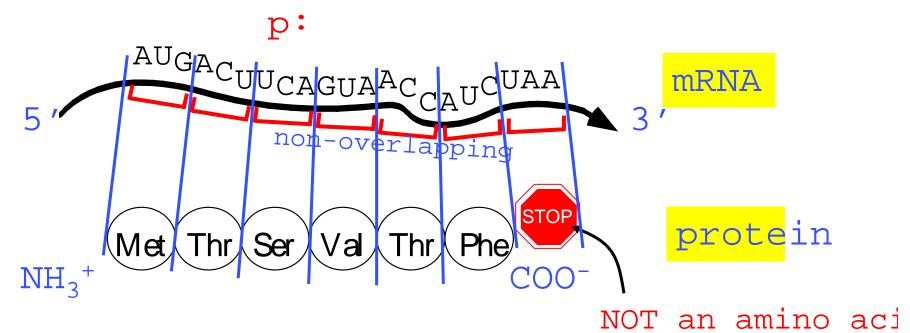


#### The triplet code

3 bases = 1 amino acid

Punctuation: sta AUG = methionine, the rt: first amino acid in sto UAA, alloppeteins



### The triplet code

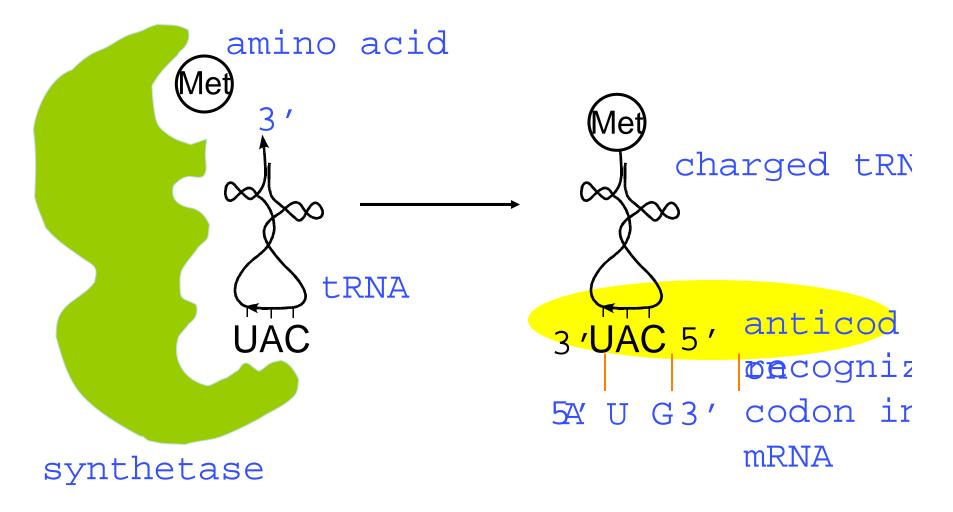
3 bases = 1 amino acid

Punctuation: sta AUG = methionine, the rt: first amino acid in sto (AAmosta, allappeteins p: AUGACUUCAGUA<sup>A</sup>CCAUCUAA mRNA 5 3 Jetc.

overlapping

The Genetic Code: Who is the interpreter? Where's the dictionary? What are the rules of grammar?

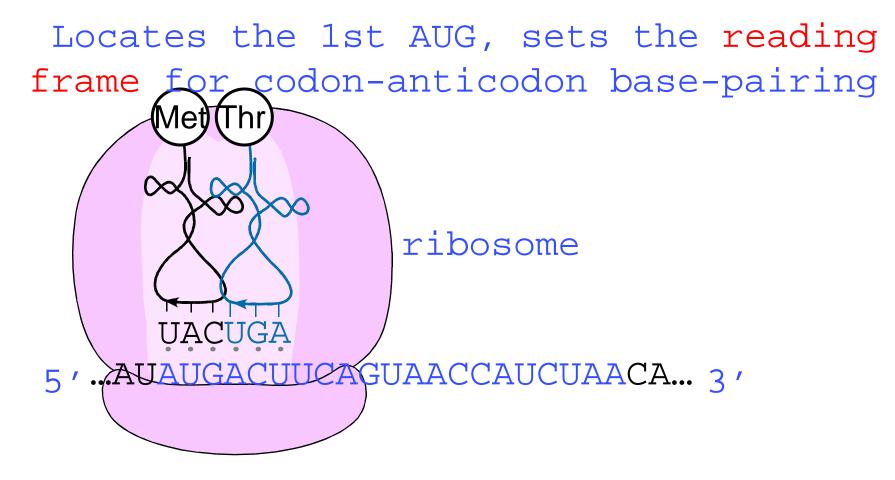
tRNA = transfer RNA



# The genetic code

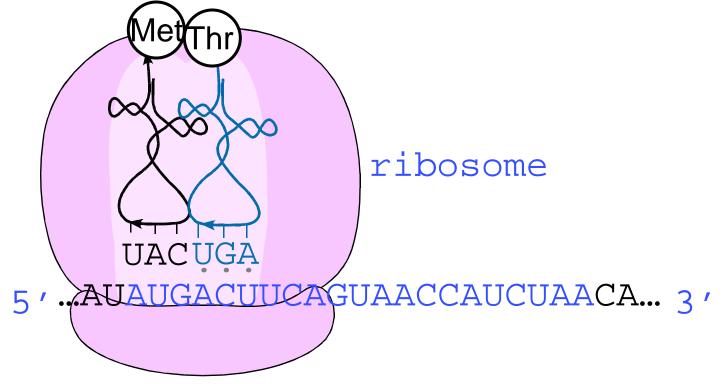
QuickTime™ and a TIFF (Uncompressed) decompressor are needed to see this picture.

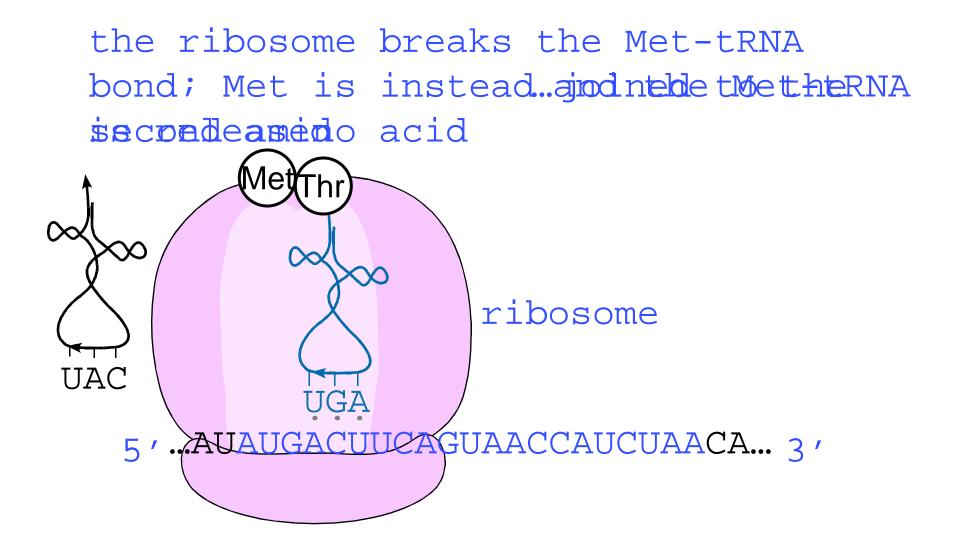
#### The **ribosome**: mediates translation



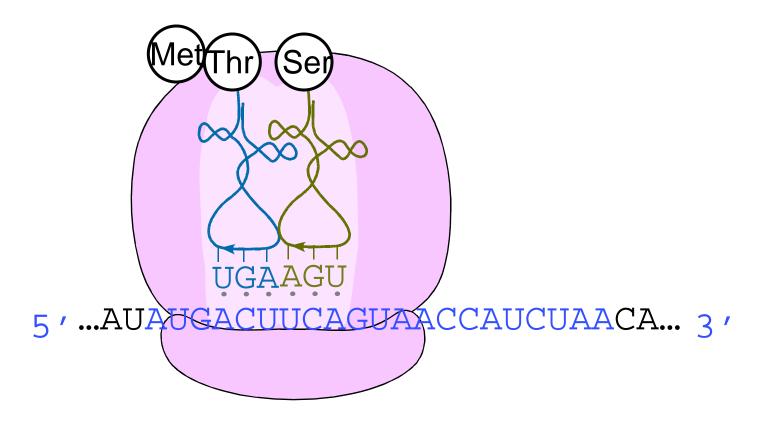
After the 1st two tRNAs have bound ...

the ribosome breaks the Met-tRNA bond; Met is instead joined to the second amino acid

