

AUTOSOMAL DNA COUSINS? NOT SO FAST!

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April 3, 2017

FAMILY TREE OF ALL LIFE

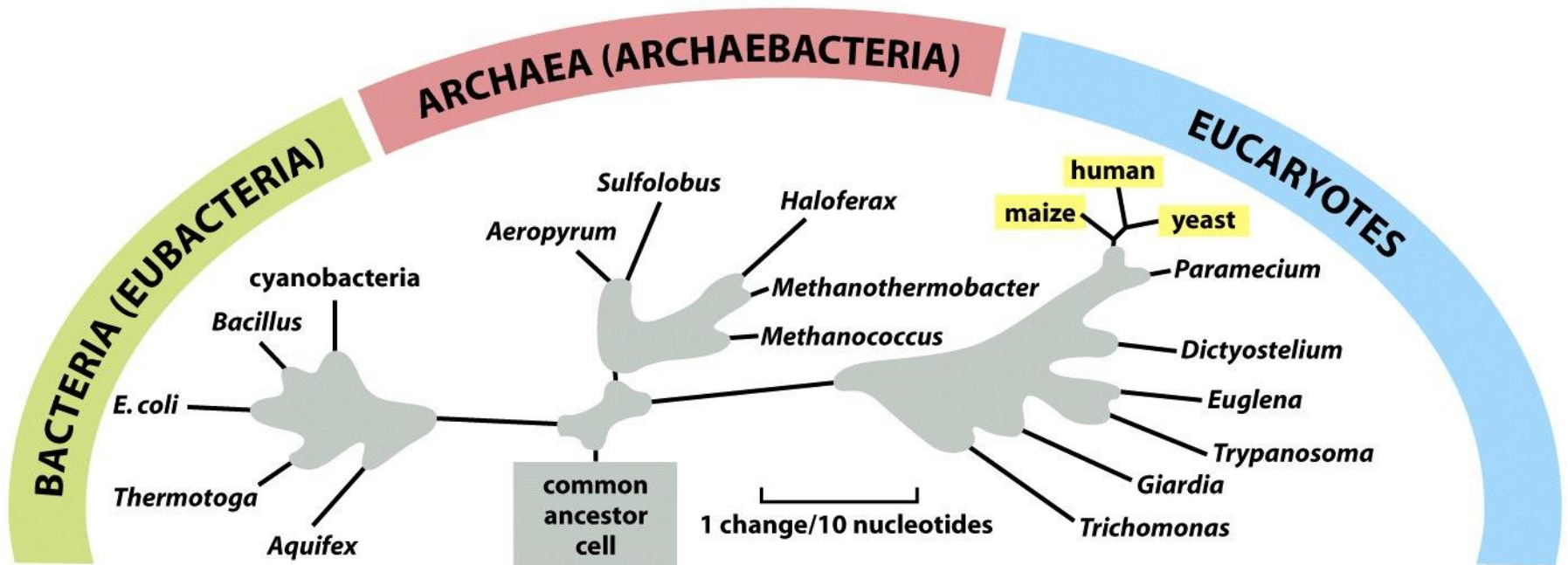


Figure 1-21 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Time span: about 3.5 billion years from the original common ancestor cell to the present. To some degree, we are cousins with every living thing on Earth today.

These are all of our cousins, so far. 2.3 million named species out of an estimated 8.7 million. 15 thousand are discovered every year. About 5% have had their DNA completely sequenced.

The Circle of Life

Lineages of all known species on earth are finally pieced together

Since Charles Darwin's day, biologists have depicted how new organisms evolve from old ones by adding branches to numerous trees that represent portions of the animal, plant and microbial kingdoms. Researchers from a dozen institutions recently completed a three-year effort to combine tens of thousands of trees into one diagram, most readable as a circle (*below*). The lines inside the circle represent all 2.3 million species that have been named. Biologists have genetic sequences for only about 5 percent of them, however; as more are finished, the relation-

ships within and across groups of species may change. Experts estimate that up to 8.7 million species may inhabit the planet (about 15,000 are discovered every year). "We expect the circle to broaden," says Karen Cranston, a computational evolutionary biologist at Duke University.

Anyone can propose updates to the database (OpenTreeOfLife.org). Greater detail could improve understanding of evolution and help scientists invent drugs, make crops more productive and better control infectious diseases. —Mark Fischetti

How to Read the Circle of Life

Primordial life begins at the center and branches out in all directions, leading to the groups of species that exist today (*colored rings*)

Outer ring: Estimated proportion of all species*

Inner ring: Proportion of the groups named to date

Each black line represents at least 500 descendant species

Dark lines: Many species have been genetically sequenced

Light lines: Few species have been genetically sequenced

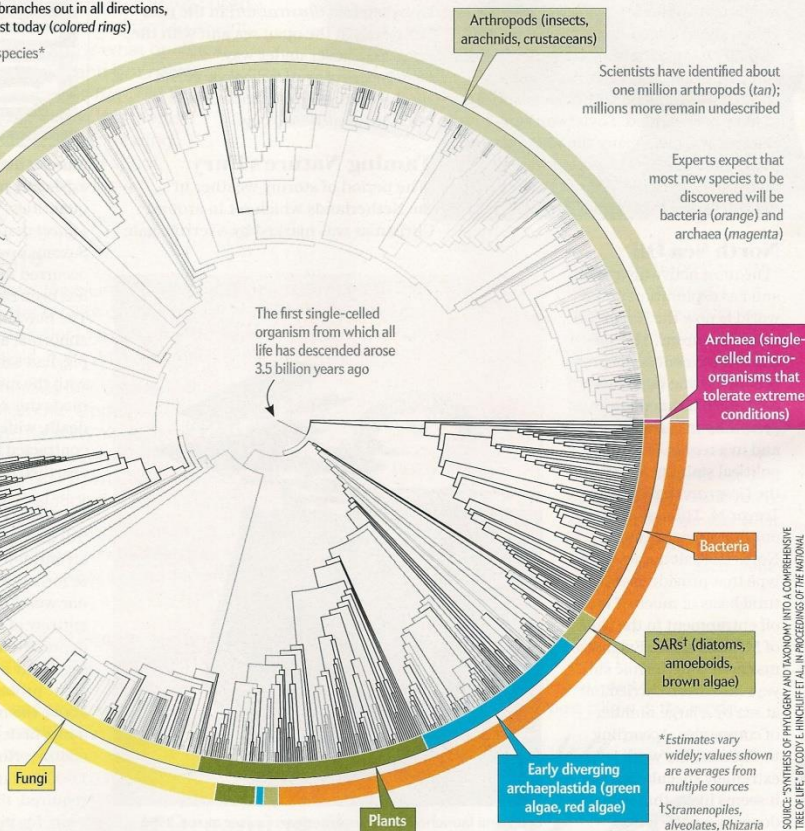
Nematodes (roundworms)

Lophotrochozoa (mollusks, segmented worms, brachiopods)

Deuterostomia (vertebrates, sea stars and urchins, certain worms)

Early diverging metazoa (cnidaria, comb jellies, sponges)

Many deuterostomia (*gold*) and plants (*dark green*) are already genetically sequenced (*dark lines*) because they are culturally or economically important (such as humans!)



*Estimates vary widely; values shown are averages from multiple sources
†Stramenopiles, alveolates, Rhizaria

SOURCE: "AN UNBIASED PHYLOGENY AND TAXONOMY INTO A COMPREHENSIVE TREE OF LIFE," BY MARK FISCETTI ET AL., IN PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES USA, NO. 41, VOL. 10, OCTOBER 13, 2015

TOTAL NUMBER OF GENOMES SEQUENCED, 2014

Organism	Completed sequences
Bacteria, (archaea)	17,420 (362)
Fungi	356
Insects	98
Plants	150
Vertebrates (mammals)	235 (80)
Marine invertebrates	16
Nematodes (worms)	17
Drosophila (fly)	21

SHARED DNA SEQUENCES AMONG DISTANT RELATIVES

GTTCCGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCC human
GCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTTAAAGGAATTGGCGGGGAGCACTACAACGGGTGGAGCCTGCGGTTTAATTGGATTCAACGCCGGGCATCTTACCA *Methanococcus*
ACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGC.ACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCT *E. coli*
GTTCCGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCC human

Figure 1-22 Molecular Biology of the Cell 5/e (© Garland Science 2008)

“Railroad ties” between sequences indicate identical bases. *E. Coli* and *Methanococcus* are eubacteria and archaebacteria, respectively.

MECHANISMS FOR CHANGING GENES

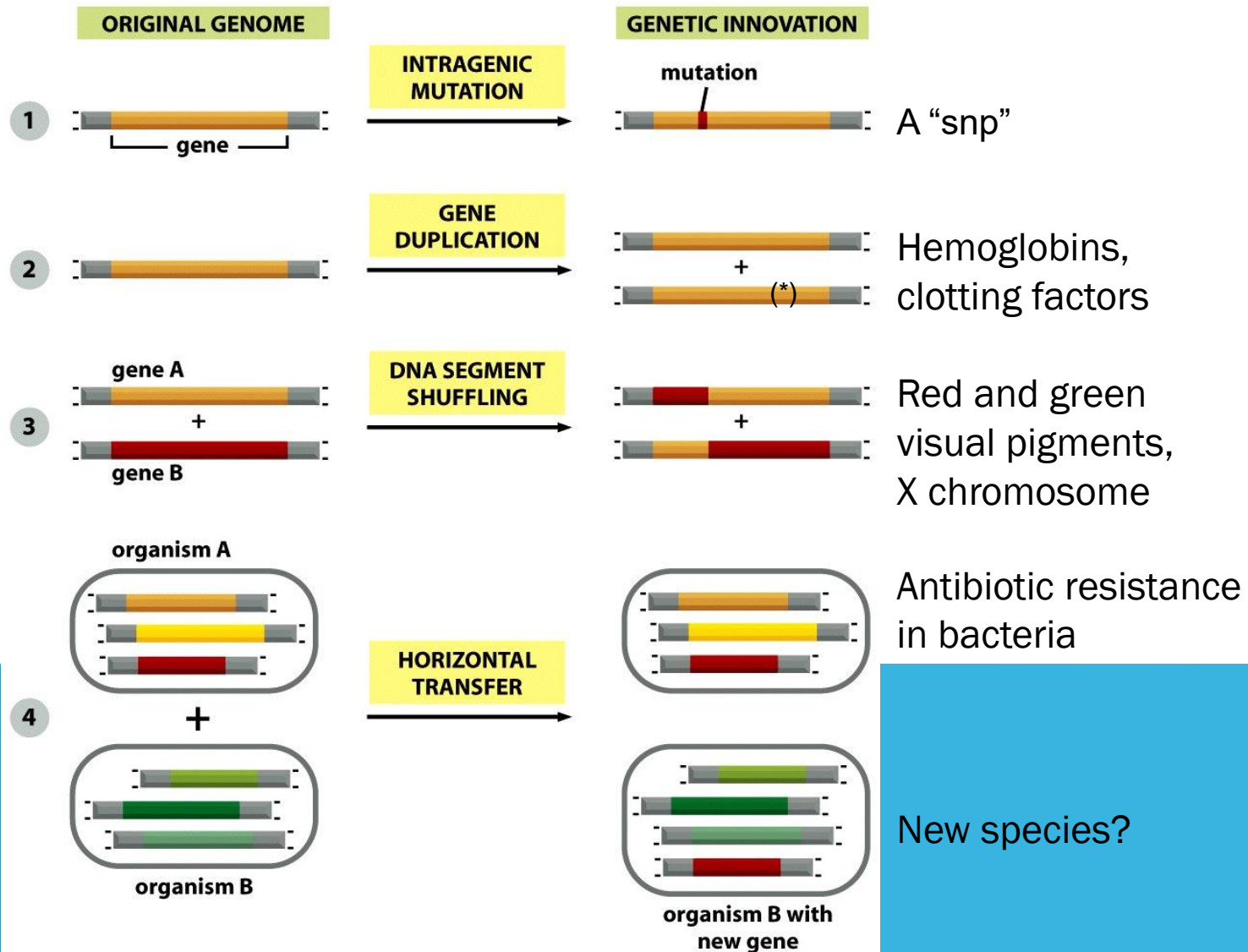


Figure 1-23 Molecular Biology of the Cell 5/e (© Garland Science 2008)

