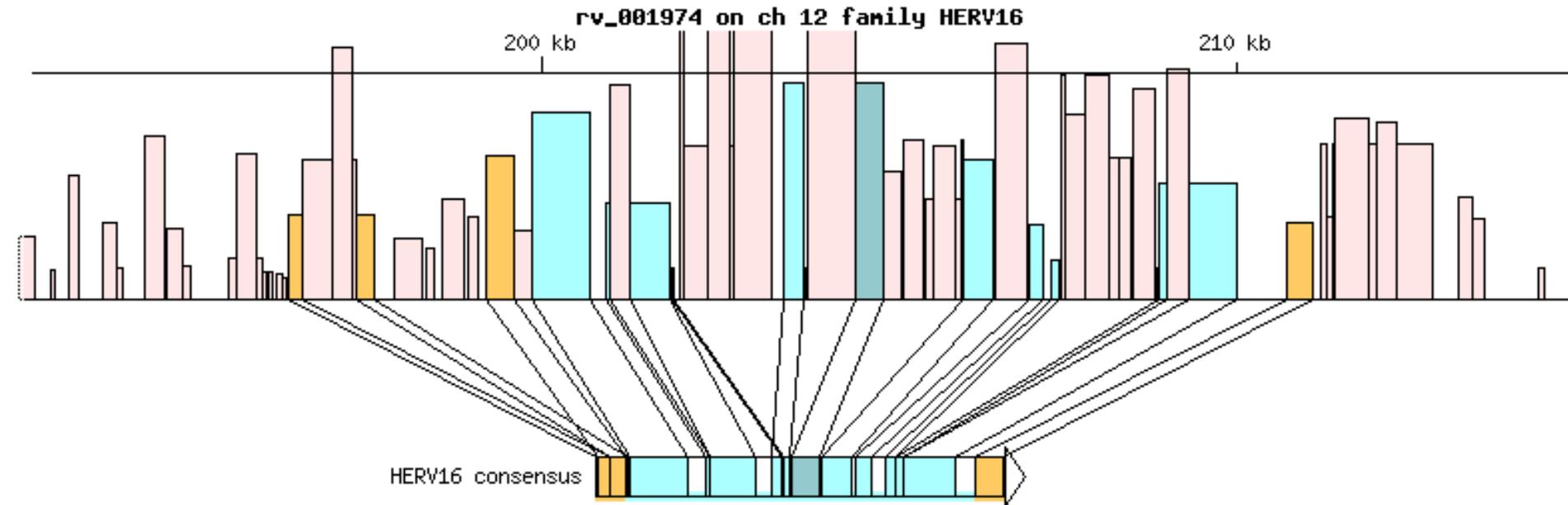
Color coding: Internal Internal used for classification LTR LTR used for classification Other HERV Other exo



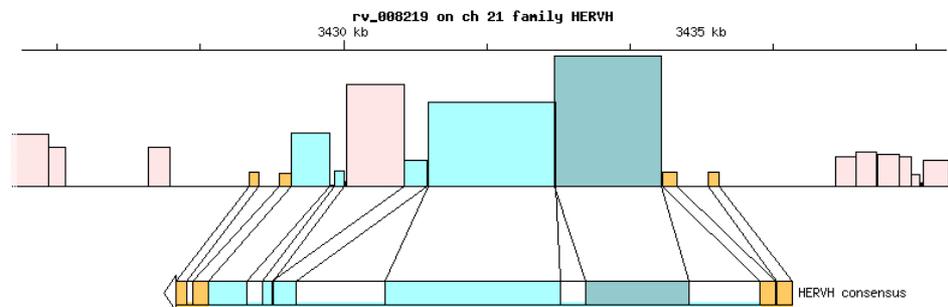
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HERV

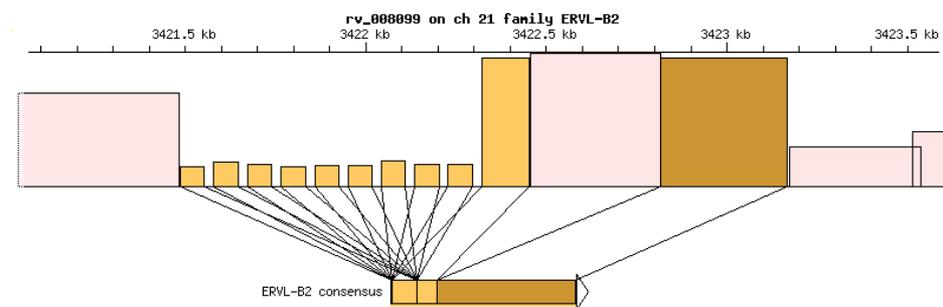
Human Endogenous Retroviruses (Example of HERV 16)



Color coding: Internal Internal used for classification LTR LTR used for classification Other HERV Other exo



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Other genes that may add to make us humans

An intelligence gene

A gene called *SRGAP2* was duplicated three times. As a result, our ancestors had several copies, some of which could evolve freely. One of the mutated copies turned out to be better than the original. It seems to have caused our brain cells to extrude more spines, allowing them to form more connections.

Added dexterity

Our hands are unusually dextrous, allowing us to make beautiful stone tools and write words. That might be partly down to a bit of DNA called *HACNS1*, which has evolved rapidly since our ancestors split from the ancestors of chimps. We don't know what *HACNS1* does, but it is active in our arms and hands as they develop.

Power to the brain

After the human line split from the chimp line, two genes mutated. *SLC2A1* and *SLC2A4* both build proteins that transport glucose in and out of cells. The tweaks may have taken glucose away from muscles and into the early hominins' brains. The glucose would then have boosted the brains, allowing them to grow bigger.

Lidský genom – etické aspekty

Důvěrnost dat

Patentování genů

Genová terapie (somatické buňky vs. zárodečné buňky)

„Pozitivní“ genové inženýrství

Lidské buňky – etické aspekty

Klonování

Embryonální kmenové buňky

Applications of Molecular Genetics

1. **Transgene organisms**

- Microorganisms producing important proteins (enzymes, hormones...)
- Higher organisms producing important proteins (e.g. in milk)
- Improved organisms (e.g. for agriculture, bioremediations...)

2. **Diagnostics** (prenatal, infections...)

3. **Forensics** (DNA tests)

4. **Gene therapy**

- Somatic cells
- Germinal cells
- „Positive“ gene engineering

5. **Protein engineering**