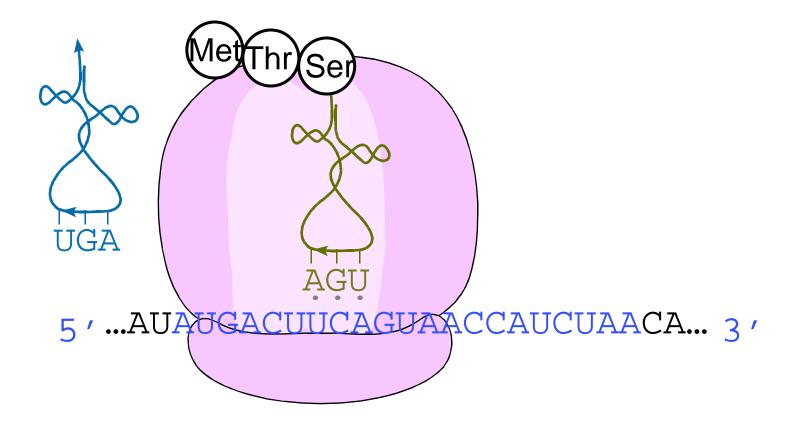


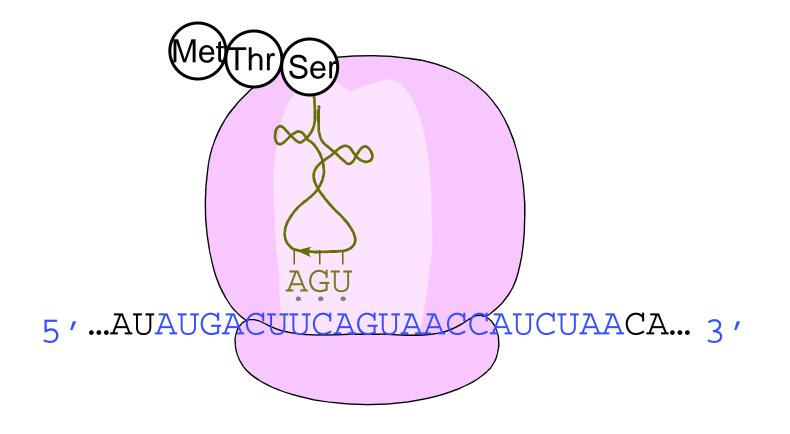


...then ribosome moves over by 1 codon in the 3' direction and the next tRNA can bind, and the process repeats

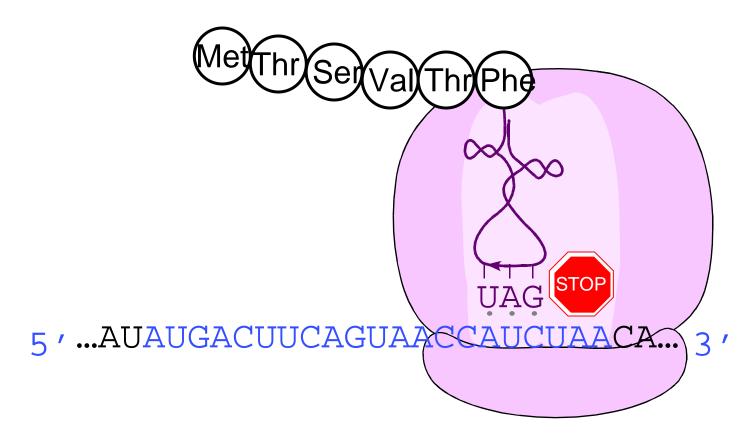


...then ribosome moves over by 1 codon in the 3' direction

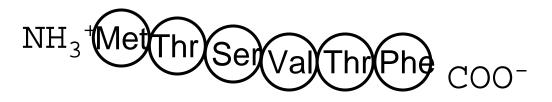




# When the ribosome reaches the Stop codon... termination



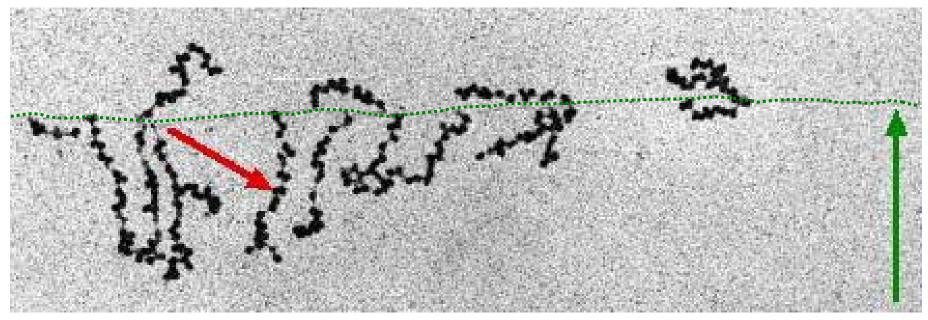
#### The finished peptide!



#### 5 · ...AUAUGACUUCAGUAACCAUCUAACA... 3 ·

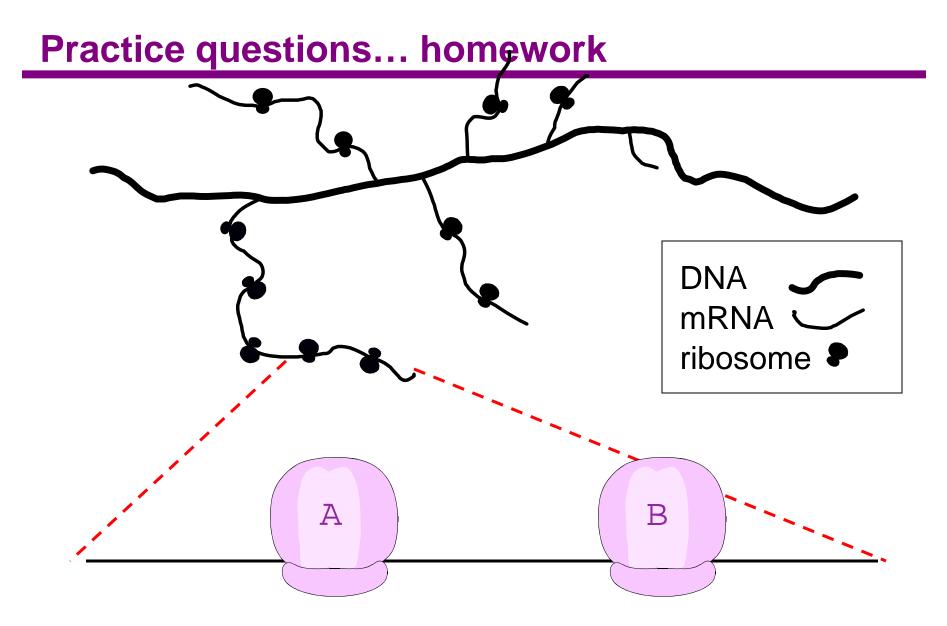
#### **Practice questions... homework**

# **Coupling of transcription and translation** . . . in prokaryotes, like E. coli.

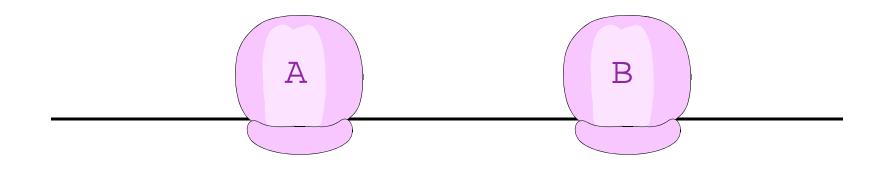


DNA

# mRNAs covered with ribosomes



1. Label the 5' and 3' ends of the mRNA, then answer the following questions:



- 2. Which way (to the right or to the left) are ribosomes A and B moving?
- 3. Toward which end (left or right) is the AUG start codon?
- 4. Which ribosome (A or B) has the shorter nascent polypeptide?
- 5. Which end of the polypeptide (amino or carboxy) has not yet been synthesized?

