

Mutaciones

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¿Cómo nació el término mutación?

Hugo De Vries (1902): *Oenothera lamarckiana*.

Individuos con una característica nueva que no estaba en sus antecesores.

→ Cambio en el factor (gen) que determinaba el carácter y que este cambio se transmite a la progenie como cualquier otro carácter hereditario.



↓

Mutación

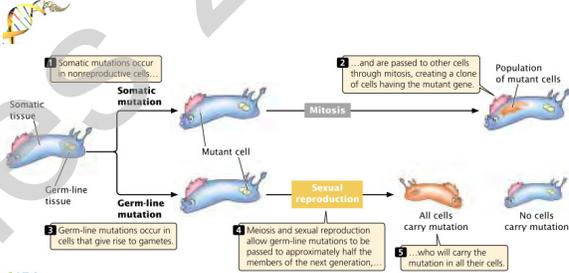
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Mutantes



Hugo De Vries, around 1920.
Photo courtesy of Cold Spring Harbor Laboratory Archives.

Mutación es una alteración o cambio en la **información genética** (genotipo) de un ser vivo que se presenta espontáneamente (o inducida), y que se puede **transmitir** a la descendencia.

17.2 There are two basic classes of mutations: somatic mutations and germ-line mutations.

Mutaciones

Genómicas o cariotípicas (Número)

↓

- ❖ Euploidía
- ❖ Aneuploidía

Cromosómicas (Estructura)

↓

- ❖ Delección
- ❖ Duplicación
- ❖ Inversión
- ❖ Translocación

Génicas (puntuales)

↓

Esta clase

Mutaciones Genómicas

Euploidía:
Afecta al conjunto de cromosomas del genoma (set de cromosomas), aumentando el número de juegos cromosómicos (poliploidía) o reduciéndolo a una sola serie (haploidía o monoploidía).



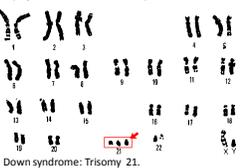
Aneuploidía:
Afecta el número de cromosomas individualmente (1 par de cromosomas).

meiosis

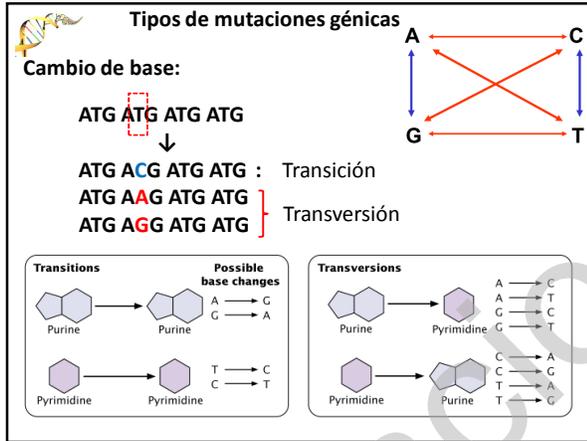
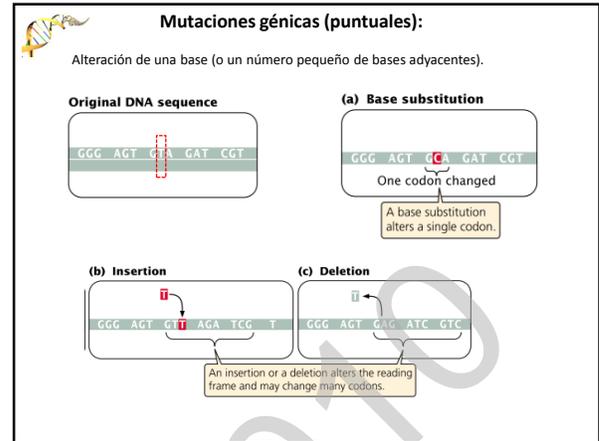
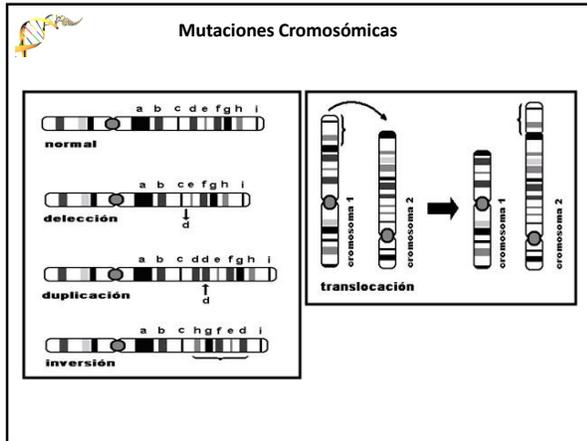
XX + XX = 4XX → aneuploidia

