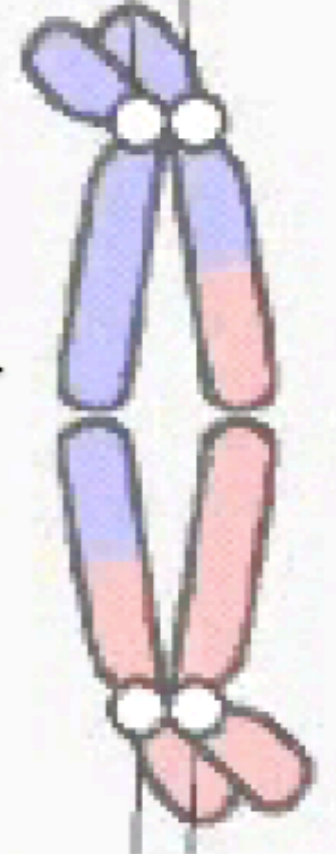
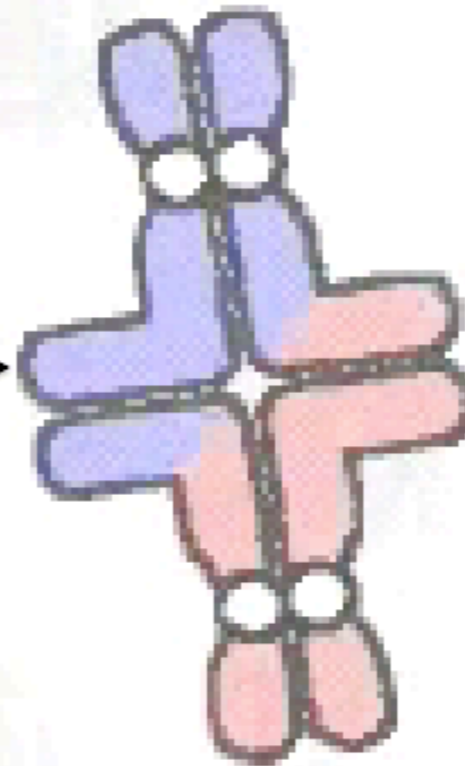
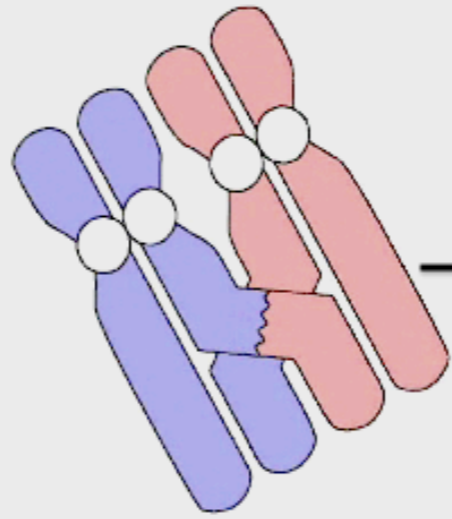
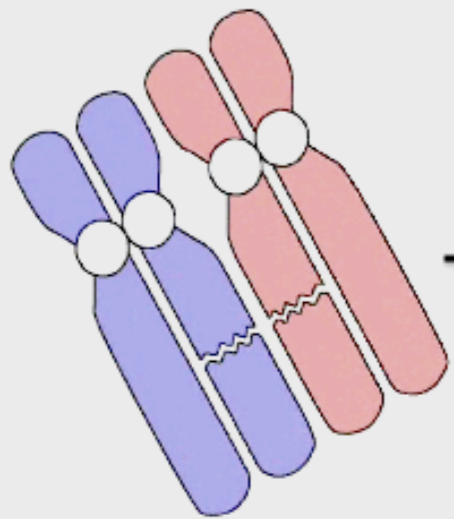