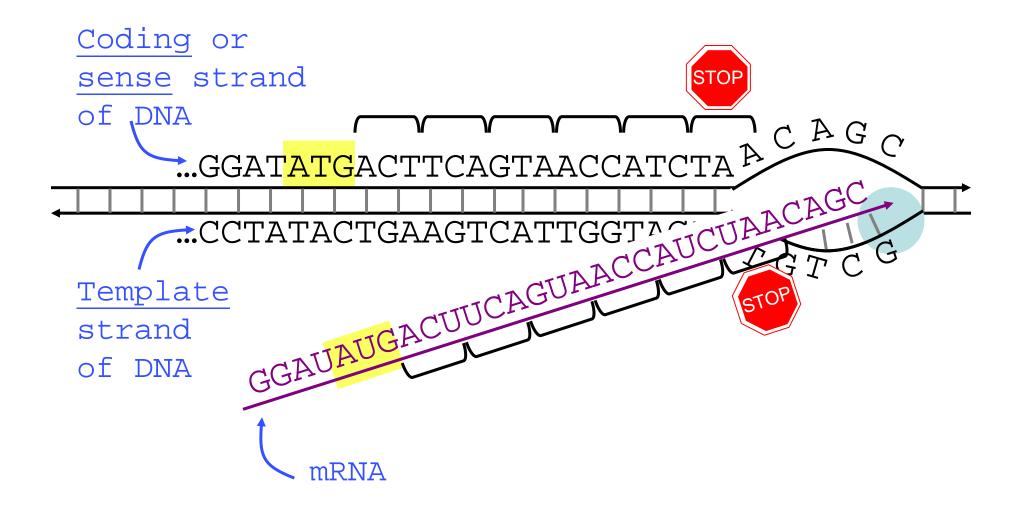
Reading Frame: the ribosome establishes the grouping of nucleotides that correspond to codons by Start counting AUG triplets from ed. this base 5'...AUAUGACUUCAGUAACCAUCUAACA... 3'

Open Reading ORF: from the first Frame: AUG to the first in-frame stop. The ORF is the information for the More generally: a reading protein frame with a stretch of codons not interrupted by

#### **Looking for ORFs**

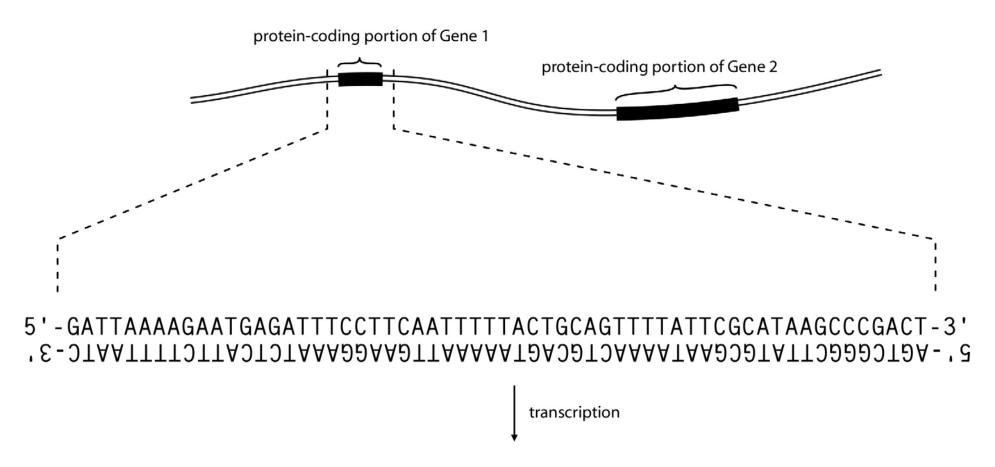
- -read the sequence 5'  $\rightarrow$  3', looking for stop
- -try each reading frame
- -since we know the genetic code-can do a virtual translation if Something to think about...
- -what might the presence of introns do to our virtual translation?

# Identifying ORFs in DNA sequence



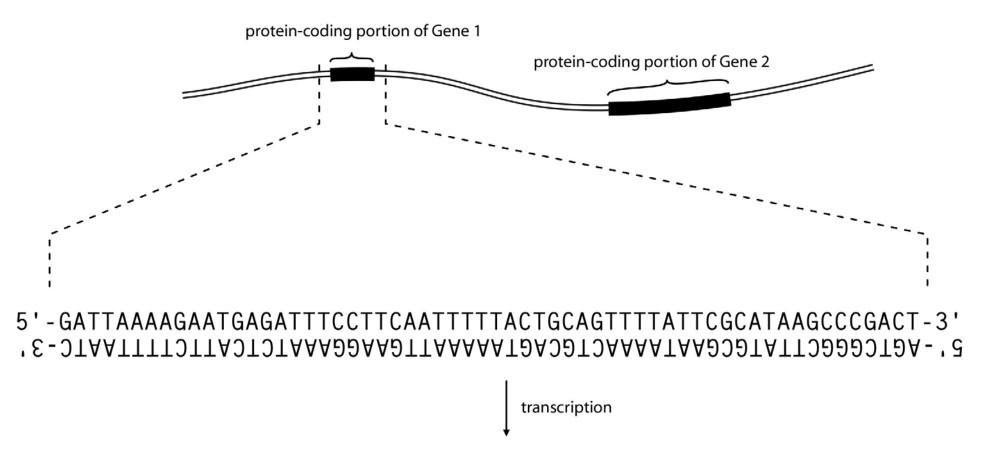
### **Looking for ORFs**

Practice question



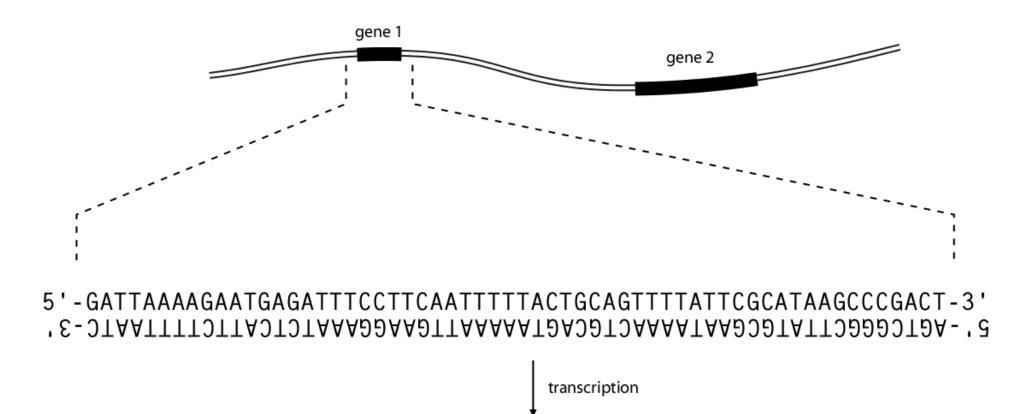
5'-AAAAGAAUGAGAUUUCCUUCAAUUUUUACUGCAGUUUUAUUCGCAUAAGCCCGACU-3'

1. Which strand on the DNA sequence is the coding (sense) strand? How can you tell?



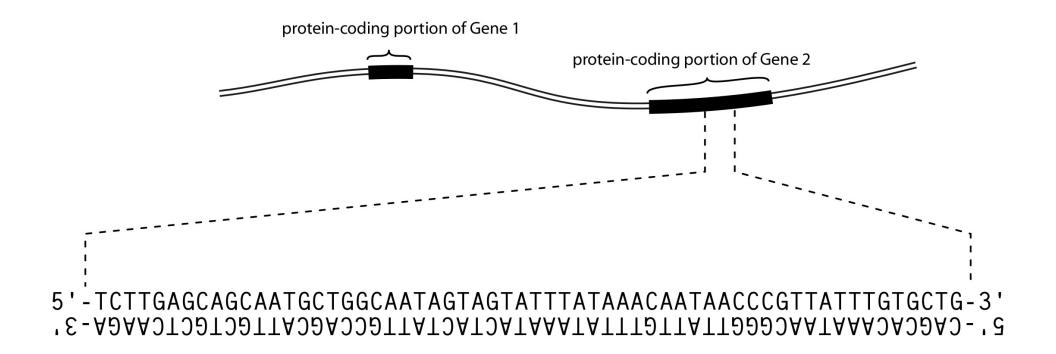
5'-AAAAGAAUGAGAUUUCCUUCAAUUUUUACUGCAGUUUUAUUCGCAUAAGCCCGACU-3'

2. On the DNA sequence, circle the nucleotides that correspond to the start codon.

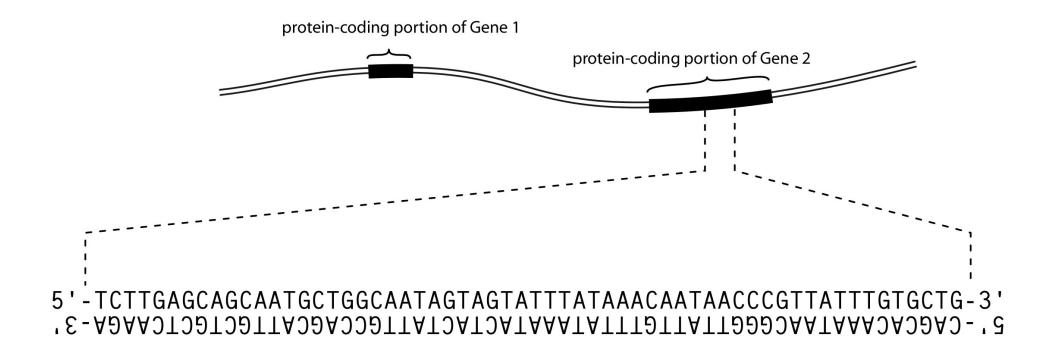


5'-AAAAGAAUGAGAUUUCCUUCAAUUUUUACUGCAGUUUUAUUCGCAUAAGCCCGACU-3'