XX + XY = 3XY → síndrome de Klinefelter

XX + XX = 3XX → síndrome de Turner

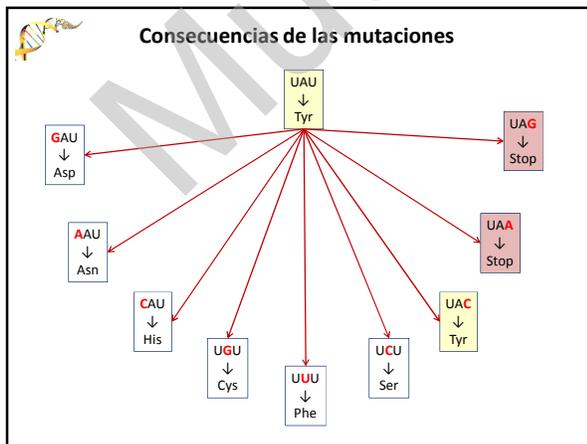


Down syndrome: Trisomy 21.



Consecuencias de las mutaciones

	Segunda base				
	U	C	A	G	
P r i m e r a	UUU } Fen	UCU } Ser	UAU } Trp	UGU } Cys	T e r c e r a
	UUC } Fen	UCC } Ser	UAC } Trp	UGC } Cys	
	UUA } Leu	UCA } Ser	UAA } Alto	UGA } Alto	
	UUG } Leu	UCG } Ser	UAG } Alto	UGG } Trp	
C	CUU } Leu	CCU } Pro	CAU } His	CGU } Arg	U C A G
	CUC } Leu	CCC } Pro	CAC } His	CGC } Arg	
	CUA } Leu	CCA } Pro	CAA } Glu	CGA } Arg	
	CUG } Leu	CCG } Pro	CAG } Glu	CGG } Arg	
A	AUU } Ile	ACU } Tre	AAU } Asn	AGU } Ser	U C A G
	AUC } Ile	ACC } Tre	AAC } Asn	AGC } Ser	
	AUA } Met inicio	ACA } Tre	AAA } Lys	AGA } Arg	
	AUG } Met inicio	ACG } Tre	AAG } Lys	AGG } Arg	
G	GUU } Val	GCU } Ala	GAU } Asp	GGU } Glu	U C A G
	GUC } Val	GCC } Ala	GAC } Asp	GGC } Glu	
	GUA } Val	GCA } Ala	GAA } Asp	GGA } Glu	
	GUG } Val	GCG } Ala	GAG } Asp	GGG } Glu	



Consecuencias de las mutaciones

Mutaciones silenciosas: AGG → CGG (mismo aa)
Arg Arg

Mutaciones sentido errado "Missense": (otro aa)

Conservativa: AAA → AGA
Lys Arg (básico) (básico)

No Conservativa: UUA → UCA
Leu Ser (hidrofóbico) (polar)

Consecuencias de las mutaciones

Mutaciones sin sentido "Nonsense": CAG → UAG
Gln Stop

17.7 Base substitutions can cause (a) missense, (b) nonsense, and (c) silent mutations.

Consecuencias de las mutaciones

Mutaciones "Frameshift" (cambio en el marco de lectura):

Adición: AAG ACT CCT... → AAG AGC TCC T...
Delección: AAG ACT CCT... → AAA CTC CT...