FAMILY TREE OF HEMOGLOBINS

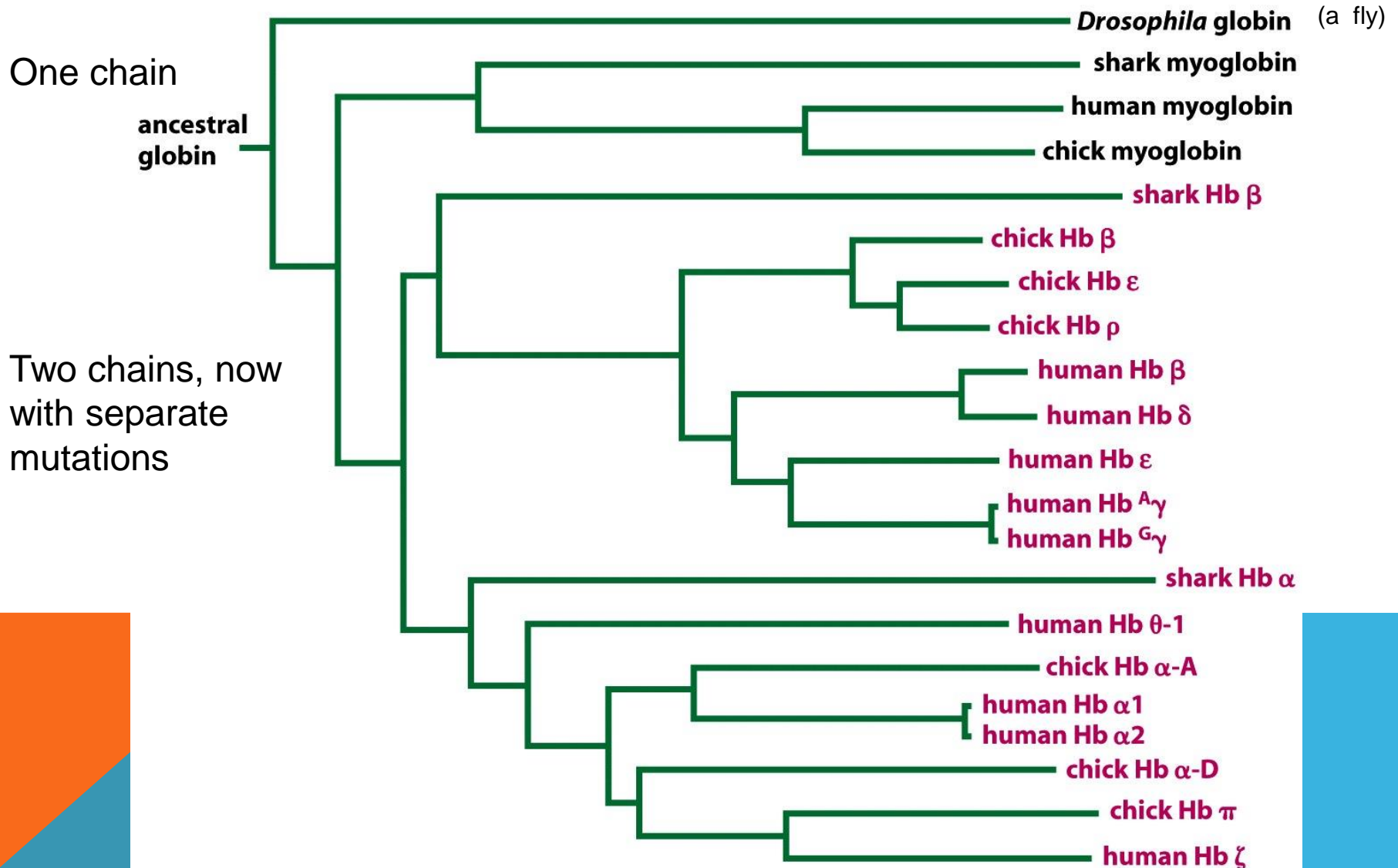


Figure 1-26 Molecular Biology of the Cell 5/e (© Garland Science 2008)

DIAGRAM OF EUKARYOTIC CELL (TRUE NUCLEUS)

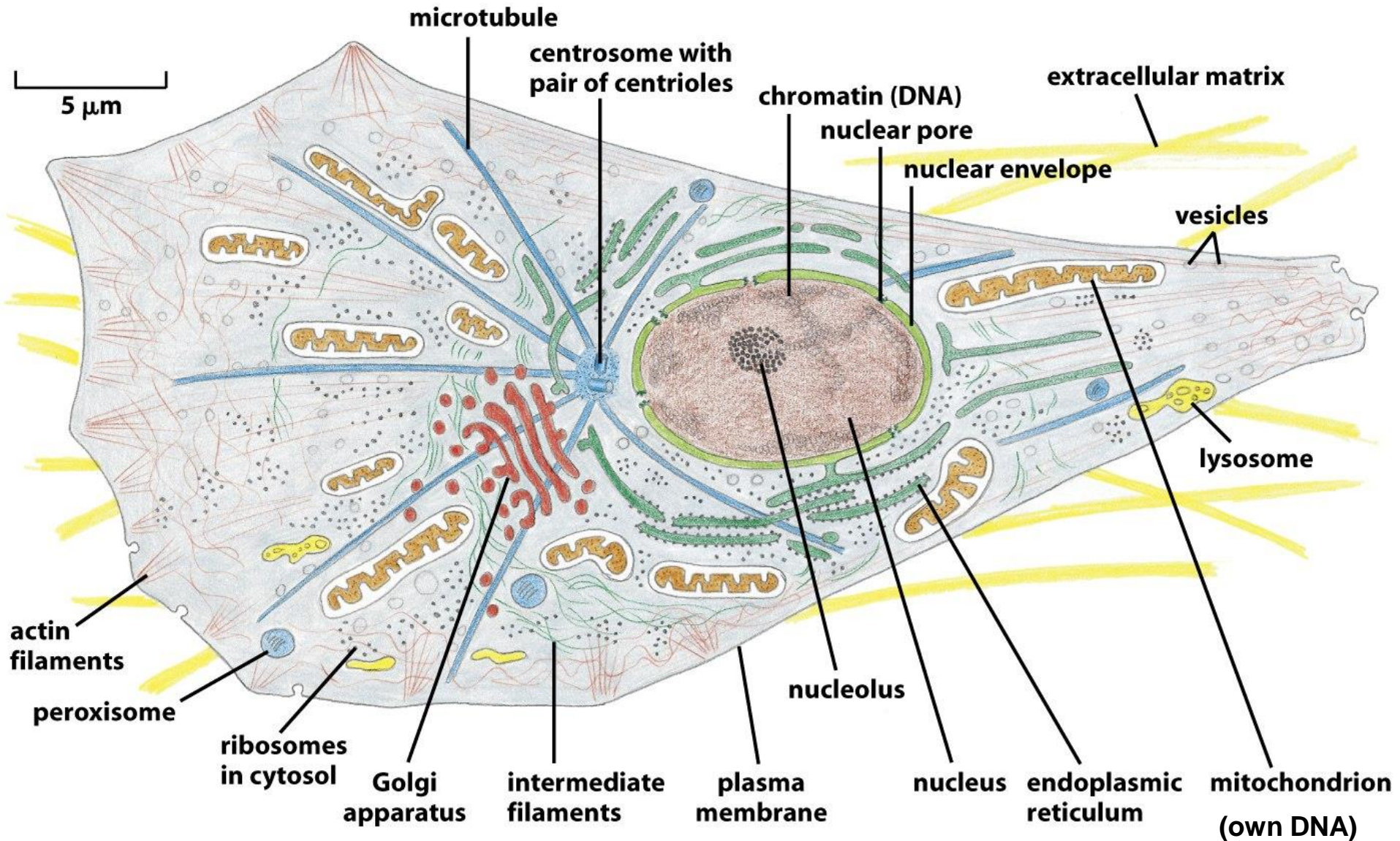
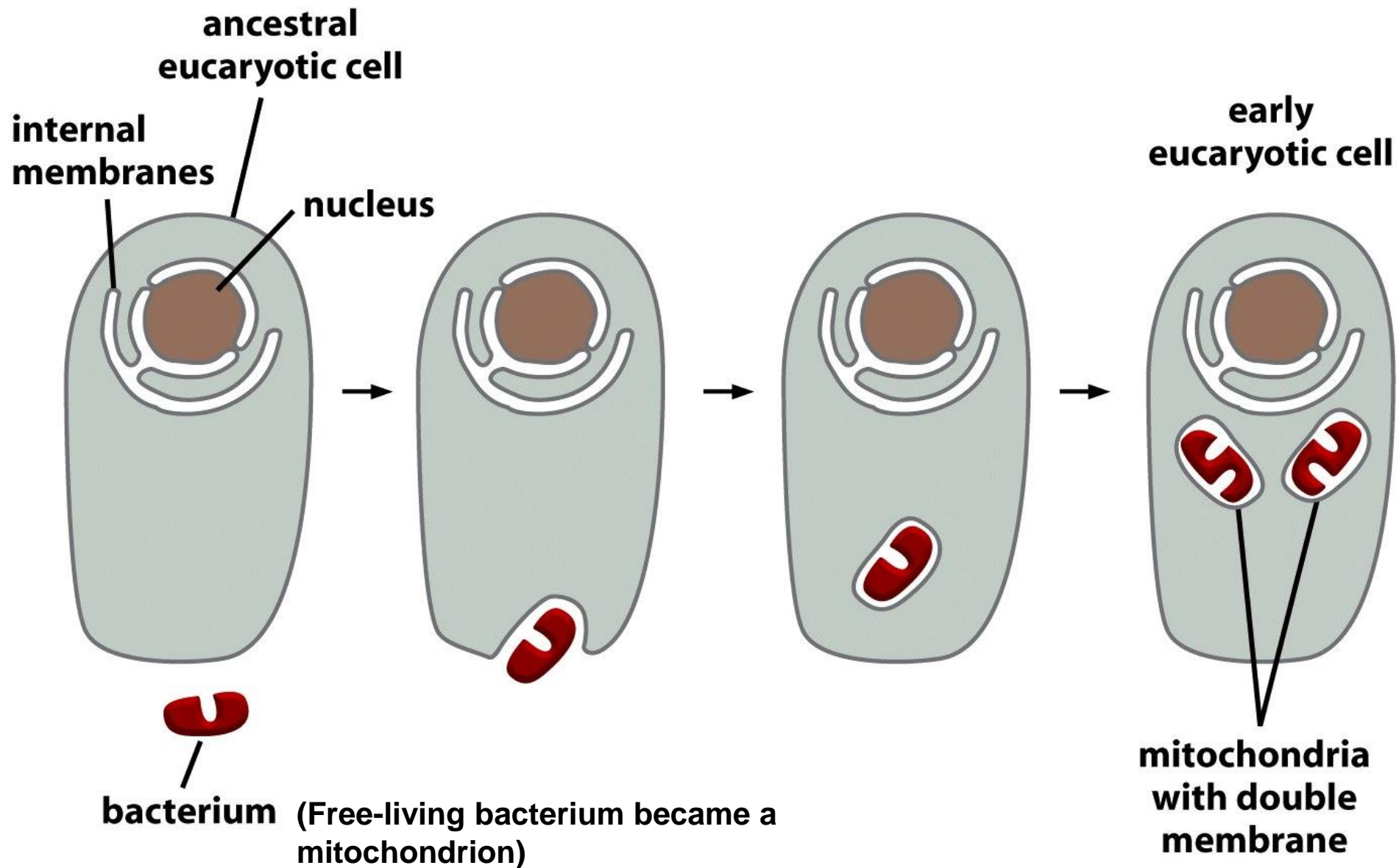
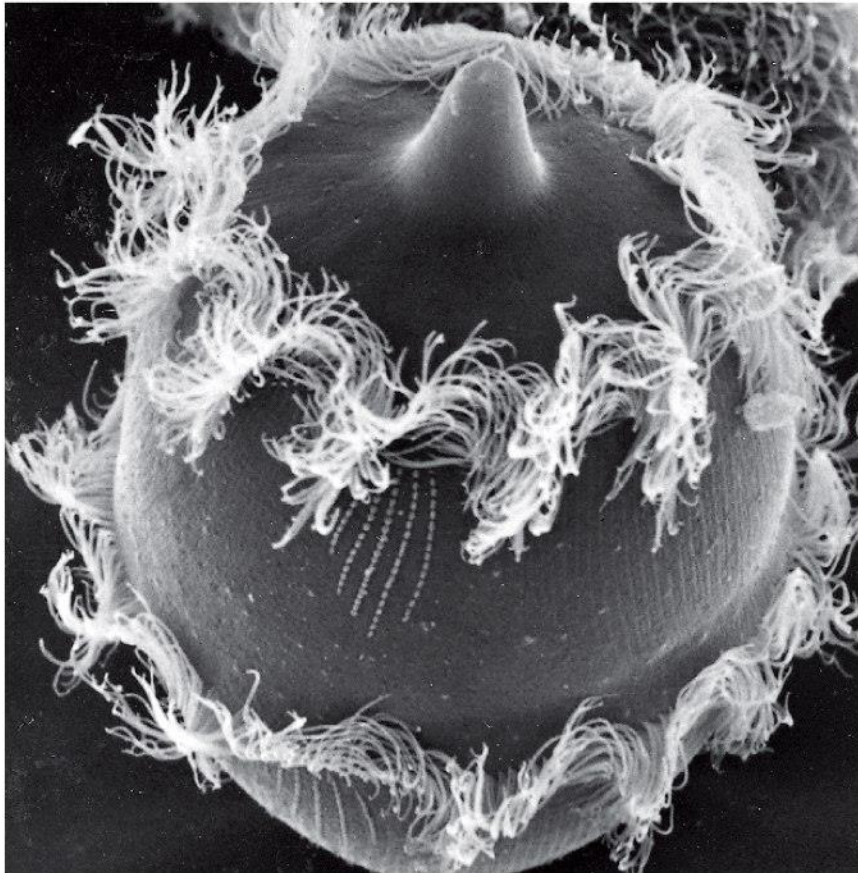