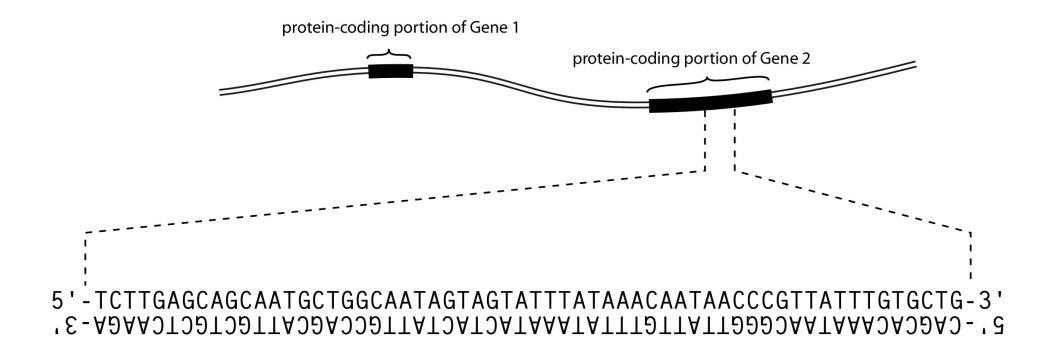
3. How many amino acids are encoded by this gene?



1. Do you expect the start and stop codons of gene 2 to be represented in the DNA sequence that is shown?



2. How many potential reading frames do you think this chunk of DNA sequence contains? How did you arrive at your answer? Would the answer be the same if you didn't know that this sequence came from the middle of a gene?



3. On the appropriate strand, mark the codons for the portion of gene 2 that is shown.

Given a chunk of DNA sequence...

**GGGTATAGAAAATGAATATAAACTCATAGAC** GATATCACTGGGAAAATAACAAAAAAATTTGC GAAAATATACGTTACCTCGTCACCGCAAAGA CGAGAGTAGCCCCTCTATGTGATGCAAAAAG CGAGGAGTTCCGAACTTTCTACAGGGATCTA GCATTGAAGTTTGTTCATTCGAAGGGAATTAT TTGGGGCGTGGAGTGCTTGTTGATTTTGGTC AAAACGATTACGACAATTATGCAAATACAAAC CCATGCATTATGCGTAATCAATATTCTCCTAA CAAGGTCGTCCACTTAAACAATGTAAATGGG ATTAAAAGGGCTAATAGAGCAGGGACTCGTG AGCACAAAGATTGATATATGGTCCGTAGGTG AAGTTTAGATGATGCGGATTCTTTGCTAGAG CGTTGCATGGATTGGGTTTCGAAGCTAGTGG GGAATTTGTTTATGATTTGCTTAATAAAGAAT CATTCGGATTTCTACAACAAGAATTACATGAC ATGGATGCTGTTGATGCCTATGAGTTGAAAAA GGTTTTGGAACAATGCTTCGAAATGGATCCT TTCAATGAATTGAATGAAAACACATATTTACT GCGAGGCAGATTTGCTCGATAAGGATGTTC

Open reading frames (termination codons?)

Splicing signals

Promoters & transcriptional termination sequences

Other features

Computer programs build models of each organism's genes and scan the genome

How do you find out if it contains a gene? How do you identify the gene?

cbdryloiaucahjdhtheflybitthedogbutnotthecatjhhajctipheq

The diagram below represents the region of cat genomic DNA that contains the *tyrosinase* gene (needed for fur pigment production). The asterisks marked (i) and (ii) show the locations of two mutations that have been found in this gene (in separate cats). Mutation (i) causes fur pigmentation to be much more intense than normal, but no amino acid changes were found in the tyrosinase protein in this mutant. Mutation (ii) is a TCA $\rightarrow$ TGA change that results in a truncated, non-functional protein.

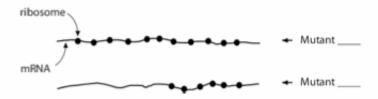
5' (i) (ii) 3' 3' \* \* 5'

(a) Based on what you have been told about mutation (i), suggest a hypothesis to explain the altered fur phenotype.

 (b) Mark the start codon of the tyrosinase gene in the diagram above by drawing a small circle at its <u>approximate</u> location on the **coding strand**. Your answer here should not contradict your answer in (a). (c) In the close-up representation of a transcription bubble in the tyrosinase gene (below), mark the coding (sense) and template strands... again, consistent with your answer in (a). Draw a circle to mark the location of the RNA polymerase and draw a short RNA transcript with its 5' and 3' ends marked. Is the promoter to the left or to the right? <u>Circle one</u>: Left Right



(d) The picture below represents electron micrographs of tyrosinase mRNAs from the two mutants (i and ii) as they are being translated by ribosomes. [The proteins being made are not shown.] Both mRNAs are in the same orientation (i.e., both have their 5' ends on the same side). Identify which mRNA is from which mutant. Then mark the 5' and 3' ends on one of the mRNAs and put a box around the approximate location of the start codon.



Genome 371, 8 Jan 2010, Lecture 2

# Chromosome segregation (mainly)

#### »Model organisms in genetics

- » Chromosomes and the cell cycle
- » Mitosis
- » (Meiosis)

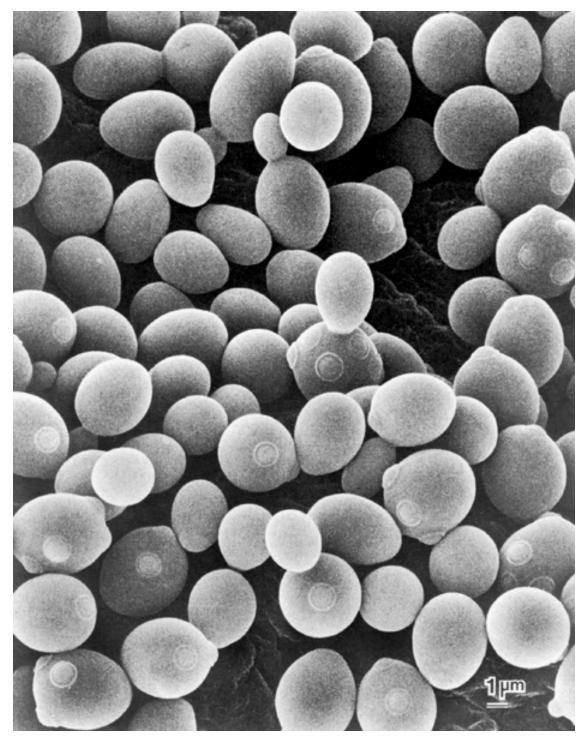
#### **Quiz Section 1** — The Central Dogma

One way of identifying genes in DNA sequence

Getting familiar with gene structure, transcription, and translation

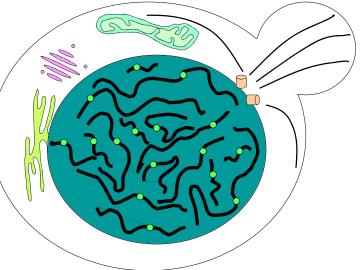
...using Baker's yeast

genome

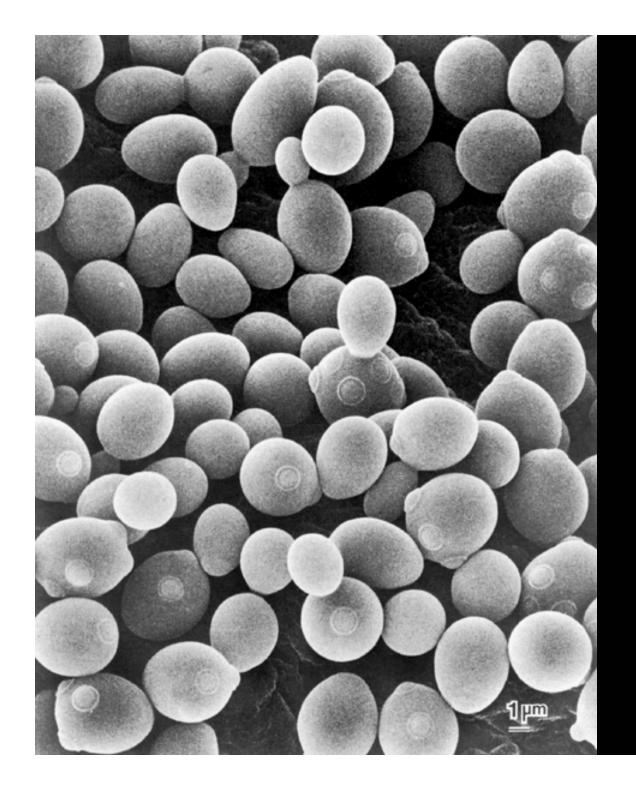


Baker's yeast = budding yeast =

Saccharomyces cerevisiae



- Yeast is a eukaryote
- 16 chromosomes
- ~6000 genes
- Very few introns



# Why yeast?

#### The use of model organisms

#### What is a model organism?

A species that one can experiment with to ask a biological question

#### Why bother with model organisms?

- Not always possible to do experiments on the organism you want
- If the basic biology is similar, it may make sense to study a simple organism rather than a