Profase I

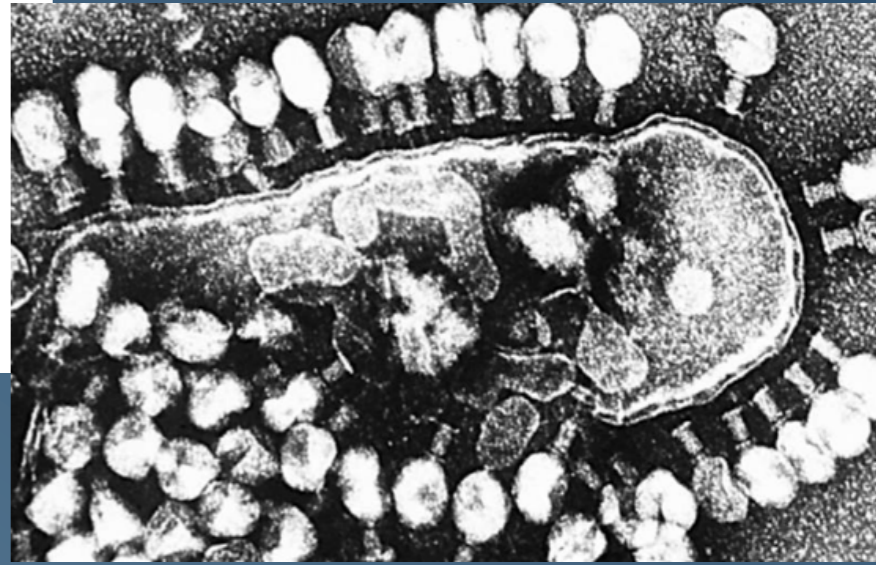
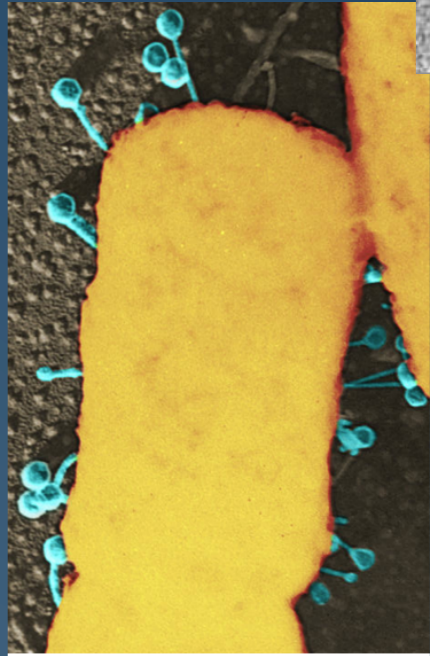
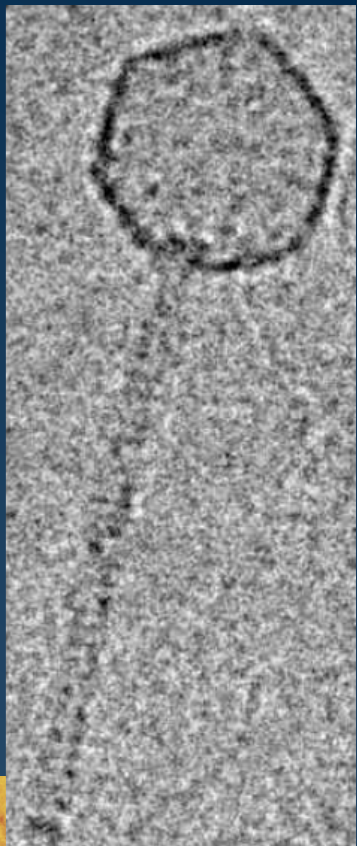
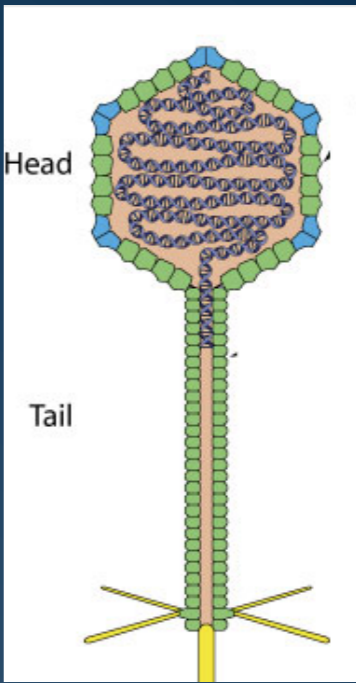
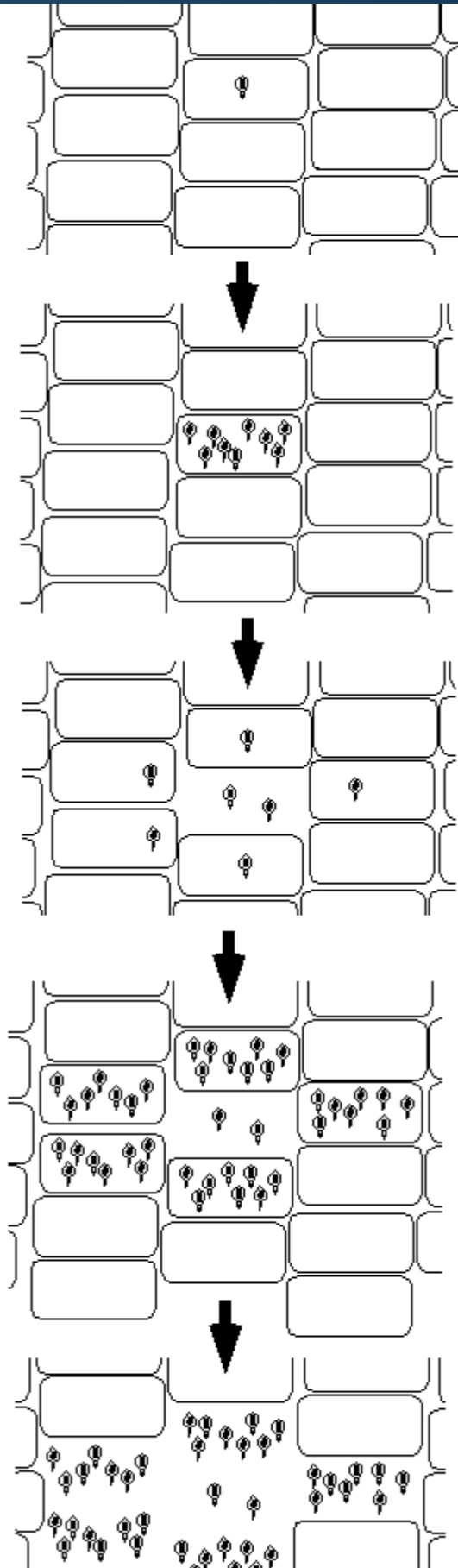
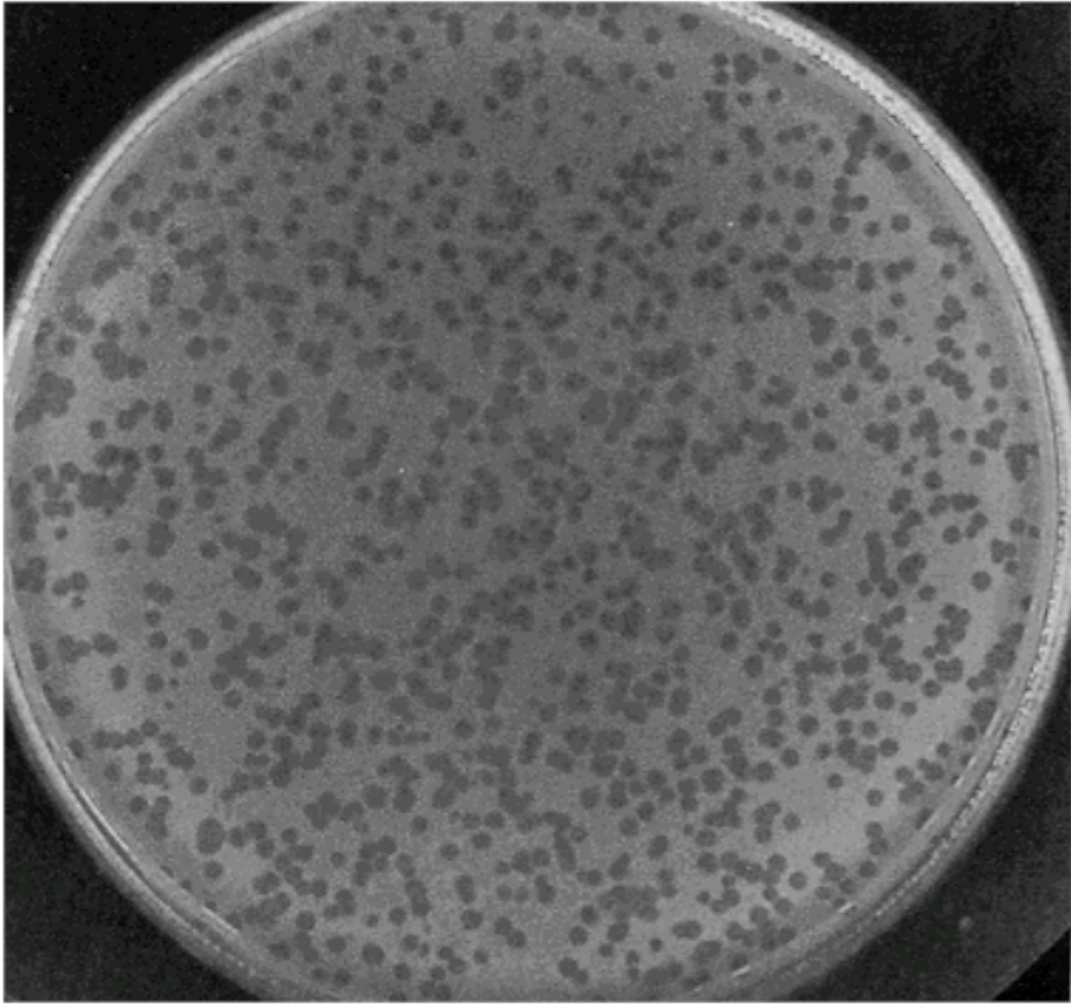
Profase I