Figure 1-30 Molecular Biology of the Cell 5/e (© Garland Science 2008)

BECOMING A MITOCHONDRION, THE CELL'S ENERGY FACTORY

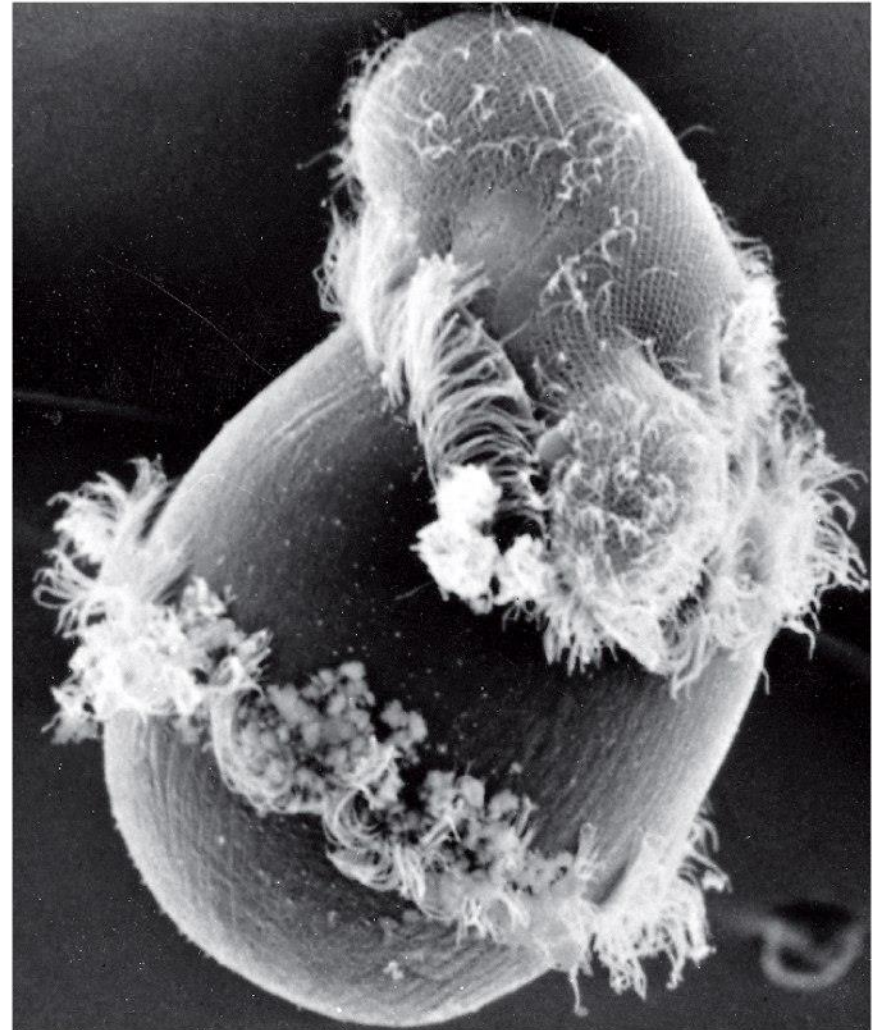


BECOMING A MITOCHONDRION TODAY - THIS PROCESS IS STILL GOING ON



(A)