#### Features of a good model organism?

- Small, easy to maintain
- Short life cycle
- Large numbers of progeny
- Well-studied life cycle, biology
- Appropriate for the question at hand
- Has a genome sequence available





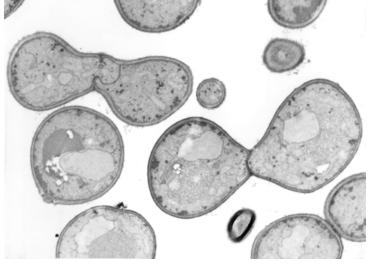
## Using model organisms... Example 1

#### February 1988:

#### Yeast STE7, STE11, and STE12 Genes Are Required for Expression of Cell-Type-Specific Genes

STANLEY FIELDS,<sup>1</sup> DEBORAH T. CHALEFF,<sup>2</sup><sup>†\*</sup> and GEORGE F. SPRAGUE, JR.<sup>3</sup>

Analysis in yeast of the role of genes encoding a cascade of protein kinases (M/) '-'page



#### Development of anticancer drugs targeting the MAP kinase pathway

Targeting the EGF receptor in ovarian cancer with the tyrosine kinase inhibitor ZD 1839 ('Iressa') Human cervical cancer cells use  $Ca^{2+}$  signalling, protein M Sewell', KG Macleo tyrosine phosphorylation and MAP kinase in regulatory volume decrease Hyperexpression of Mitogen-activated Protein Kinase in Human Breast Cancer Vimala S. Sivaraman,\* Hsien-yu Wang,‡ Gerard J. Nuovo,§ and Craig C. Malbon/ Mitogen-Activated Protein Kinase Kinase Kinase 1 Activates Androgen Receptor-Dependent Transcription and Apoptosis in Prostate Cancer

MARIA T. ABREU-MARTIN,<sup>1</sup> AJAI CHARI,<sup>2,3</sup> ANDREW A. PALLADINO,<sup>1</sup> NOAH A. CRAFT,<sup>2,3</sup> AND CHARLES L. SAWYERS<sup>2,3\*</sup>

## Some commonly used model organisms





Round worm — *Caenorhabditis ele<u>gans</u>* 



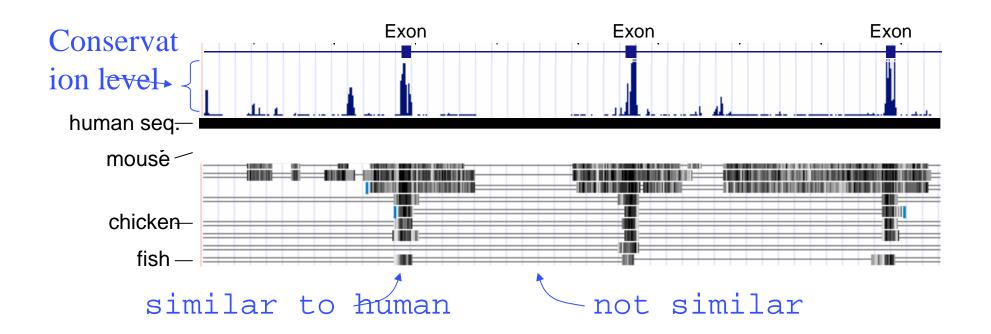
Fruit fly — Drosophila melanog



Thale cress — Arabidops is thaliana

## Sequence conservation across species

Comparison of human sequences to those of other organisms:



Even for yeast:

~50% of yeast genes have at least one similar human gene;

~50% of human genes have at least one similar yeast gene

## Using model organisms... Example 2

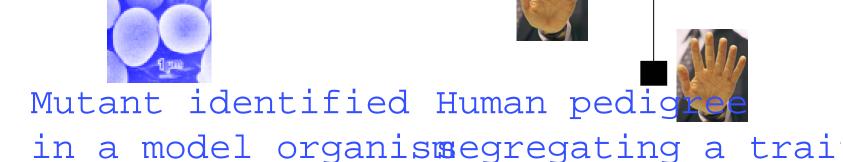
# What is the basis of human skin color differences?

QuickTime<sup>™</sup> and a TIFF (Uncompressed) decompressor are needed to see this picture.

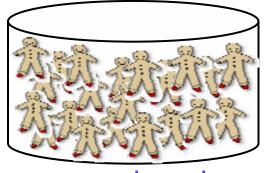
Science, 16 Dec 2005

How would a geneticist approach this question?

#### Linking genotype & phenotype: model organisms



### Protein acting in a biological process



Association s

946 ATT GTC TGT AGC CGA TTG GAG GAG TAC AAC AGC CAT 1009 GGA CCT TTA CGG CGT AAT CCT GGA AAC CAT GAC AAA 1072 GCT GAT GTA GAA TTT TGC CTG AGT TTG ACC CAA TAT 1135 AAT TTC AGC TTT AGA AAT ACA CTG GAA GGA TTT GCT 1198 TCT CAA AGC AGC ATG CAC AAT GCC TTG CAC ATC TAT 1261 GGA TCT GCC AAC GAT CCT ATC TTC CTT CTT CAC CAT 1324 TGG CTC CGA AGG CAC CGT CCT CTT CAA GAA GTT TAT

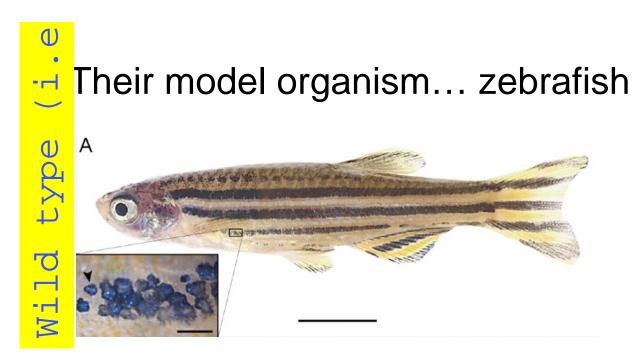
## A genetic approach...

Pick a model organism

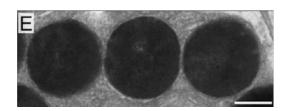
QuickTime<sup>™</sup> and a TIFF (Uncompressed) decompressor are needed to see this picture.

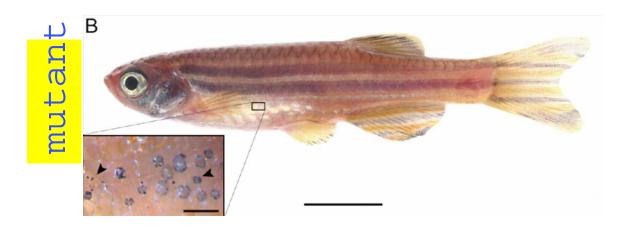
Find mutant(s)
with "interesting"
phenotypes

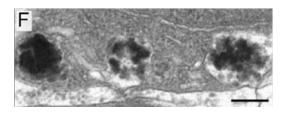
Rebecca Lamason et al., Science, 16 Dec 2005



#### Melanosomes in EM







Pick a model organism Find mutant(s) Map the gene that has been mutated Identify genes in the region Find which of these genes is the "culprit"

#### But what does it have to do with humans?

Find which of these genes is the "culprit"

Do humans have a similar gene?

If so, does the human version also control pigmentation?
Are there different alleles corresponding to different.

mutan
t +
human
gene!