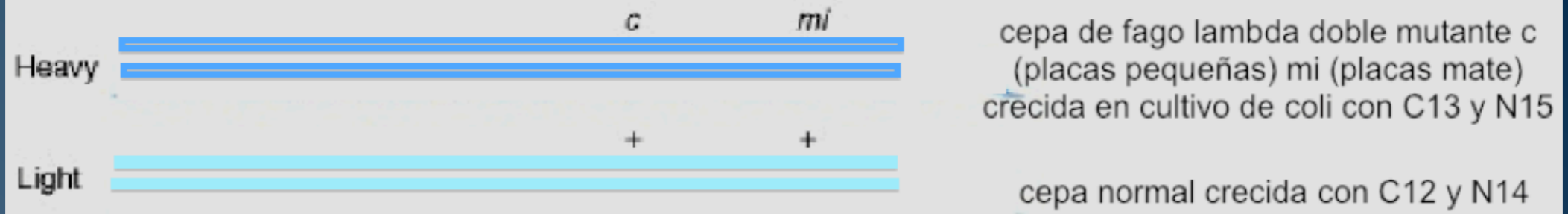
Metafase I

Anafase I



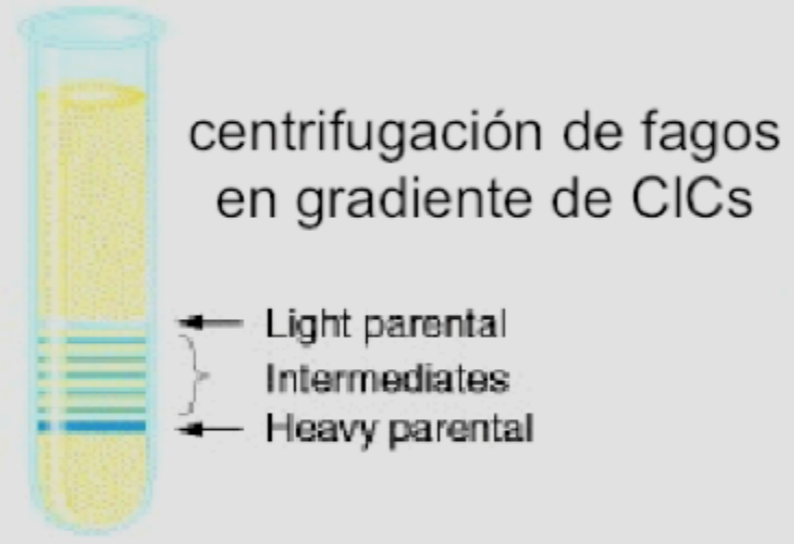
Cultivo de bacteriófagos y fenotipos en placas de lisis





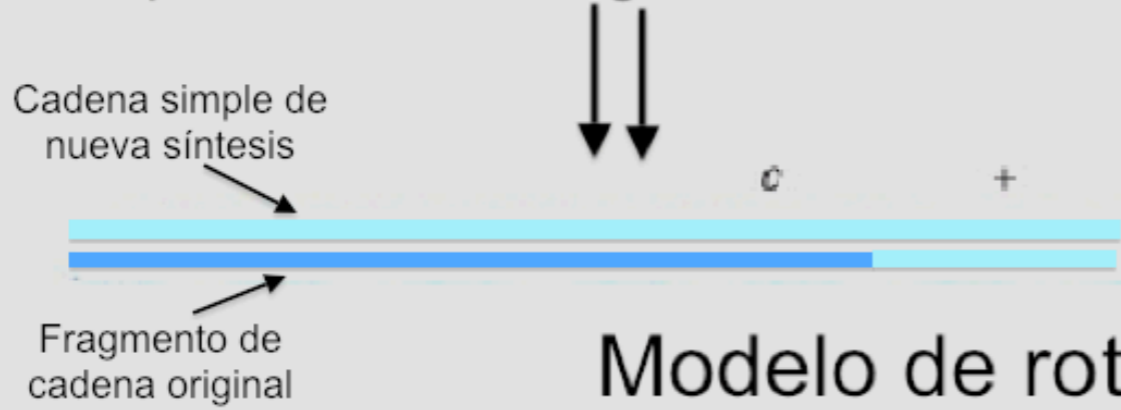
coinfeción de cultivo líquido de coli con C12 N14