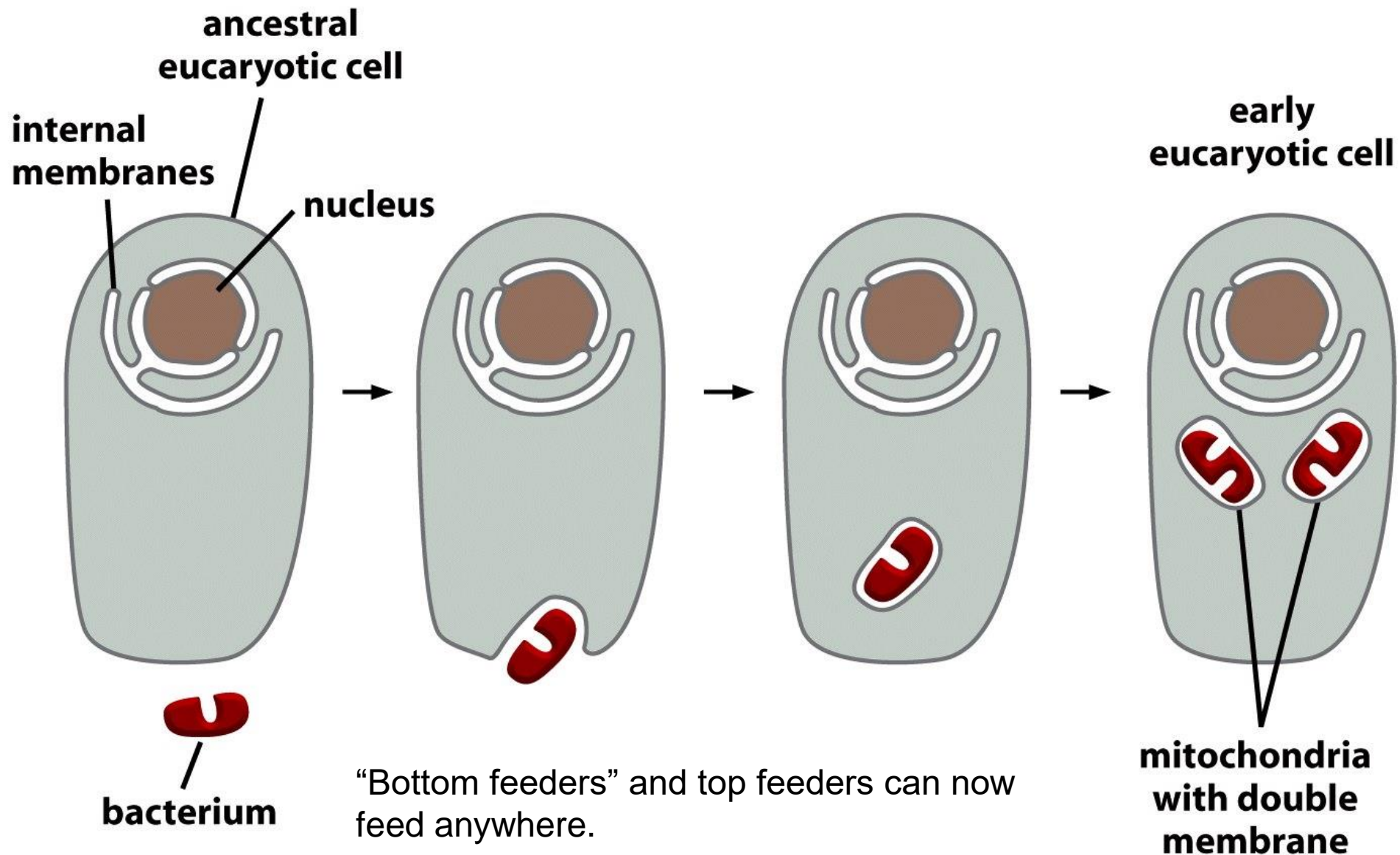
100 μm



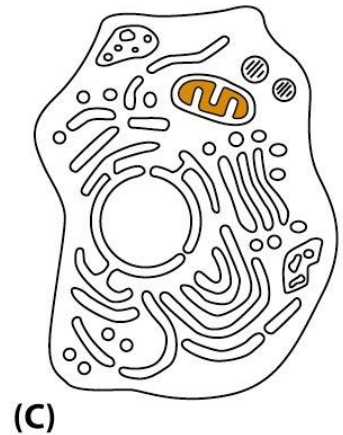
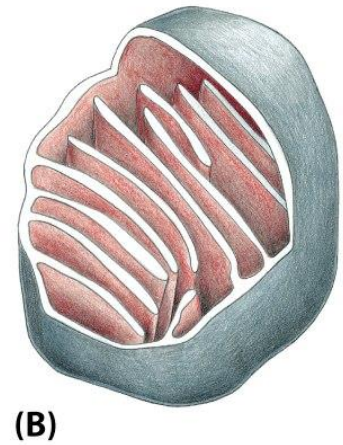
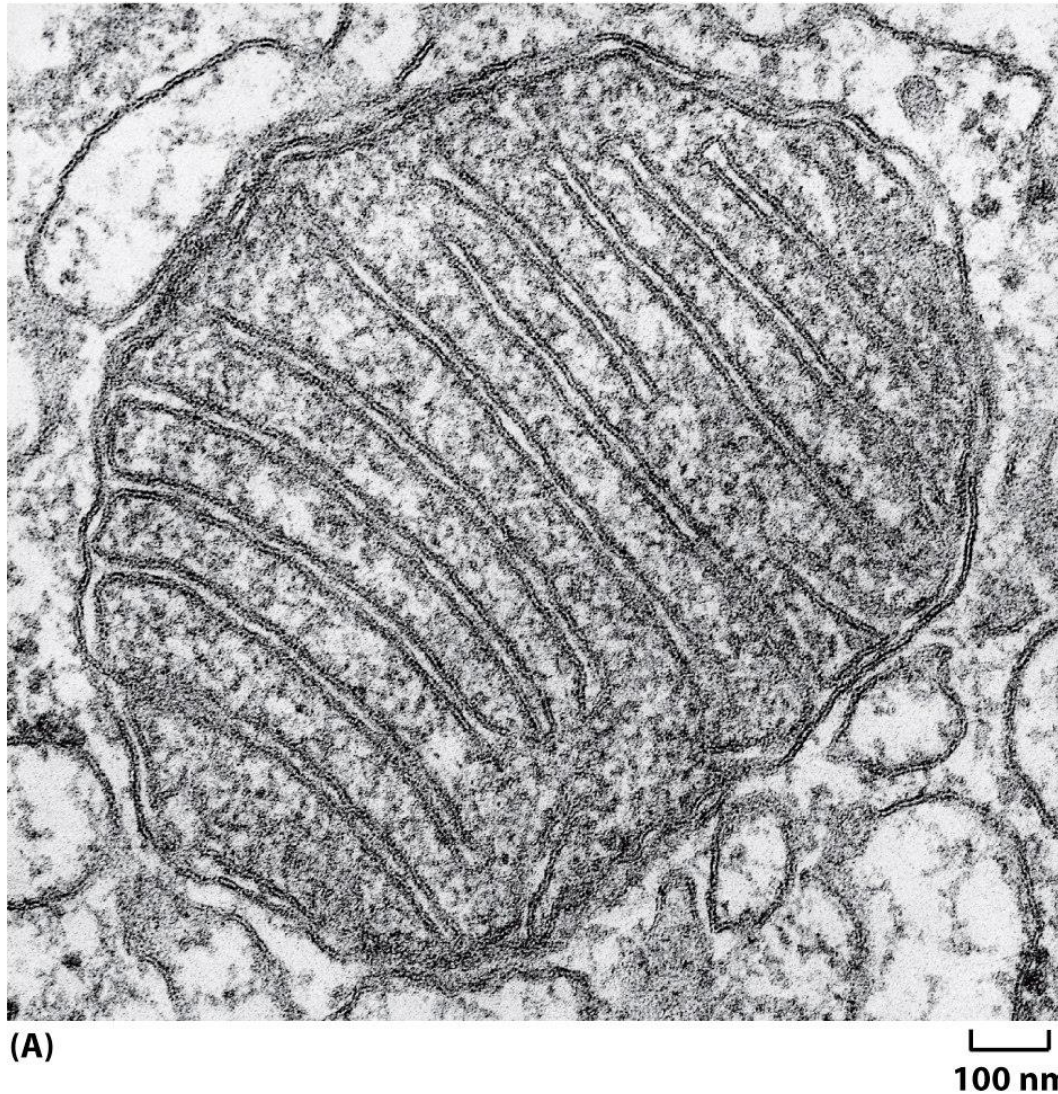
(B)

Cell on bottom eating cell on top

BECOMING A MITOCHONDRION, SYMBIOSIS - ONE ORGANISM ANEROBIC; ONE AEROBIC



MITOCHONDRIAL STRUCTURE - LINES OF MEMBRANES FOR ELECTRON AND ENERGY TRANSPORT. DNA NOT SHOWN

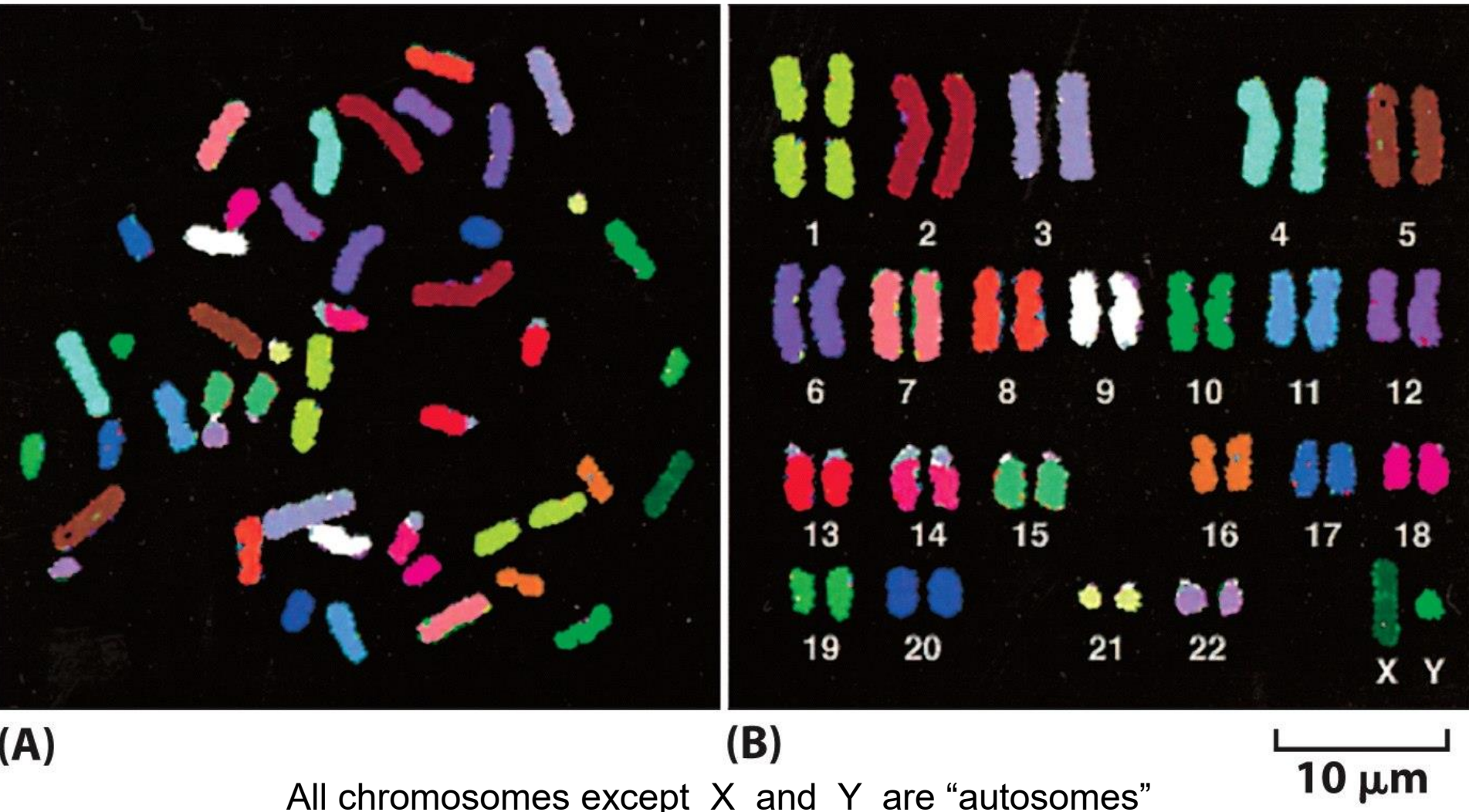


**TWO “COUSINS” SHARING THE SAME GENE (KIT)
WITH THE SAME MUTATION: THE GENE IS A TYROSINE
KINASE THAT FUNCTIONS IN NORMAL DEVELOPMENT AND
IS ALSO RESPONSIBLE FOR SOME MALIGNANCIES**

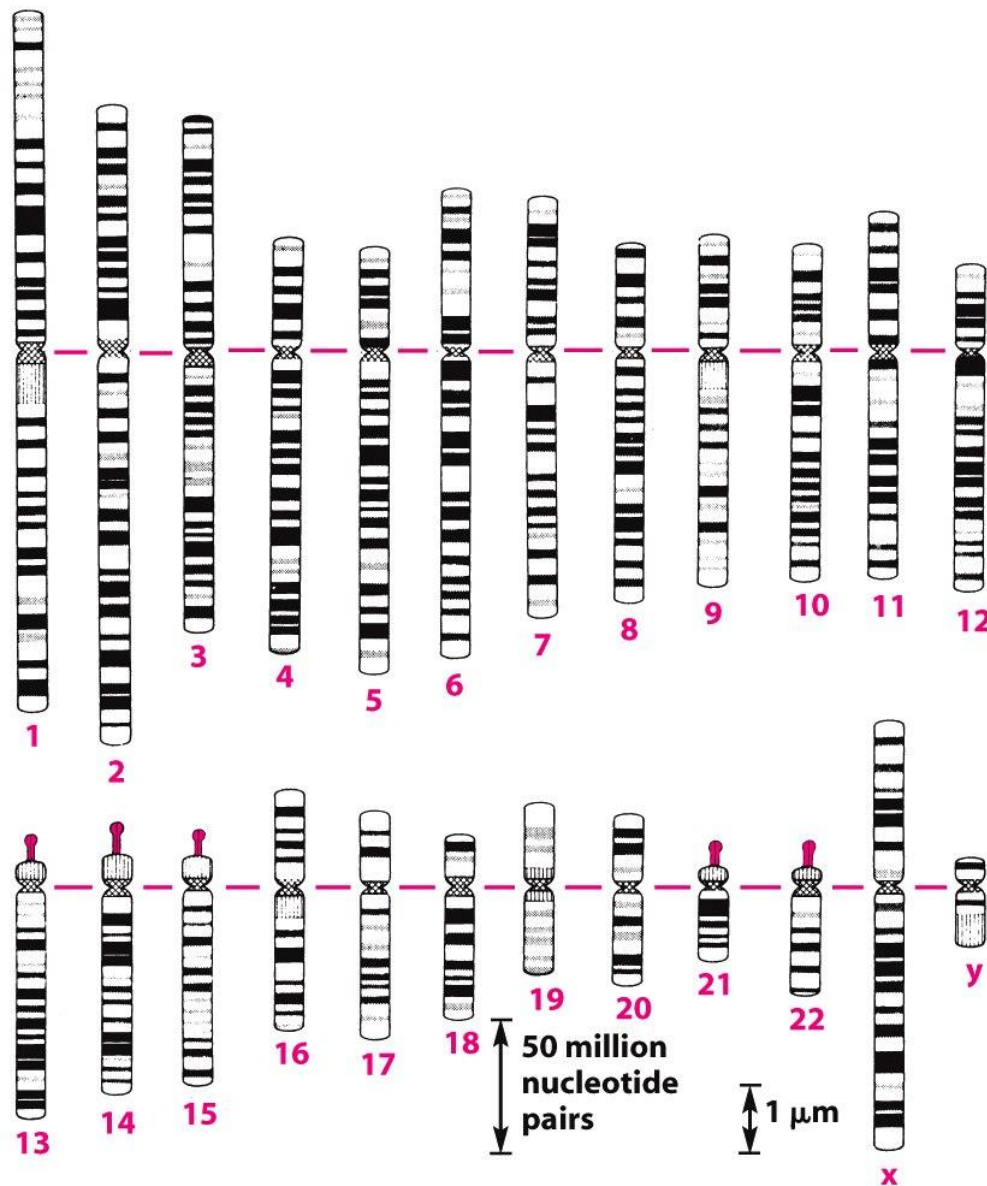


Figure 1-53 Molecular Biology of the Cell 5/e (© Garland Science 2008)