#### mutant

A somewhat different path... Example 3

Huntington Disease (HD)

- A neurodegenerative disorder
- movement disorder ("chorea")
- lack of coordination
- cognitive changes
- invariably lethal
- no known cure

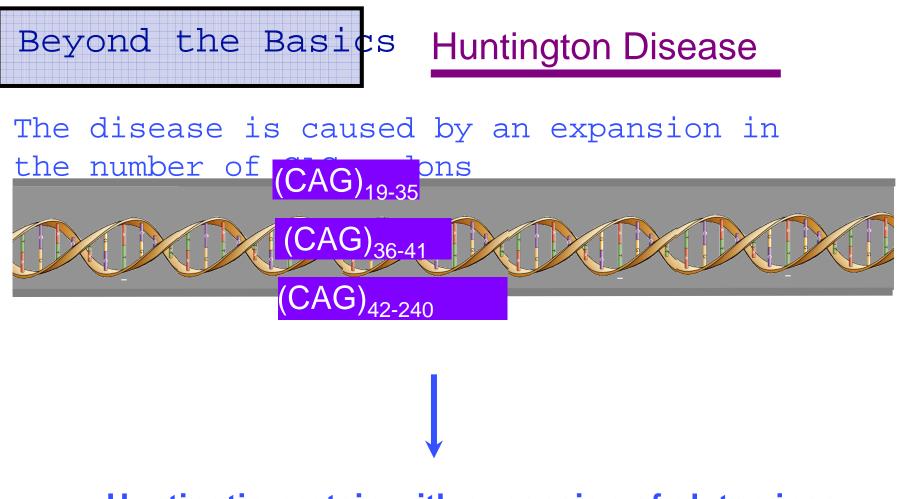
#### Linking genotype & phenotype: human pedigrees

## Mutant identified Human pedig in a model organismsegregating a trai Protein acting in Association a biological process S 946 ATT GTC TGT AGC CGA TTG GAG GAG TAC AAC AGC CAT 1009 GGA CCT TTA CGG CGT AAT CCT GGA AAC CAT GAC AAA 1072 GCT GAT GTA GAA TIT TGC CTG AGT TTG ACC CAA TAT

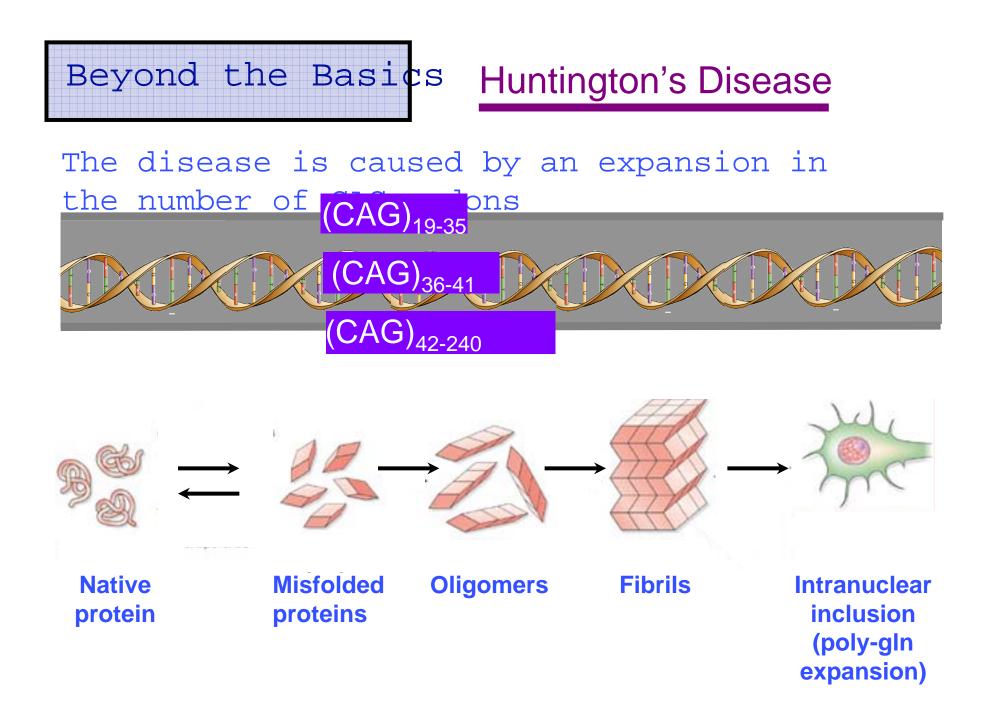
1135 AAT TTC AGC TTT AGA AAT ACA CTG GAA GGA TTT GCT 1198 TCT CAA AGC AGC ATG CAC AAT GCC TTG CAC ATC TAT 1261 GGA TCT GCC AAC GAT CCT ATC TTC CTT CTT CAC CAT Sequence analysi 1324 TGG CTC CGA AGG CAC CGT CCT CTT CAA GAA GTT TAT

```
Pick a model
  organism
    Find
  mutant(s)
Map the gene
that has been(HD)
   mutated
  Identify
genes in the
   region
Find which of
 these genes
   is the
  "culprit"
```

```
Pick a model (mouse)
     organism
                 → what can we learı
Make——Find
    mutant(s)
Map the gene in
humans that has (HD)
 been mutated
     Identify
   genes in the
      region
  Find which of
   these genes
      is the
    "culprit"
```



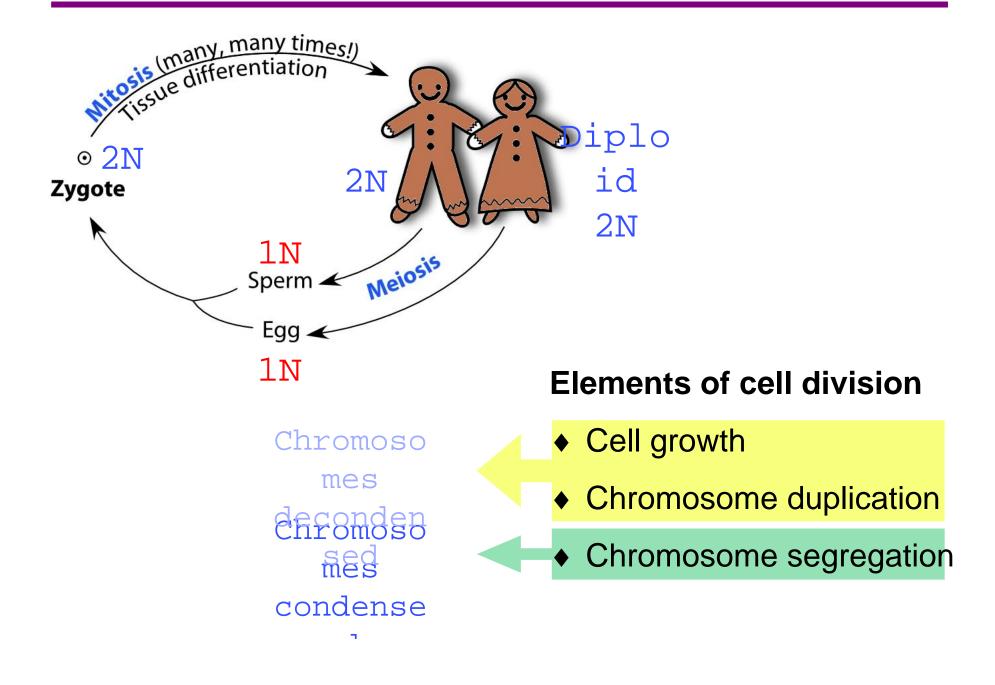
#### Huntingtin protein with expansion of glutamines



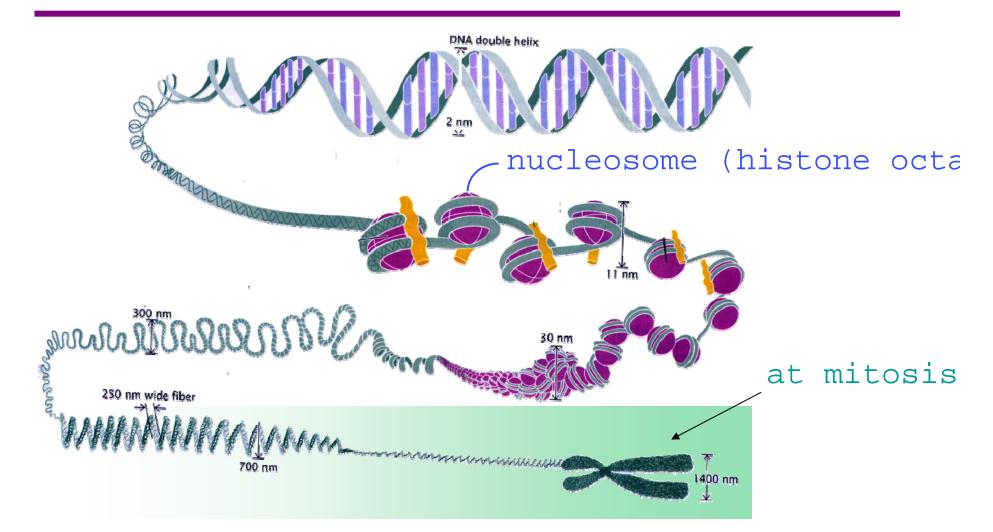
## »Model organisms in genetics

»Chromosomes and the cell
cycle
»Mitosis
» (Meiosis)