lisis y purificación de fagos



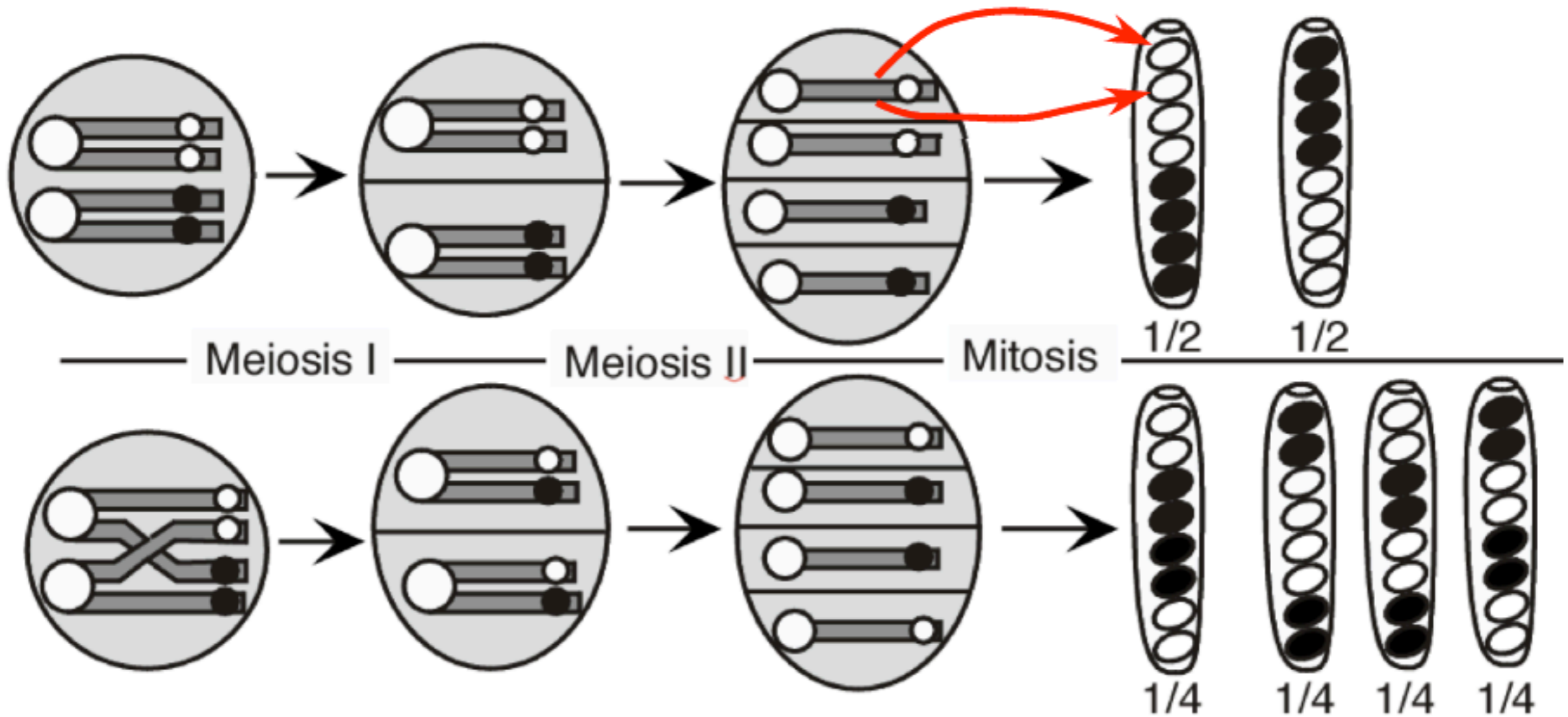
extracción de fracciones y fenotipado para los marcadores

Las primeras fracciones (más pesadas) tenían fenotipo c mi . Las siguientes eran de fenotipo c $+$.



Modelo de rotura-reunión

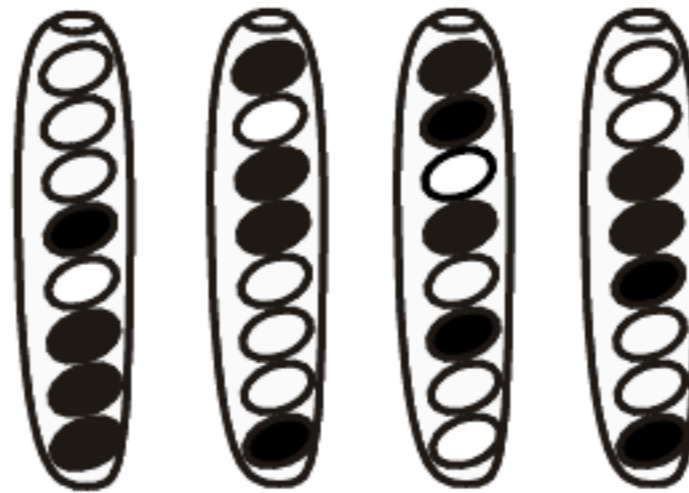
Segregación típica de un gen en ascas ordenadas



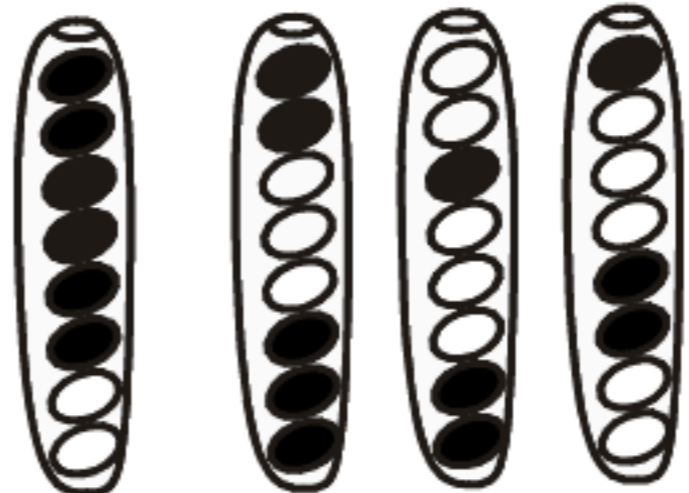
Ascas con disposiciones infrecuentes

ASCAS INFRECUENTES

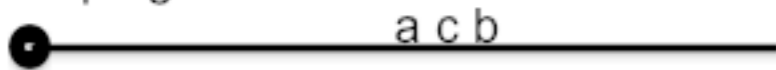
Proporciones mendelianas



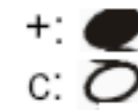
Conversión génica



Mapa genético:

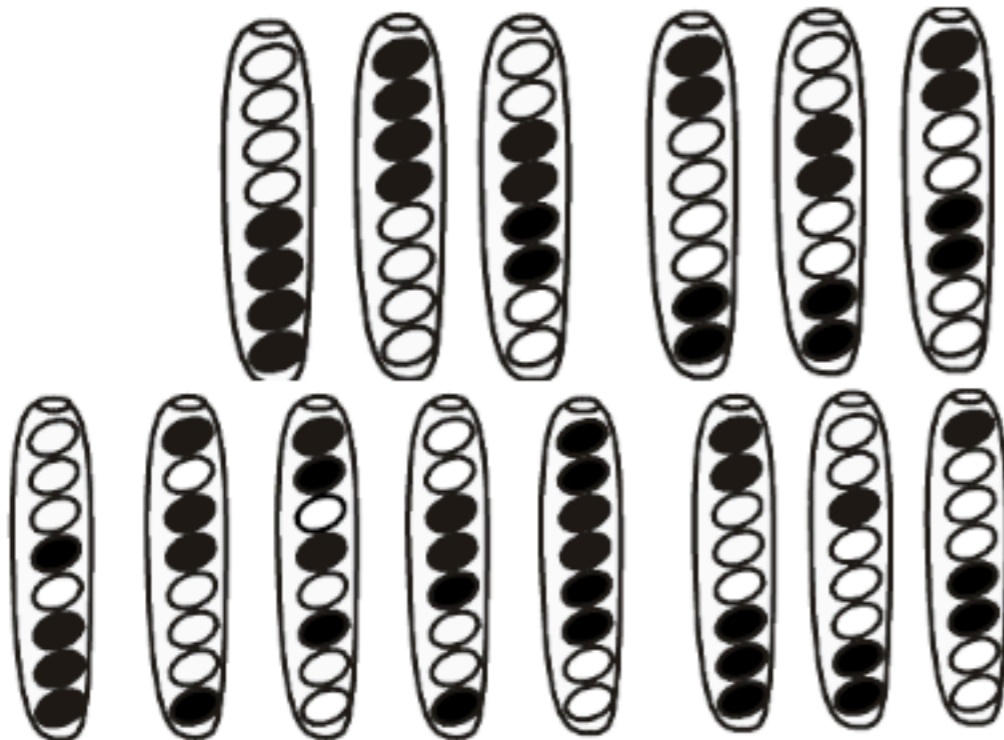


Fenotipos del gen central:

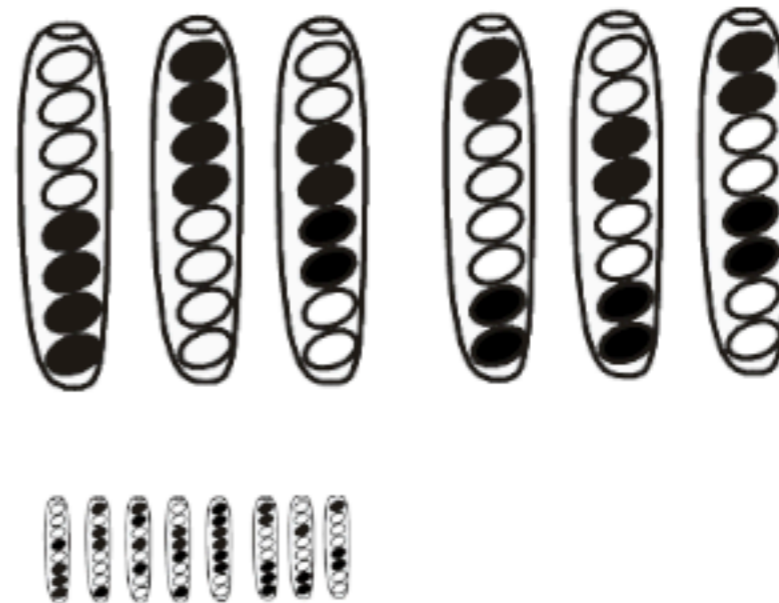


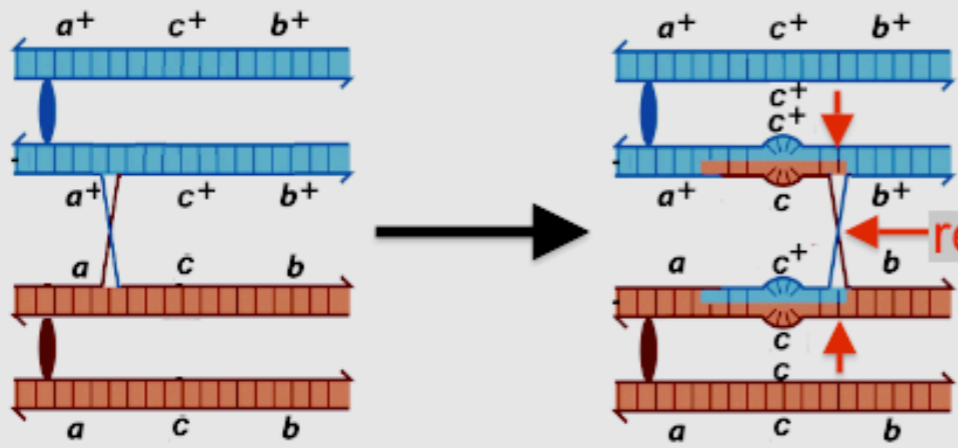
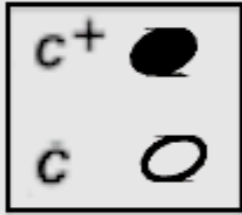
a c b x + + +