“PAINTED” HUMAN CHROMOSOMES, DIFFERENT GROUPS OF GENES CAN BE STAINED DIFFERENT COLORS



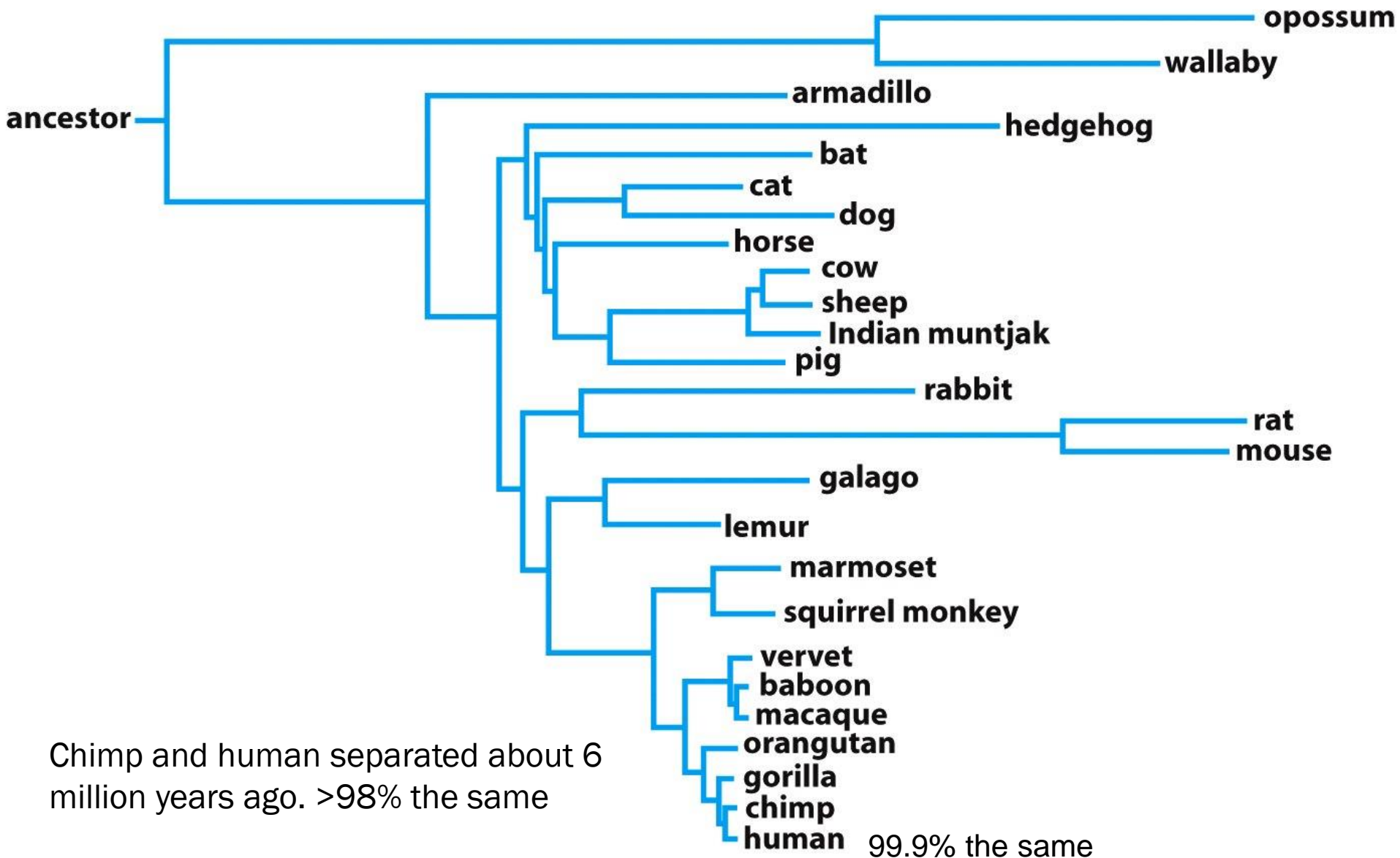
HUMAN CHROMOSOME DIAGRAM, DIFFERENT DNA SEQUENCES ARE DARK OR LIGHT



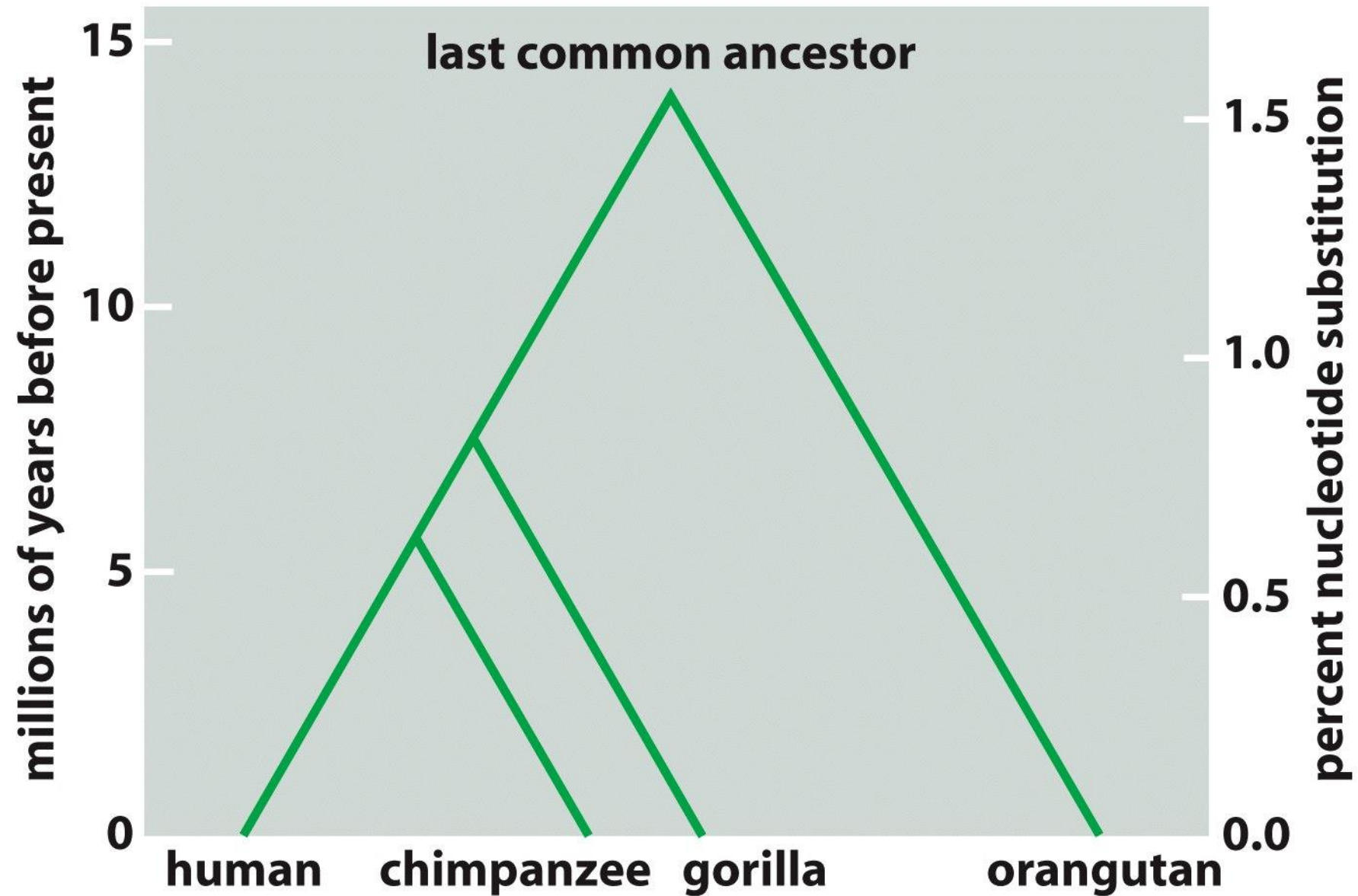
All but X and Y
are called
autosomes

Three billion total nucleotide pairs. All
autosomes can pair with each other
and exchange genes. One autosome
from mom, one from dad.

FAMILY TREE OF DISTANT RELATIVES (COUSINS)



FAMILY TREE OF CLOSER RELATIVES



SHARED GENES AMONG “COUSINS”