## Cell division and the life cycle

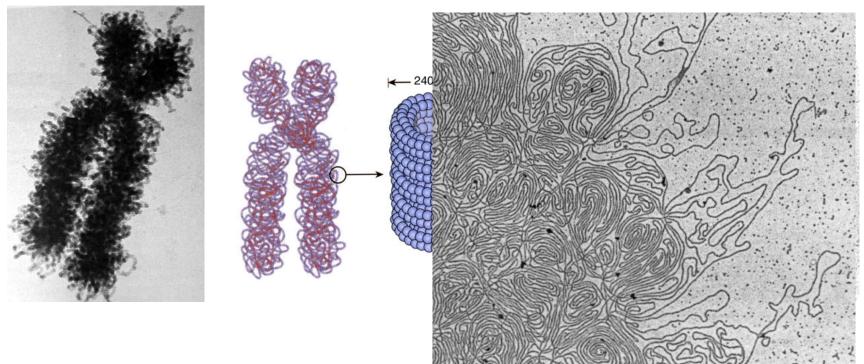


## **Chromosome structure: coils of coils of coils...**



Local unpacking of chromatin...to allow gene expression & replication

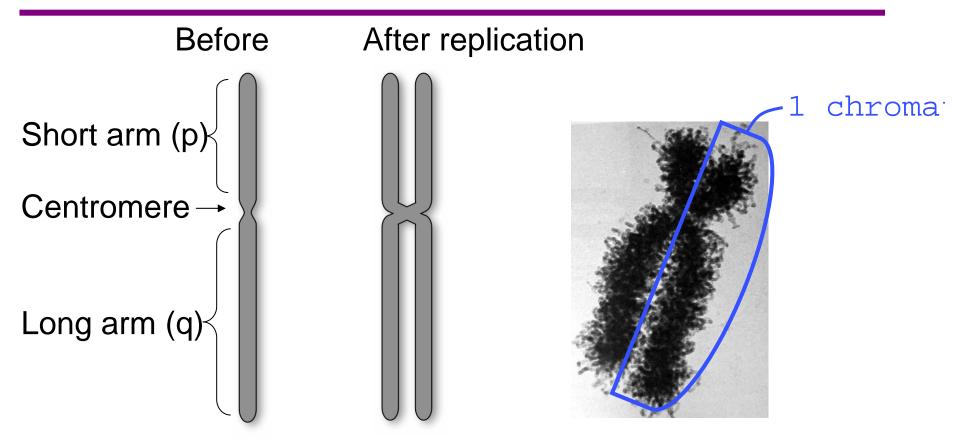
## **Chromosome structure: coils of coils of coils...**



How packed is the DNA?

- 1 human cell has ~ 2 meters of DNA
- 1 average human body: DNA length equivalent to ~600+ round-trips to the sun!

## **Chromosome structure (cont'd)**

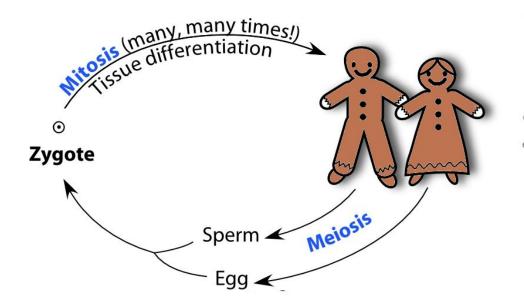


After a chromosome is replicated but before the two copies are separated... (sister) chromatids

#### **Chromosome folding pattern is reproducible**

Each chromosome has its own characteristic folding pattern...

variations in level of folding → banding
patterns (when stained)
karyotype: picture of human chromosome set from 1 individu



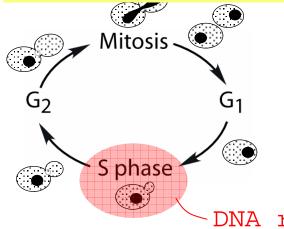
A STREET			)[	Í.	(l	
)(	the second		(j		2	
13	14		16	(1.948);	2 6	18
19	20	21 21	2	2	×	ð,

Two copies of each chromosome type... homologous pairs

#### The cell division cycle

#### **Elements of cell division**

- Cell growth
- Chromosome duplication
- Chromosome segregation



Cell cycle genetics— originally from yeast mutants

- cell and nuclear morphology reflect cell cycle stage
- haploid life style → recessive phenotypes revealed

DNA replication mutants relatively easy to find

#### Segregating the replicated chromosomes

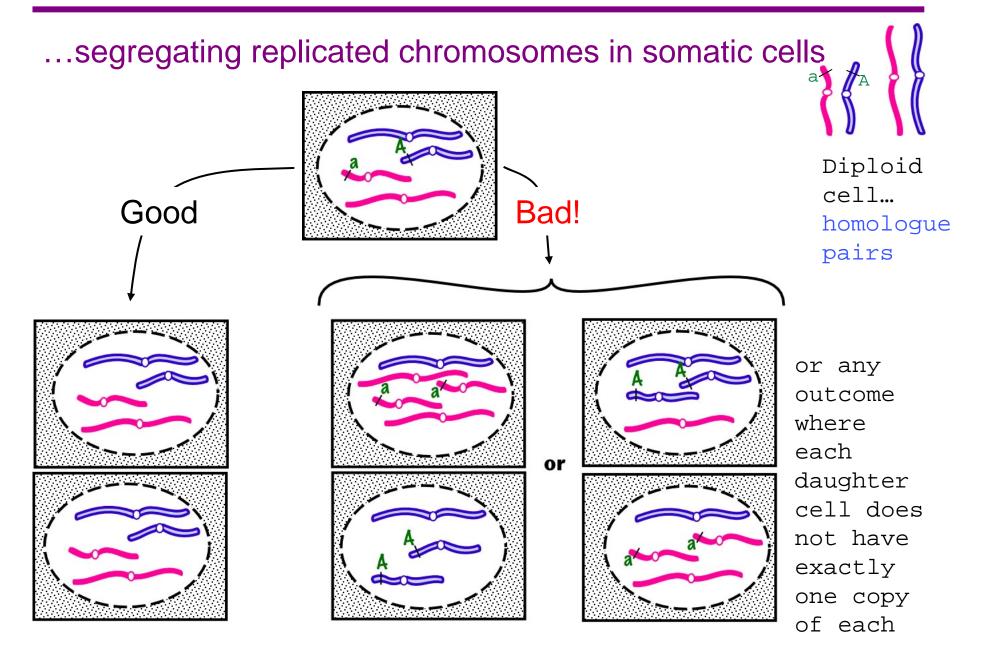
What happens to the replicated chromosomes? ... depends on the goal of the division

- to make more "vegetative" cells: mitosis

daughter cells' chromosome set should be identical to parental cell's

#### - to make gametes: meiosis

each daughter cell should have half the number of chromc If parental cell was diploid (2N)... daughters should be Will a normal haploid cell undergo meiosis? No



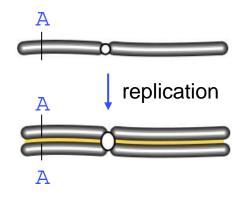
#### The problem

Partitioning replicated chromosomes so that each daughter cell gets one copy of each chromosome

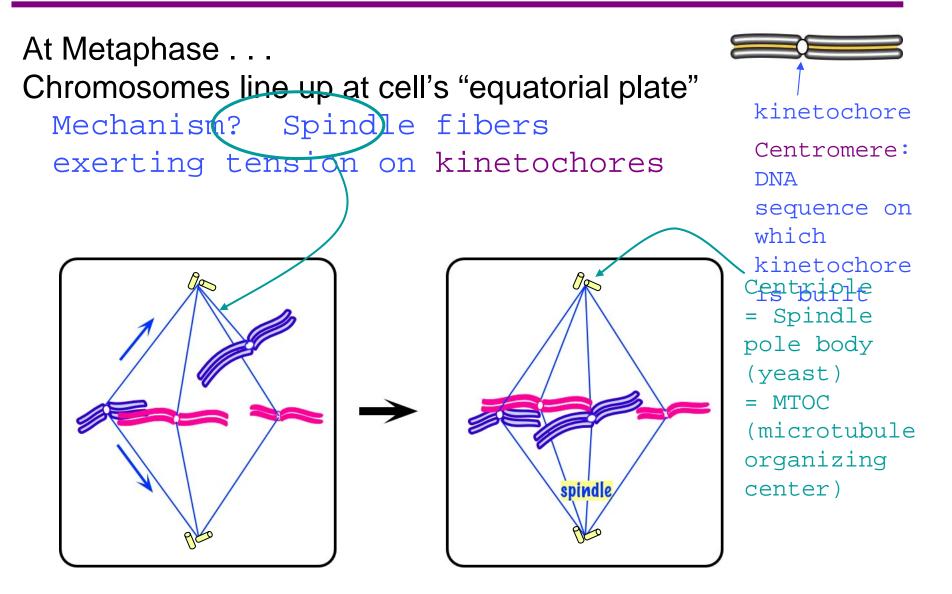
#### The solution

After replication of a chromosome...