Mutaciones "Frameshift" (cambio en el marco de lectura):

Change of one letter: Substitution (Point mutation)
Loss of one letter: Deletion (Frameshift mutation)
Gain of one letter: Insertion (Frameshift mutation)

Example sentences:
Original: THE CAT SAW THE DOG
Substitution: THE BAT SAW THE DOG / THE CAT SAW THE HOG / THE CAT SA T THE DOG
Deletion: THE ATS AWT HED OG (Loss of C)
Insertion: THE CMA TSA WTH EDO G (Insertion of M)

Mutaciones supresoras

1 A forward mutation changes the wild type into a mutant phenotype.
2 A reverse mutation restores the wild-type gene and the phenotype.
3 A suppressor mutation occurs at a site different from that of the original mutation...
4 ...and produces an individual that possesses both the original mutation and the suppressor mutation...
5 ...but has the wild-type phenotype.

Genotype: Wild type A⁺B⁺ → Mutation A → Reverse of mutation A⁻ → Mutation A⁻B⁻ → Suppressor mutation B⁺ → Mutations A⁻B⁺

Phenotypes: Red eyes → White eyes → Red eyes

17.8 Relation of forward, reverse, and suppressor mutations.

Intrigénicas **Intergénicas**

Mutaciones supresoras: Intrigénica

1 A missense mutation alters a single codon.
2 A second mutation at a different site in the same gene...
3 ...may restore the original amino acid.

DNA: AAT → Mutation → AAG → Intragenic suppressor mutation → GAA
mRNA: UUA → UUU → CUU
Protein: Ser → Phe → Leu

17.9 An intragenic suppressor mutation occurs in the same gene that contains the mutation being suppressed.

Mutaciones supresoras: Intergénica

(a) With the wild-type sequence...
1 A base substitution at one site produces a premature stop codon...
2 Leu is incorporated into a protein.
3 ...which halts protein synthesis, resulting in a non-functional protein.
4 Termination of translation. Shortened, nonfunctional protein.

(b) At site 2, a gene encoding tyrosine-tRNA...
1 A base substitution produces an incorrect base (G...)
2 ...the resulting mutant tRNA has anticodon AUC (instead of AUA)...
3 ...which can pair with the stop codon UAG...
4 Translation continues past the stop codon. Tyr is incorporated into the protein.
5 Full-length, functional protein.



Mutaciones espontáneas o inducidas

Table 14-1 Mutation Frequencies Obtained with Various Mutagens in *Neurospora*

Mutagenic treatment	Exposure time (minutes)	Survival (%)	Number of <i>ad-3</i> mutants per 10 ⁶ survivors
No treatment (spontaneous rate)	–	100	–0.4
Amino purine (1–5 mg/ml)	During growth	100	3
Ethylmethanesulfonate (1%)	90	56	25
Nitrous acid (0.05 M)	160	23	128
X rays (2000 r/min)	18	16	259
Methyl methanesulfonate (20 mM)	300	26	350
UV rays (600 erg/mm ² /min)	6	18	375
Nitrosoguanidine (25 mM)	240	65	1500
ICR-170 acridine mustard (5 mg/ml)	480	28	2287

Note: The assay measures the frequency of *ad-3* mutants. It so happens that such mutants are red, so they can be detected against a background of white *ad-3⁻* colonies.

Mutaciones espontáneas

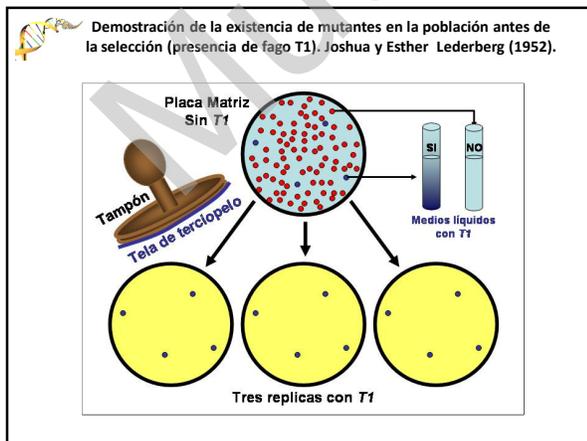
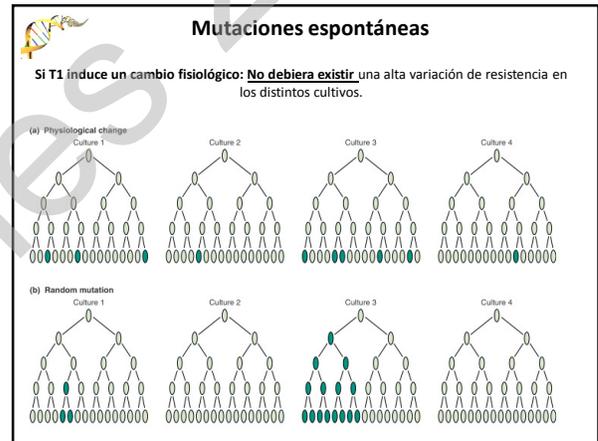
Luria y Delbrück (1943) “test de la fluctuación”:

Con cierta frecuencia aparecían bacterias resistentes al fago T1:

¿Fago T1 induce un cambio fisiológico que produce la resistencia? o ¿La resistencia en las bacterias se produce de forma aleatoria?

20 cultivos independientes de *E. coli* → plaqueo en presencia de fago T1:
Variación en el número de colonias resistentes a T1 en los distintos cultivos.

20 muestras de 1 cultivo de *E. coli* → plaqueo en presencia de fago T1:
Número similar de colonias resistentes a T1 en las distintas muestras.



- ### Mutaciones espontáneas:
- Errores en la replicación
 - Tautómeros
 - “Balanceo”
 - Deslizamiento de la hebra de DNA
 - Cambios químicos espontáneos
 - Depurinación
 - Desaminación

Tautomerismo de las bases nitrogenadas.

Tautómeros: isómeros que se diferencian sólo en la posición de sus átomos.

Figure 14-6 Mismatched bases. Rare tautomeric forms of bases result in mismatches.

Tautomerismo de las bases nitrogenadas.

Table 12.4 Pairing Relationships of DNA Bases in the Normal and Tautomeric Forms

Base	In Normal State Pairs with	In Tautomeric State Pairs with
A	T	C
T	A	G
G	C	T
C	G	A

Template transition—tautomerization of adenine in the template. Substrate transition—tautomerization of incoming adenine.

“Balanceo” por flexibilidad en la estructura del DNA.

Non-Watson-Crick base pairing

17.12 Nonstandard base pairings can occur as a result of the flexibility in DNA structure. Thymine and guanine can pair through wobble between normal bases. Cytosine and adenine can pair through wobble when adenine is protonated (has an extra hydrogen).

17.13 Wobble base pairing leads to a replicated error.

Deslizamiento de la hebra de DNA.

Figure 14-21 A model for indel mutations resulting in frameshifts. dr = deoxyribose.

Depurización y Desaminación:

17.16 Depurination, loss of a purine base from the nucleotide, produces an apurinic site.

17.17 Deamination alters DNA bases.

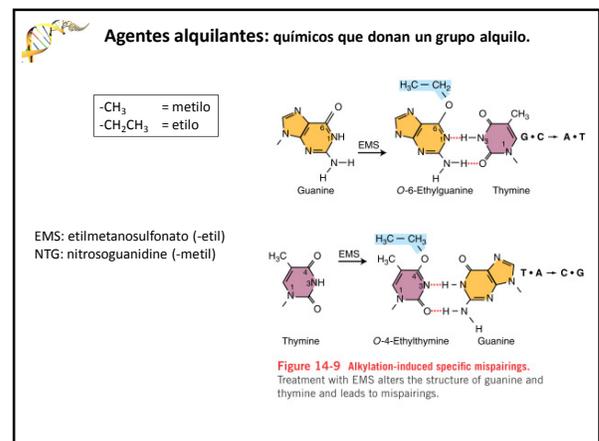
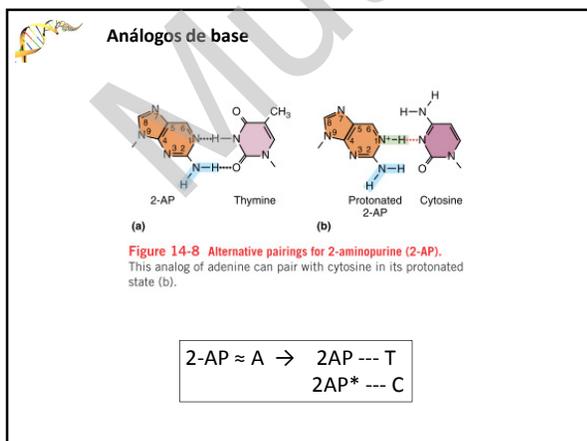
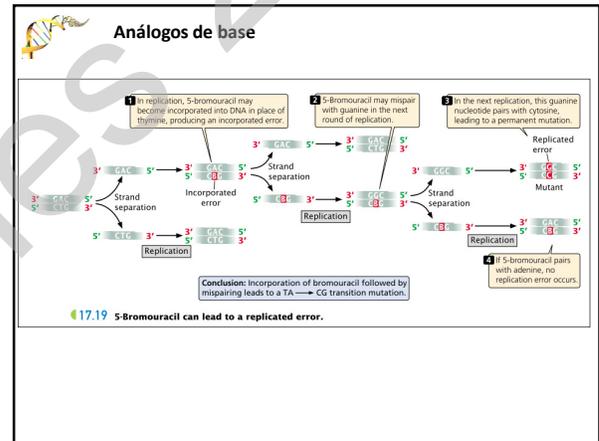
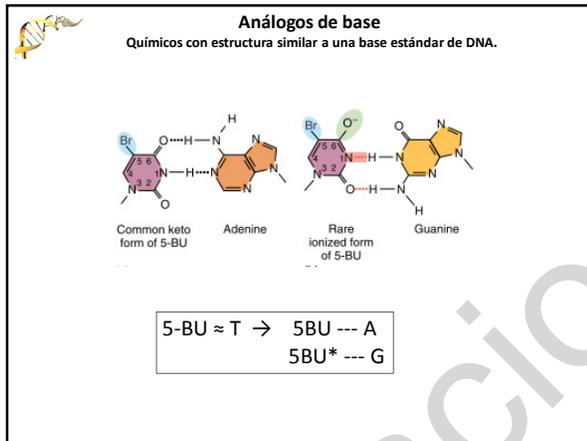
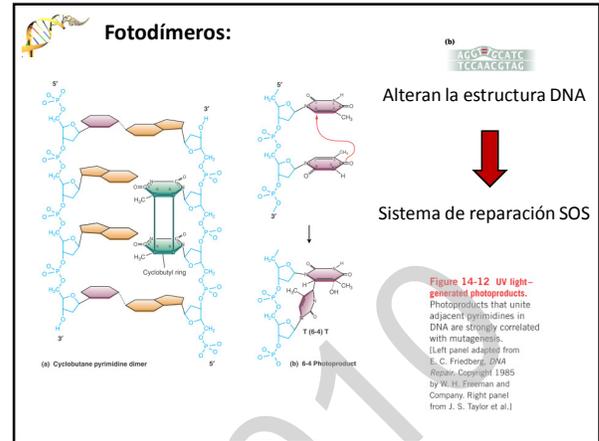
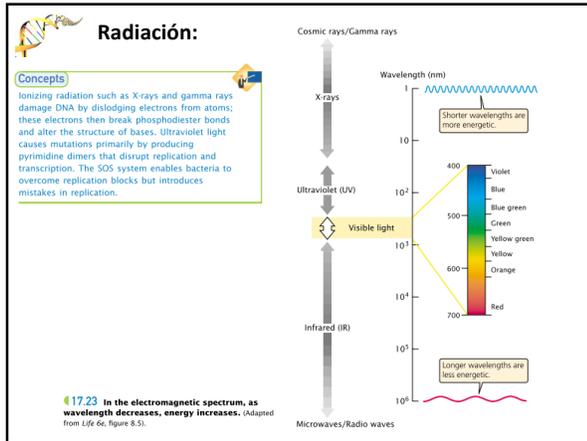
(a) Cytosine → Uracil

(b) 5-Methylcytosine (5mC) → Thymine

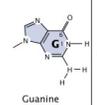
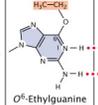
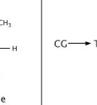
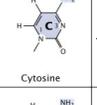
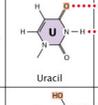
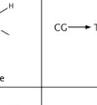
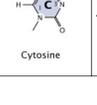
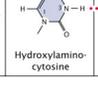
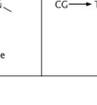
Mutaciones inducidas:

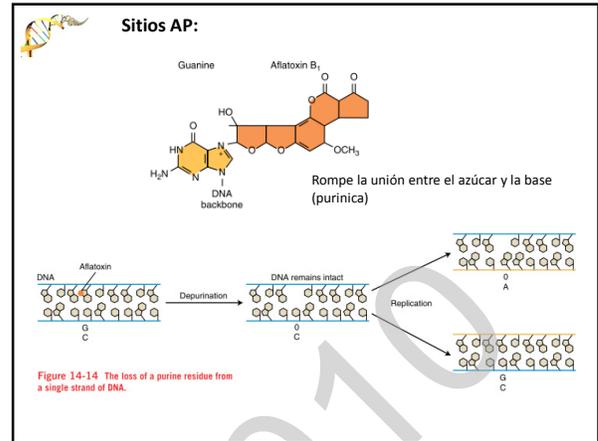
- Físicos (radiación):
 - Radiación ionizante (Rayos X y gamma)
 - UV
- Químicos:
 - Análogos de Base
 - Agentes modificadores de base:
 - Alquilantes
 - Deaminación
 - Hydroxylamina
 - Reacciones oxidativas
 - Agentes Intercalantes

Concepts
Chemicals can produce mutations by a number of mechanisms. Base analogs are inserted into DNA and frequently pair with the wrong base. Alkylating agents, deaminating chemicals, hydroxylamine, and oxidative radicals change the structure of DNA bases, thereby altering their pairing properties. Intercalating agents wedge between the bases and cause single base insertions and deletions in replication.



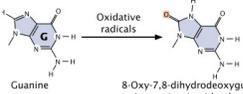
Modificadores de base:

	Original base	Mutagen	Modified base	Pairing partner	Type of mutation
(a)	 Guanine	EMS	 O ⁶ -Ethylguanine	 Thymine	CG → TA
(b)	 Cytosine	Nitrous acid (HNO ₂)	 Uracil	 Adenine	CG → TA
(c)	 Cytosine	Hydroxylamine (NH ₂ OH)	 Hydroxylaminocytosine	 Adenine	CG → TA

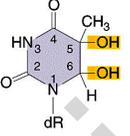


Reacciones oxidativas:

$O_2 + e^- \rightarrow O_2^-$: Superóxido
 $O_2 + e^- + 2H^+ \rightarrow H_2O_2$: Peróxido de hidrógeno
 $H_2O_2 + e^- + H^+ \rightarrow H_2O + OH\cdot$: Radical hidroxilo
 $OH\cdot + e^- + H^+ \rightarrow H_2O$



Guanine → 8-Oxy-7,8-dihydroxyguanine (may mispair with adenine)



dR
Glicol de timidina

17.21 Oxidative radicals convert guanine into 8-oxy-7,8-dihydroxyguanine, which frequently mispairs with adenine instead of cytosine.

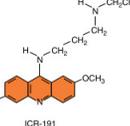
Agentes intercalantes:



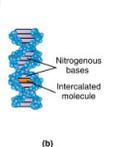
Proflavin



Acridine orange



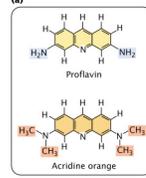
ICR-191



Nitrogenous bases
Intercalated molecule

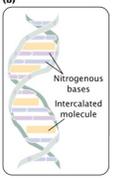
Figure 14-10 Intercalating agents. (a) Structures of common intercalating agents and (b) their interaction with DNA. [From L. S. Lerman, Proc. Natl. Acad. Sci. USA 39, 1963, 94.]

(a)



Proflavin
Acridine orange

(b)



Nitrogenous bases
Intercalated molecule



InDel

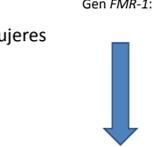
17.22 Intercalating agents such as proflavin and acridine orange insert themselves between adjacent bases in DNA, distorting the three-dimensional structure of the helix and causing single-nucleotide insertions and deletions in replication.

Algunos casos de mutaciones en humanos:

Síndrome X-frágil: retraso mental.
1 cada 1500 hombres y 1 cada 2500 mujeres



Gen *FMR-1*:

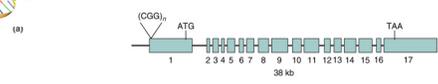


(CGG)_n; se transcribe, pero no se traduce

17.5 The fragile-X chromosome is associated with a characteristic constriction (fragile site) on the long arm. [Visuals Unlimited.]