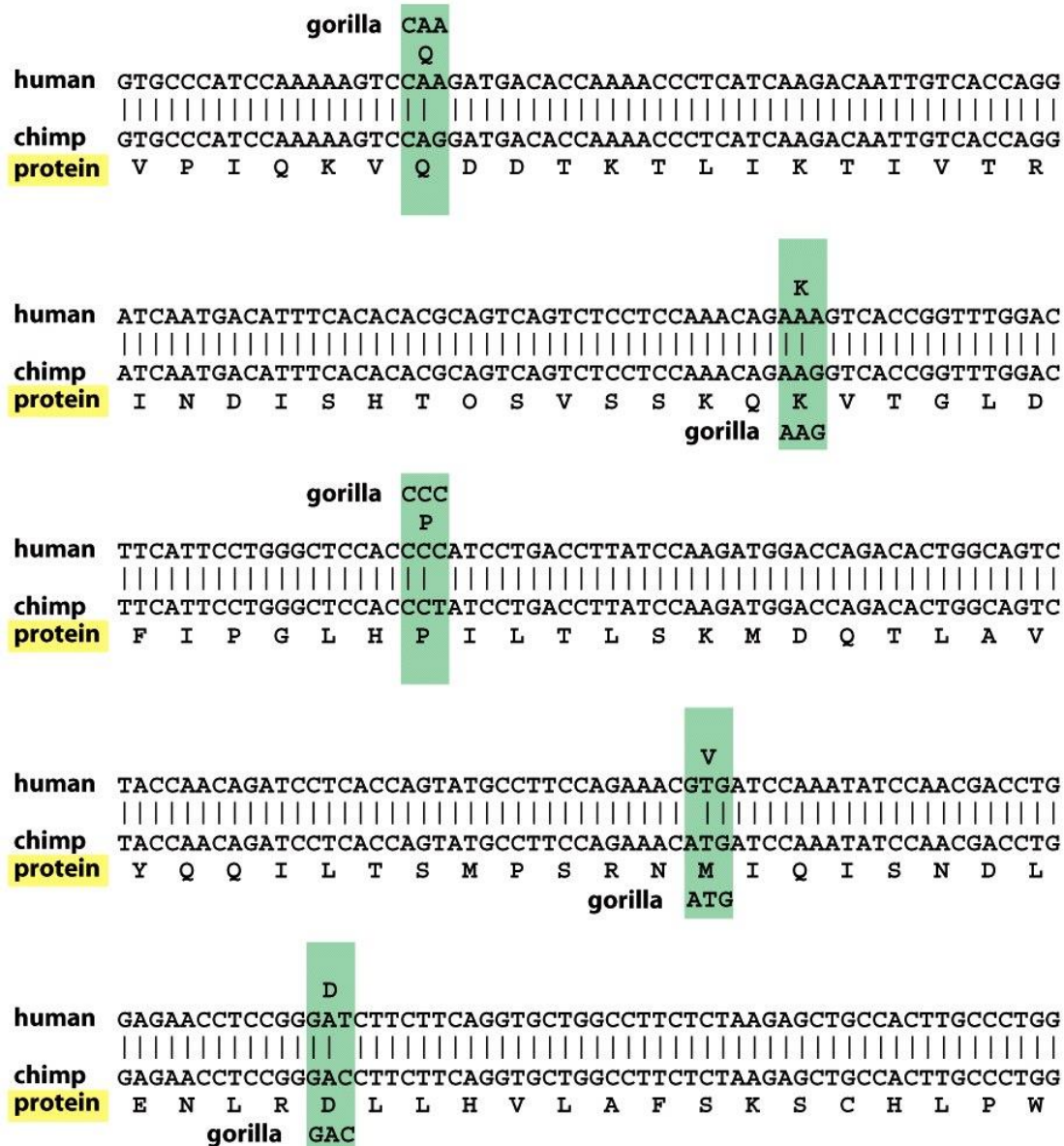


Figure 4-76 Molecular Biology of the Cell 5/e (© Garland Science 2008)

NEUTRAL VERSUS OTHER MUTATIONS

In some languages, some words that mean the same thing are spelled differently:

“Grey” and “gray” mean the same thing as do “color” and “colour.” Tyre, tire, jail, gaol. These are neutral mutations.

However, between different languages (species) words that have been separated for a long time usually vary more in spelling

In German, “grau” means “gray.”

In Italian, “tavola” means “table.”

By comparing large groups of such words linguists can estimate the length of time that two languages have been separated.



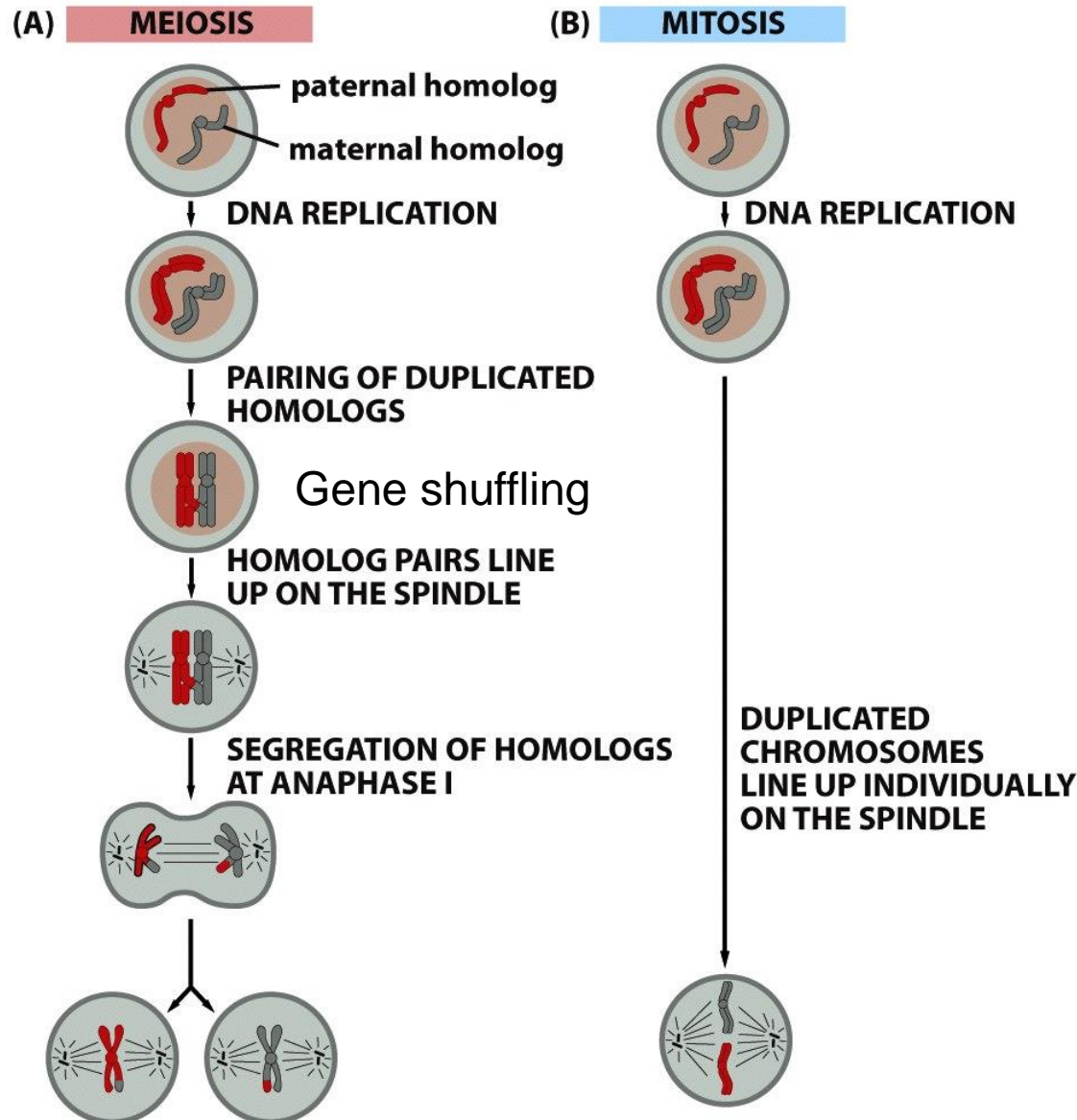
SHARED DNA SEQUENCES AMONG DISTANT RELATIVES

GTTCCGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCC	human
GCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTTAAAGGAATTGGCGGGGAGCACTACAACGGGTGGAGCCTGCGGTTTAATTGGATTCAACGCCGGGCATCTTACCA	<i>Methanococcus</i>
ACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGC . ACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCT	<i>E. coli</i>
GTTCCGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAACCTCACCC	human

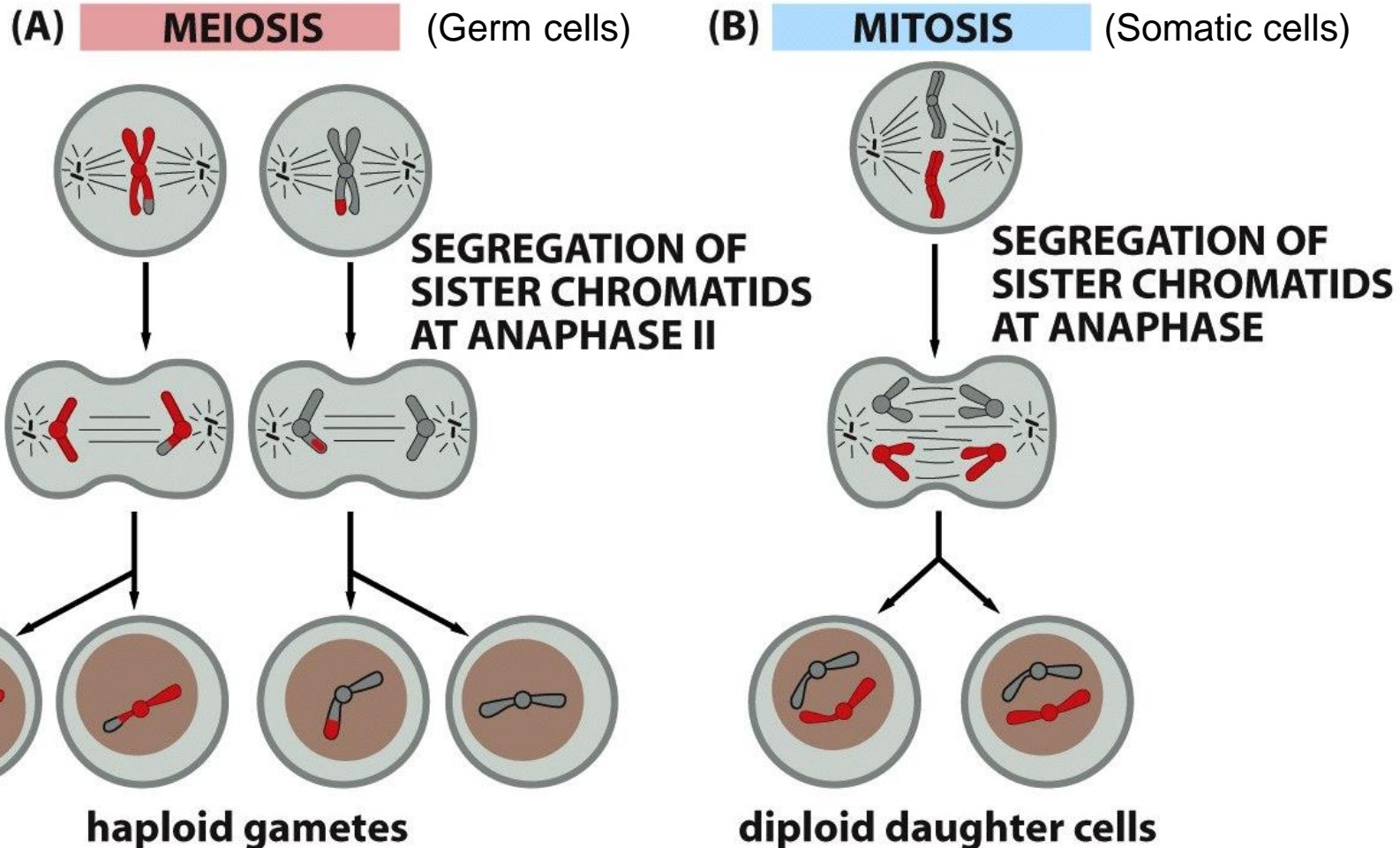
Figure 1-22 Molecular Biology of the Cell 5/e (© Garland Science 2008)

“Railroad ties” between sequences indicate identical bases. *E. Coli*, *Methanococcus*, and humans have been separated longer than humans and chimpanzees. Human siblings, cousins, second cousins, etc. have been separated for even shorter times.

MEIOSIS - HOW GENES GET SHUFFLED DURING GAMETOGENESIS (SPERM AND EGG)



MEIOSIS – HOW GENES GET SHUFFLED



WHAT DOES SHUFFLING DO FOR YOU?