ascas con esporas
recombinantes entre a y b:
(a ? + y + ? b)



ascas sin esporas
recombinantes entre a y b





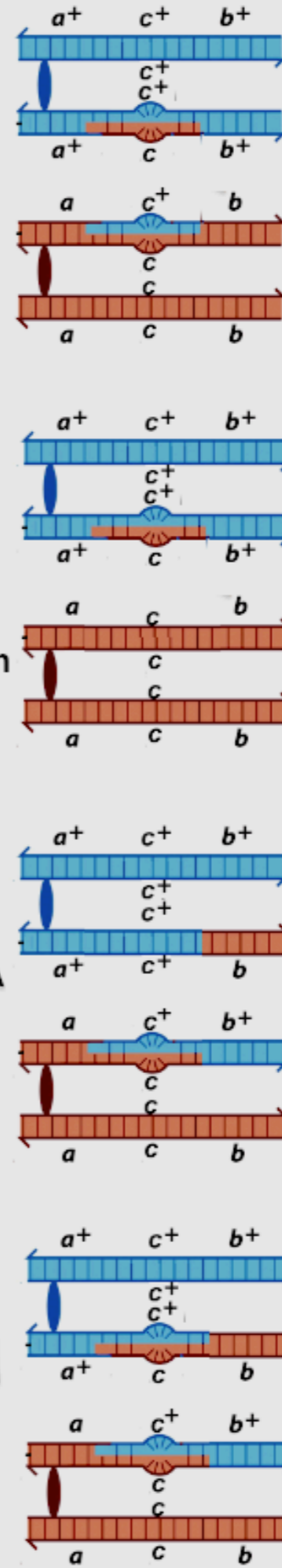
Horizontal sin reparación

Horizontal con reparación (ejemplo)

Vertical con reparación (ejemplo)