The *FMR-1* gene involved in fragile X syndrome.

(a) Exon structure and upstream CCG repeat. (b) Transcription and methylation in normal, premutation, and full mutation alleles. The red circles are methyl groups.



	<i>FMR-1</i> gene	Phenotype	Transmission	Methylation	Transcription
Normal		Normal	Stable	No	Yes
Premutation		Largely normal	Unstable, prone to expansion	No	Yes
Full mutation		Affected	Unstable	Yes	No

Figure 14-24 The *FMR-1* gene involved in fragile X syndrome. (a) Exon structure and upstream CCG repeat. (b) Transcription and methylation in normal, premutation, and full mutation alleles. The red circles are methyl groups. [W. T. O'Donnell and S. T. Warren, Ann. Rev. Neuroscience 25, 2002, 315-338, Figure 1.]

Enfermedad de Huntington: trastorno genético hereditario, trastorno neuropsiquiátrico. Degeneración neuronal constante y progresiva.

Gen de la huntingtina: expansión de repeticiones del trinucleótido CAG (Gln).

17.6 The number of copies of a trinucleotide may increase by strand slippage in replication.

Table 17.1 Examples of genetic diseases caused by expanding trinucleotide repeats

Disease	Repeated Sequence	Number of Copies of Repeat	
		Normal Range	Disease Range
Spinal and bulbar muscular atrophy	CAG	11–33	40–62
Fragile-X syndrome	CGG	6–54	50–1500
Jacobson syndrome	CGG	11	100–1000
Spinocerebellar ataxia (several types)	CAG	4–44	21–130
Autosomal dominant cerebellar ataxia	CAG	7–19	37–220
Myotonic dystrophy	CTG	5–37	44–3000
Huntington disease	CAG	9–37	37–121
Friedreich ataxia	GAA	6–29	200–900
Dentatorubral-pallidolusian atrophy	CAG	7–25	49–75
Myoclonus epilepsy of the Unverricht-Lundborg type*	CCCCCGGG	2–3	12–13

*Technically not a trinucleotide repeat but does entail a multiple of three nucleotides that expands and contracts in similar fashion to trinucleotide repeats.

Concepts
Expanding trinucleotide repeats are regions of DNA that consist of repeated copies of three nucleotides. Increased numbers of trinucleotide repeats are associated with several genetic diseases.

Table 17.2 Characteristics of different types of mutations

Type of Mutation	Definition
Base substitution	Changes the base of a single DNA nucleotide
Transition	Base substitution in which a purine replaces a purine or a pyrimidine replaces a pyrimidine
Transversion	Base substitution in which a purine replaces a pyrimidine or a pyrimidine replaces a purine
Insertion	Addition of one or more nucleotides
Deletion	Deletion of one or more nucleotides
Frameshift mutation	Insertion or deletion that alters the reading frame of a gene
In-frame deletion or insertion	Insertion or deletion of a multiple of three nucleotides that does not alter the reading frame
Expanding trinucleotide repeats	Repeated sequence of three nucleotides (trinucleotide) in which the number of copies of the trinucleotide increases
Forward mutation	Changes the wild-type phenotype to a mutant phenotype
Reverse mutation	Changes a mutant phenotype back to the wild-type phenotype
Missense mutation	Changes a sense codon into a different sense codon, resulting in the incorporation of a different amino acid in the protein
Nonsense mutation	Changes a sense codon into a nonsense codon, causing premature termination of translation
Silent mutation	Changes a sense codon into a synonymous codon, leaving unchanged the amino acid sequence of the protein
Neutral mutation	Changes the amino acid sequence of a protein without altering its ability to function
Loss-of-function mutation	Causes a complete or partial loss of function
Gain-of-function mutation	Causes the appearance of a new trait or function or causes the appearance of a trait in inappropriate tissues or at inappropriate times
Lethal mutation	Causes premature death
Suppressor mutation	Suppresses the effect of an earlier mutation at a different site
Intragenic suppressor mutation	Suppresses the effect of an earlier mutation within the same gene
Intergenic suppressor mutation	Suppresses the effect of an earlier mutation in another gene

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