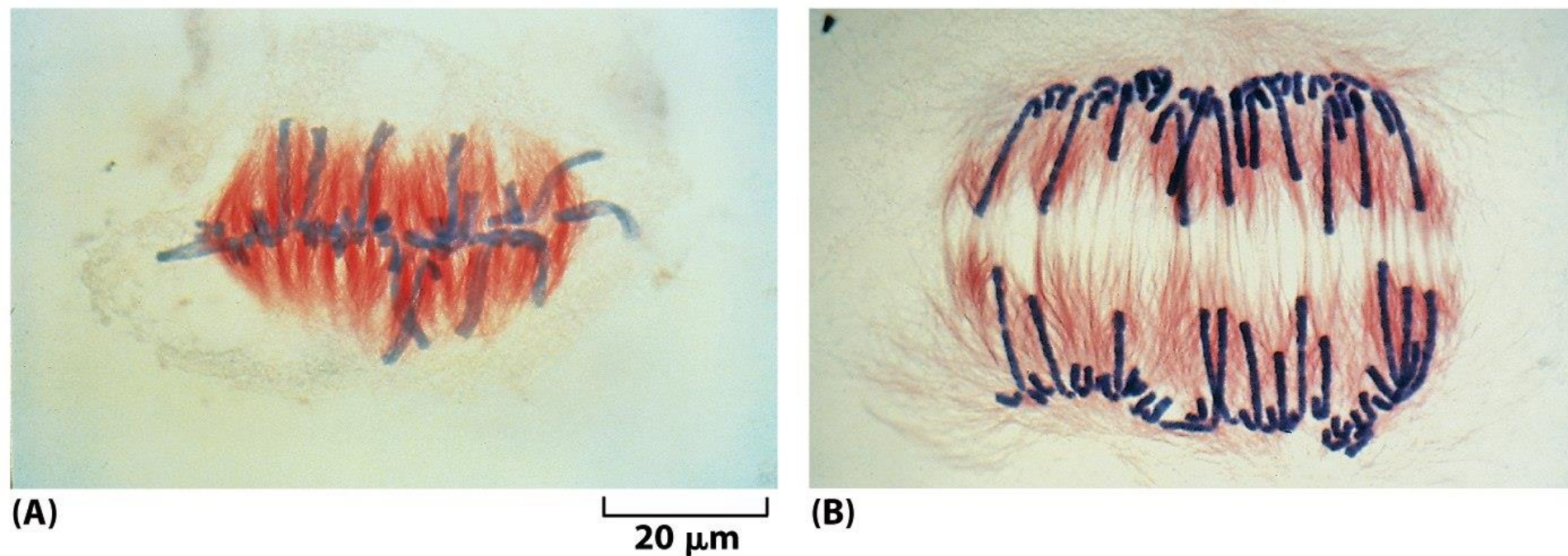
Gene shuffling puts genes from mother and father next to each other in new relationships. Thus the offspring, though sharing genes from both mother and father, have new mixtures that have never been tried out before in the species. In the case of immune response genes, this makes it very unlikely that a new organism such as a mutated influenza virus or smallpox, or HIV will ever be able to completely wipe out all individuals in a species.

This process also gives a baby “mommy’s eyes” and “daddy’s nose.” It is useful for babies to look something like their parents so the mothers will nurse them and the fathers won’t eat them.



CELL DIVISION: MITOTIC SPINDLE

BLUE STRUCTURES ARE CHROMOSOMES



MITOTIC FIGURE APPARATUS: SPINDLE

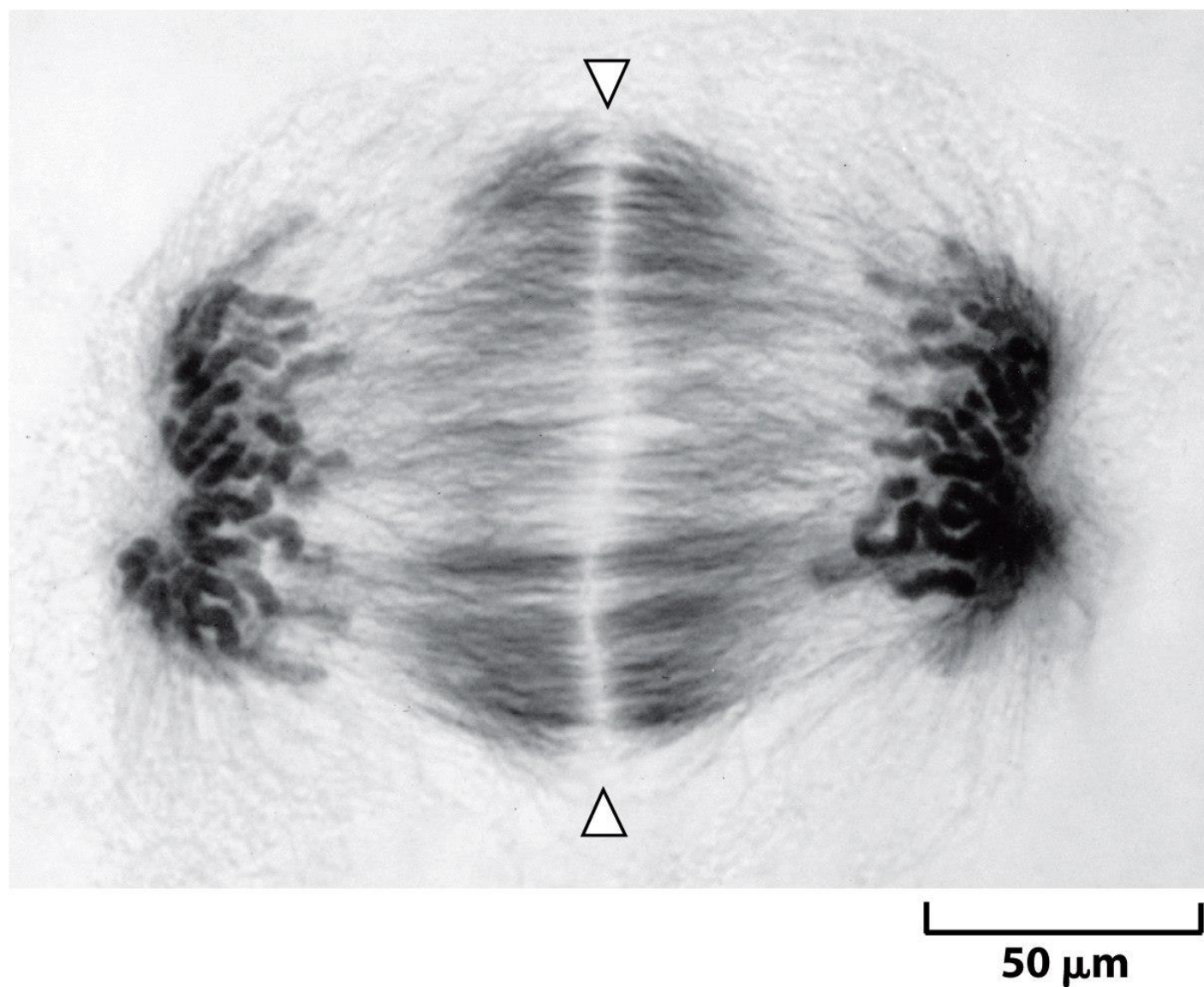
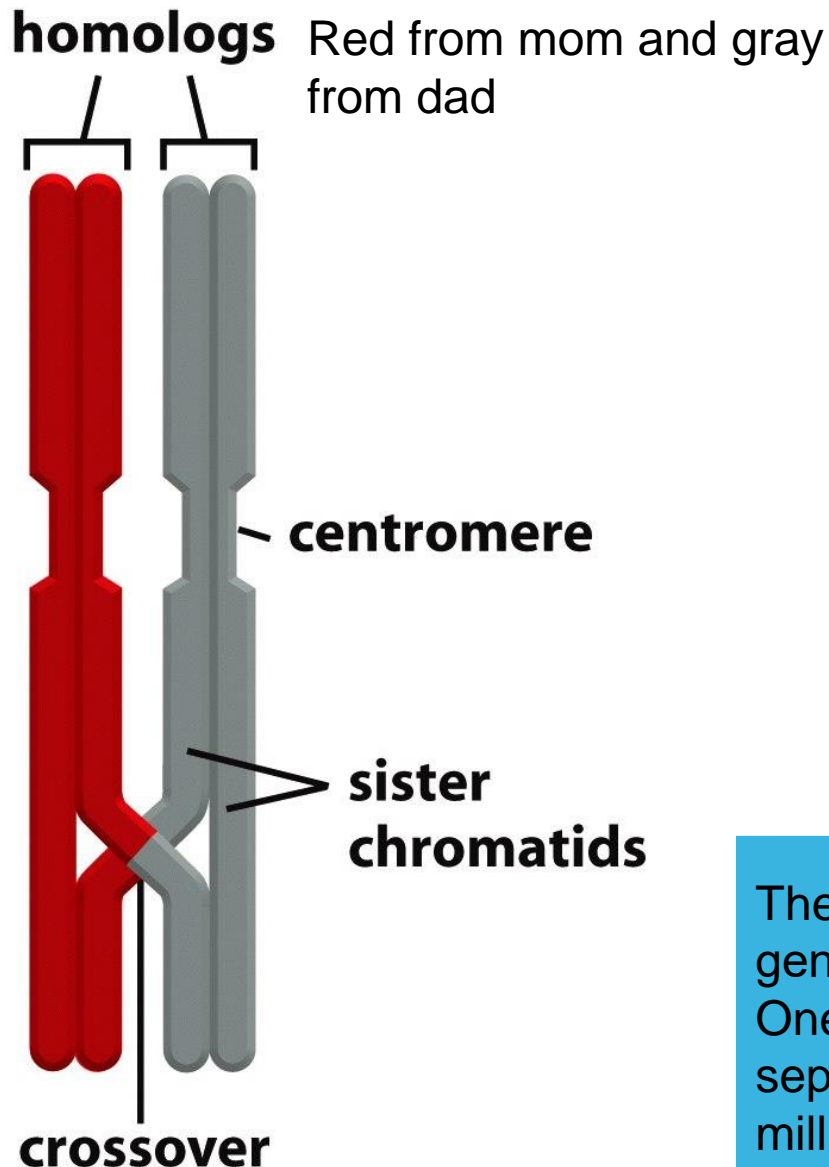


Figure 17-56 Molecular Biology of the Cell 5/e (© Garland Science 2008)