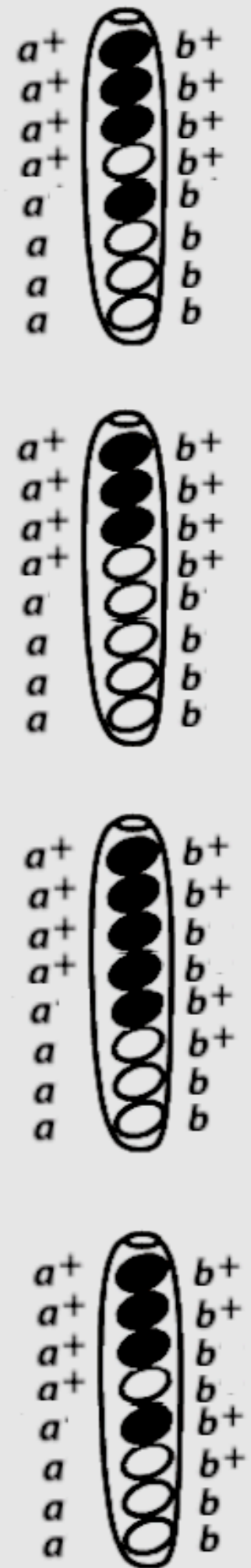
Vertical sin reparación

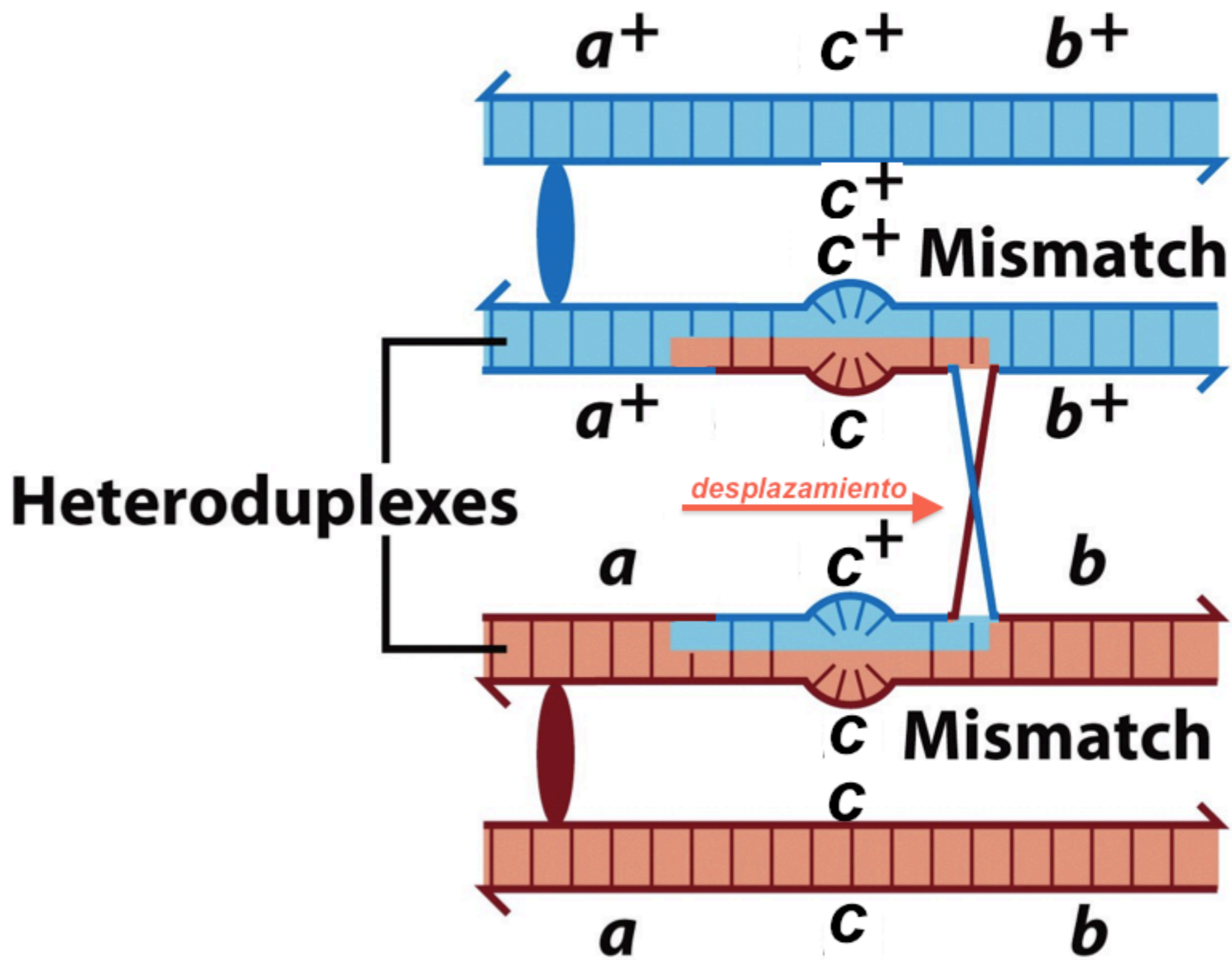
resolución



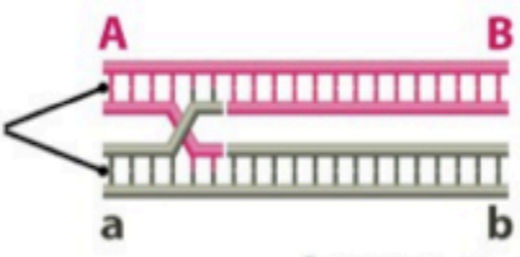
sin sobrecruzamiento

llevan a sobrecruzamiento



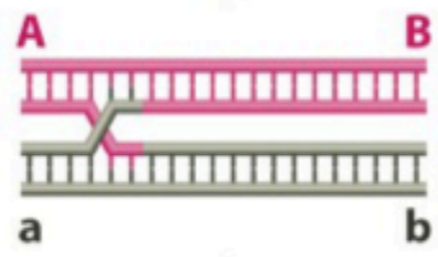


Two homologous DNA molecules



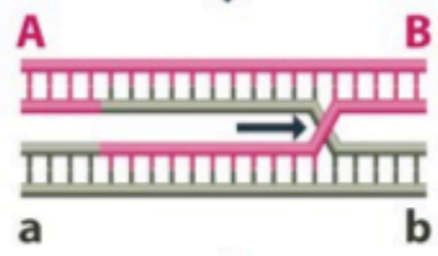
Exchange of polynucleotides sets up the heteroduplex

↓ DNA ligase

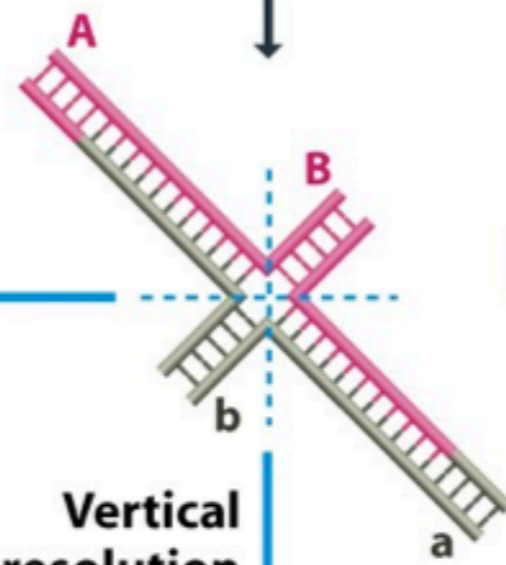


Holliday structure

↓ Branch migration



↓

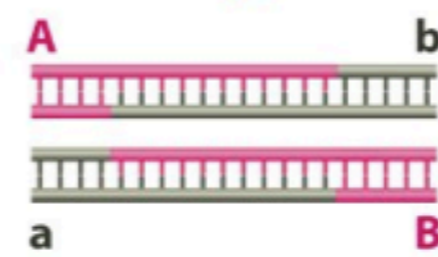
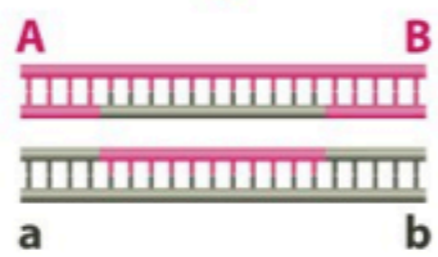