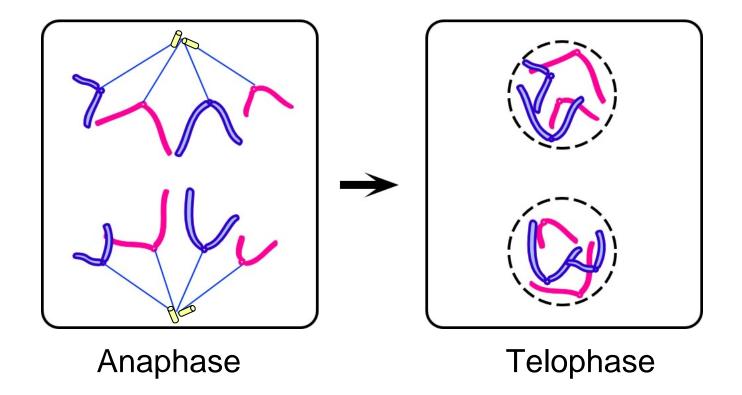
- hold the two sister chromatids together
- target them to opposite poles
- then separate the sisters



#### Mitosis (cont'd)



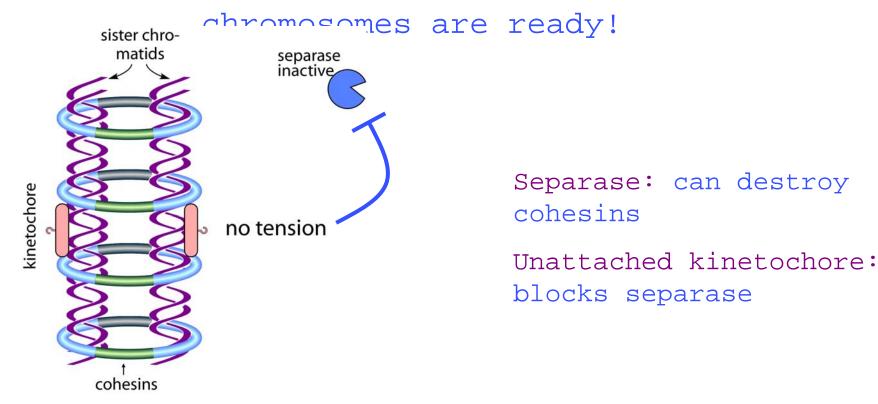
At anaphase... cohesion between sister chromatids dissolved, sisters pulled to opposite poles



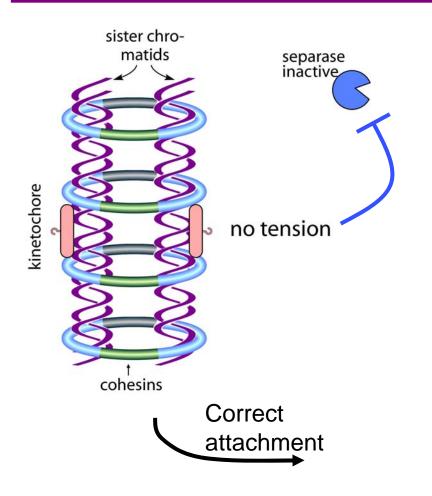
#### Monitoring correct attachment to spindle

Sister chromatids are held together by **cohesin** proteins...

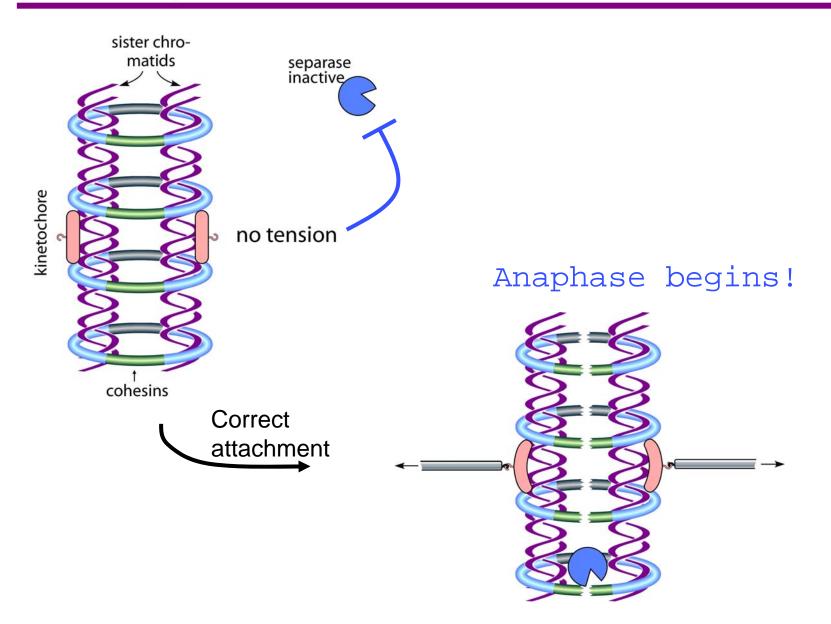
Any kinetochore not experiencing tension  $\rightarrow$  block destruction of cohesins so, no sister separation until all



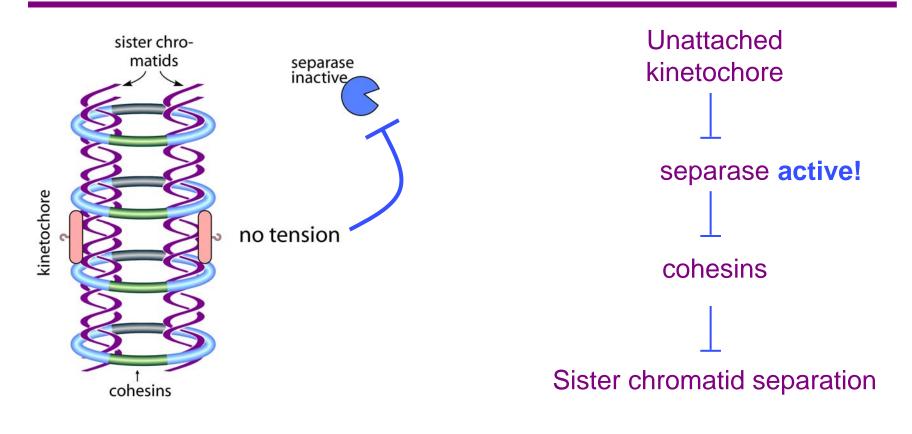
#### Monitoring correct attachment to spindle (cont'd)



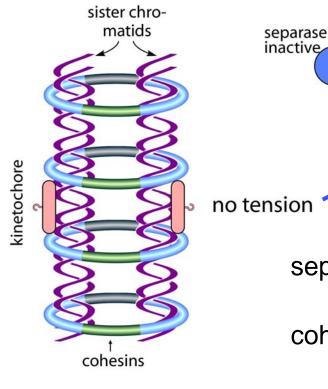
#### Monitoring correct attachment to spindle (cont'd)



#### The anaphase entry checkpoint



#### The anaphase entry checkpoint—genetic analysis



\*how to keep the strains alive? ...use temperature sensitive mutants

## **Checkpoints**

Cellular surveillance systems to monitor the integrity of the genome and of cellular structures

Enforce the correct order of execution of cellular events.

Examples:

- -Chromosomes not attached to spindle  $\rightarrow$  block onset of anaphase
- -DNA is damaged  $\rightarrow$  halt the cell cycle to allow repair
- -Irreparable DNA damage  $\rightarrow$  trigger cell death

## A tiny practice question

The haploid chromosome number in honey bees is 16. Male honey bees are haploid while females are diploid. A single cell isolated from a bee's body was found to have 32 double-stranded DNA molecules. Was the cell from a male, a female, or is it not possible to make a definite conclusion from the information given? Explain BRIEFLY.