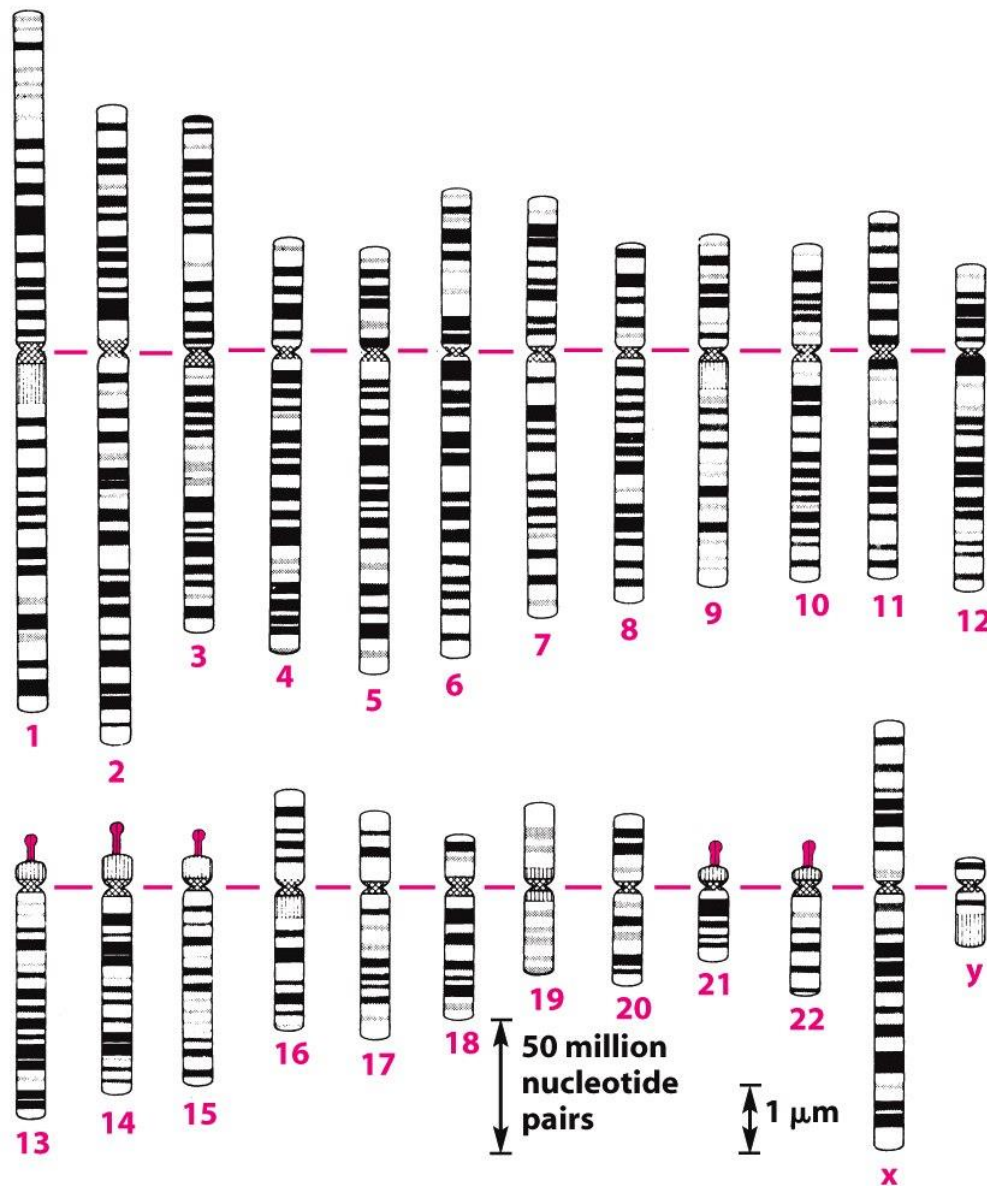
CROSSING OVER: THE KEY TO UNDERSTANDING GENE SHUFFLING



Sister chromatid exchange occurs during meiosis and the generation of sperm and egg. Maternal and paternal genes are rearranged rather randomly: mother's nose and father's eyes.

The probability of crossing over between any two gene loci is described by the "centiMorgan, cM." One cM is a likelihood of .01 that two genes will be separated in one generation. Its size is about a million base pairs. (Genome is 3 billion base pairs)

HUMAN CHROMOSOME DIAGRAM, DIFFERENT DNA SEQUENCES ARE DARK OR LIGHT



All but X and Y
are called
autosomes

Three billion total nucleotide pairs.
~25,000 genes. All autosomes can
pair with each other and exchange
genes. One autosome from mom, one
from dad.

USE OF GENE SHUFFLING TO FIND RELATIVES

- ❖ A genealogical DNA test examines the nucleotides at specific locations on a person's DNA for genetic genealogy purposes. The test results are not meant to have any informative medical value and do not determine specific genetic diseases or disorders; they are intended only to give genealogical information. Genealogical DNA tests generally involve comparing the results of living individuals to historic populations.
- ❖ The Family Finder test matches you confidently with any cousin within five generations. The science is simple - shared blocks of DNA across the 22 autosomal chromosomes are matched between two people. The degree of matching yields evidence for the relationship.
- ❖ The closer the relationship the more likely that different genes will stick together because there have been fewer shuffles

HUMAN RELATIONSHIPS

YOU	1
PARENTS	2
GRANDPARENTS	4
GENERATION 10	1024
GENERATION 20	1 MILLION
GENERATION 30	1 BILLION
GENERATION 40 (1,000 years)	1 TRILLION

- ❖ Total population of Earth ~ 7.5 billion
- ❖ Current best estimates are that about 100-1,000 humans migrated from Africa to fill the rest of the world about 100,000 years (5,000 generations ago) Human generation time is about 20-25 years and getting longer.
- ❖ Inbreeding within human populations must have occurred
- ❖ That's why all humans are 99.9% the same.

CARD (GENE) SHUFFLING

LONGEST SEQUENTIAL RUN RELATED TO NUMBER OF SHUFFLES

Shuffle #	Hearts	Diamonds	Clubs	Spades
0	13	13	13	13
1	6	6	9	4
2	4	6	4(2)	3
3	3	6	4(2)	3
4	3	4	4(1)	3
8	2	2	3	1

SHARED GENE SEQUENCES AMONG RELATIVES

Sibling	2350 cM	~18-2800 cM
½ Sib	1730 cM	790-2130
1 st cousin	880	80-1500
2 nd cousin	245	50-760
3 rd cousin	90	0-330
4 th cousin	50	0-120
5 th cousin	25	0-?
Anybody *	~10	0-?

* Shared sequences depend on geographical closeness of ancestors and restrictions on mating (ghettoized Jews in the European Middle Ages)

READING AND INTERPRETING YOUR REPORT

[Download Your Family Finder Results](#)

Filter Matches By:	Relation: Close and Immediate	<input type="checkbox"/> Exact Spelling for Surname Matches	<input type="checkbox"/> Hide 3rd Party Results
Advanced Filters:	Name: <input type="text"/>	Ancestral Surnames: <input type="text"/>	<input type="button" value="Filter"/>
Export To File:	<input type="button" value="Excel"/>	<input type="button" value="CSV"/>	

Name	GENEALOGICAL MATCHES BASED ON DNA				KNOWN GENEALOGY	
	<u>Suggested Relationship</u>	<u>Relationship Range</u>	<u>Shared cM</u>	<u>Longest Block</u>	<u>Known Relationship</u>	<u>Ancestral Surnames</u> (Bolded names match your surnames)
Helmut Schwab  	2nd Cousin	2nd Cousin - 3rd Cousin	187.91	17.50	<input type="button" value="Assign"/>	
Ashley Floyd Fields  	2nd Cousin	2nd Cousin - 3rd Cousin	142.16	8.16	<input type="button" value="Assign"/>	Feldman Osterman
Alice Lieberman  	2nd Cousin	2nd Cousin - 3rd Cousin	141.24	15.34	<input type="button" value="Assign"/>	Ransahoff Sternau (Stern?) Loeb Fred

More distant relationships (4th – 5th cousins)

<div>Daniel Gideon Krasnegor</div> <div></div>	-	5th Cousin - Distant Cousin	99.20	7.92	<div>Assign</div> <div>Botwinick (Minsk Belarus) Krasnegor (Shepetivka Ukraine) Seefer (Mlinov)</div>
<div>Harold Katz</div> <div></div>	-	4th Cousin - Distant Cousin	99.13	11.08	<div>Assign</div>
<div>Larry Heisler</div> <div></div>	-	5th Cousin - Distant Cousin	98.83	7.81	<div>Assign</div>
<div>Sigrid Esther Belinkoff</div> <div></div>	-	5th Cousin - Distant Cousin	98.72	8.91	<div>Assign</div> <div>Peyser (Lithuania or Poland) Rubin (Belarus) Shanedling (Lithuania) Harris (Poland) Krein (Lithuania)</div>
<div>Bennett Greenspan</div> <div></div>	4th Cousin	3rd Cousin - 5th Cousin	98.40	12.69	<div>Assign</div> <div>Borchonoysky Braun Garrop Gorobzoff Greenspan</div>

CARD (GENE) SHUFFLING

LONGEST SEQUENTIAL RUN RELATED TO NUMBER OF SHUFFLES

Shuffle #	Hearts	Diamonds	Clubs	Spades
0	13	13	13	13
1	6	6	9	4
2	4	6	4(2)	3
3	3	6	4(2)	3
4	3	4	4(1)	3
8	2	2	3	1

WHAT IS THE PROBABILITY THAT MY RELATIVE AND I SHARE ENOUGH DNA SEQUENCE TO BE DETECTED BY FAMILY FINDER?

Relationship	Match Probability
2 nd cousins or closer	> 99%
3 rd cousin	> 90%
4 th cousin	> 50%
5 th cousin	> 10%
6 th cousin and more distant	Remote (typically less than 2%)

Lots of people from the same geographical area, Scotland, for example, share enough DNA to be said to be related at the sixth cousin level. People in the same town, county, country, continent, marry each other.

LINEAL vs GEOGRAPHICAL “COUSINS”

- Lineal cousins share named grandparents, great grandparents, etc.
- Geographic cousins share the same autosomal gene pool which repeatedly shuffles but the genes being shuffled are just like the cards in a 52-card deck
- Many lineal male cousins will share the same Y chromosome
- Many lineal male and female cousins will share the same mtDNA
- Many geographic cousins may also share Y chromosome or mtDNA haplogroups because they are common in that geographic area, i.e **I1a** Y chromosome haplogroup in Norway and Scotland (That's me)
- However, lineal cousins will tend to share longer blocks of genes than geographic cousins because there have been fewer shuffles from their most recent common ancestor

Bottom line: All humans are related at about the sixth or seventh cousin level. At about this level of relationship, if you can prove it on paper, your lineal relative will be no more related to you genetically than any other person on Earth.

INSIDE EDITION ACCURACY TESTS

23andMe, Family Tree DNA, and Ancestry DNA were all tested for accuracy on two sets of identical, female triplets and one set of identical, male quadruplets

Triplet set 1: all 99% European but one girl was 11% French and German, another was 18%, and a third was 22 percent.

Triplet set 2: British Isles ancestry was 59%, 66%, and 70% on the three girls

Quadruplet set: all results essentially identical. The boys did not show the variation that the girls did.

How could this happen?

Small mutations in genes always occur during life, even in identical twins, triplets, etc.

Females have two X chromosomes: one from mom and one from dad.

Females randomly inactivate one or the other in all somatic cells. If any of the genes scored for country of origin, are on the X, they would give different results in different females. Males have only one X.

These results might also reflect the “error bars” in the laboratory test and computer algorithms.



The cemetery of Geneva, Kansas, where two centuries of our maternal ancestors rest. We placed my sister, Janet's ashes there on 2/25/2016.

The Mabie family plot, one of the founding families of Geneva, Kansas, a town that no longer exists. Edmund Mabie and Clara May Esse were the parents of my grandmother, Alice Miller (Mabie.)
I am placing some of Janet's ashes with the Mabies.



The Esse (Ess) family plot.
They were another of the
founding families of Geneva.
We placed some of Janet's
ashes with each of her
ancestral families.



Grandpa Ben Miller and
Grandma Alice were the
parents of our mother,
Lois Miller Baird.



The gravestone of our mother,
Lois Miller Baird and my sister,
Janet.



Letting the Kansas wind take
the rest of Janet's ashes away.