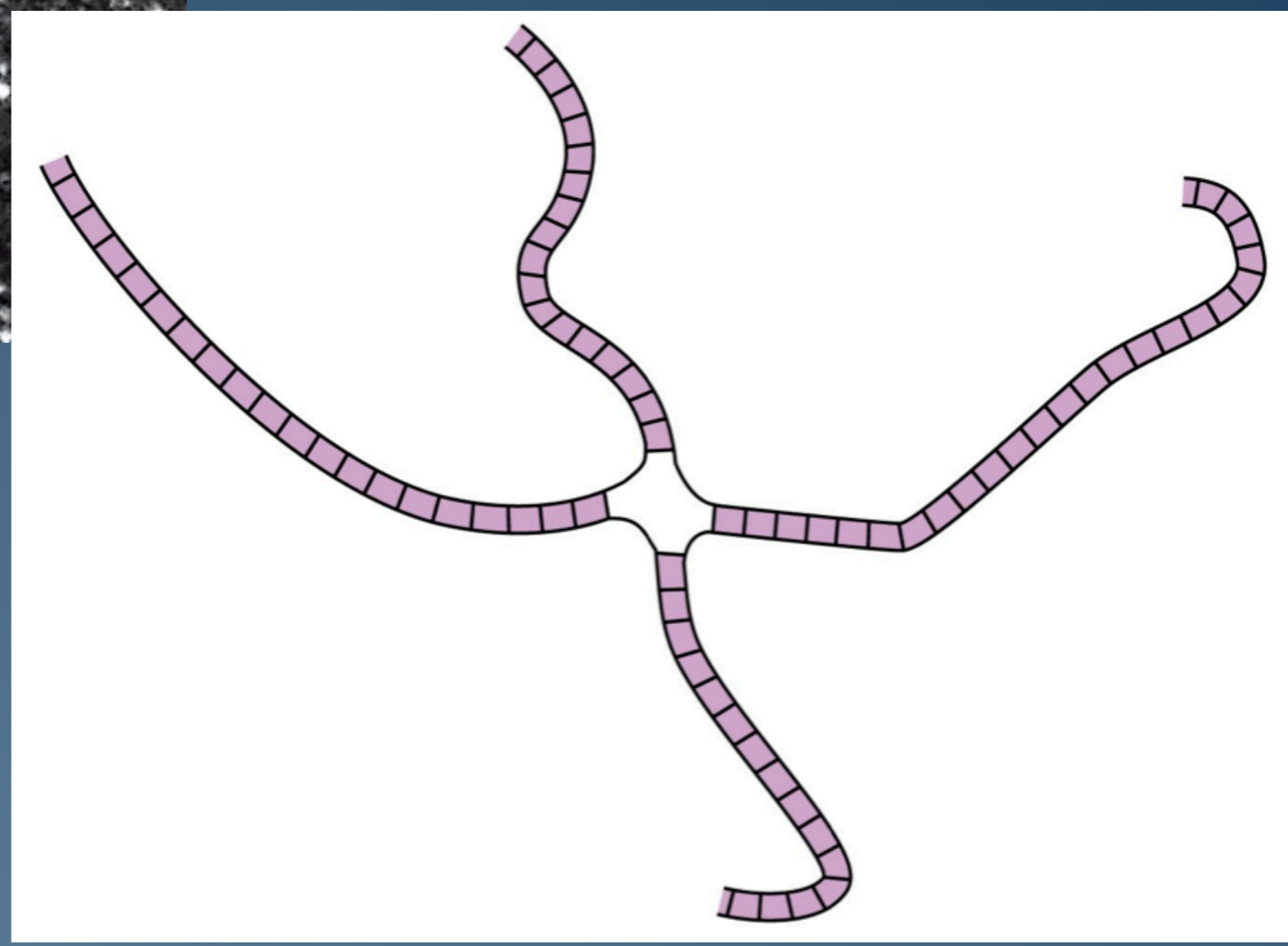
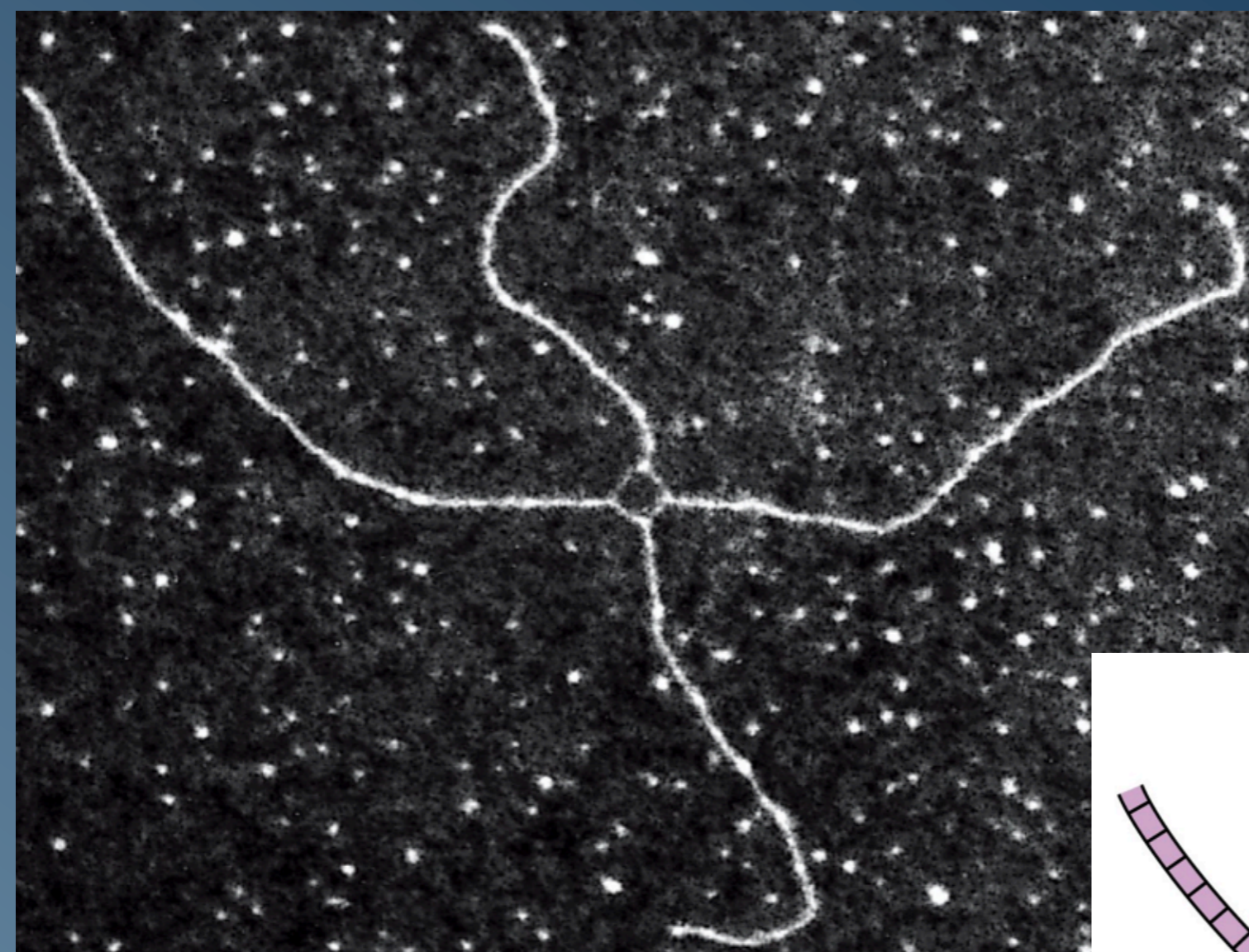
chi form

Horizontal resolution

Vertical resolution

Reciprocal strand exchange



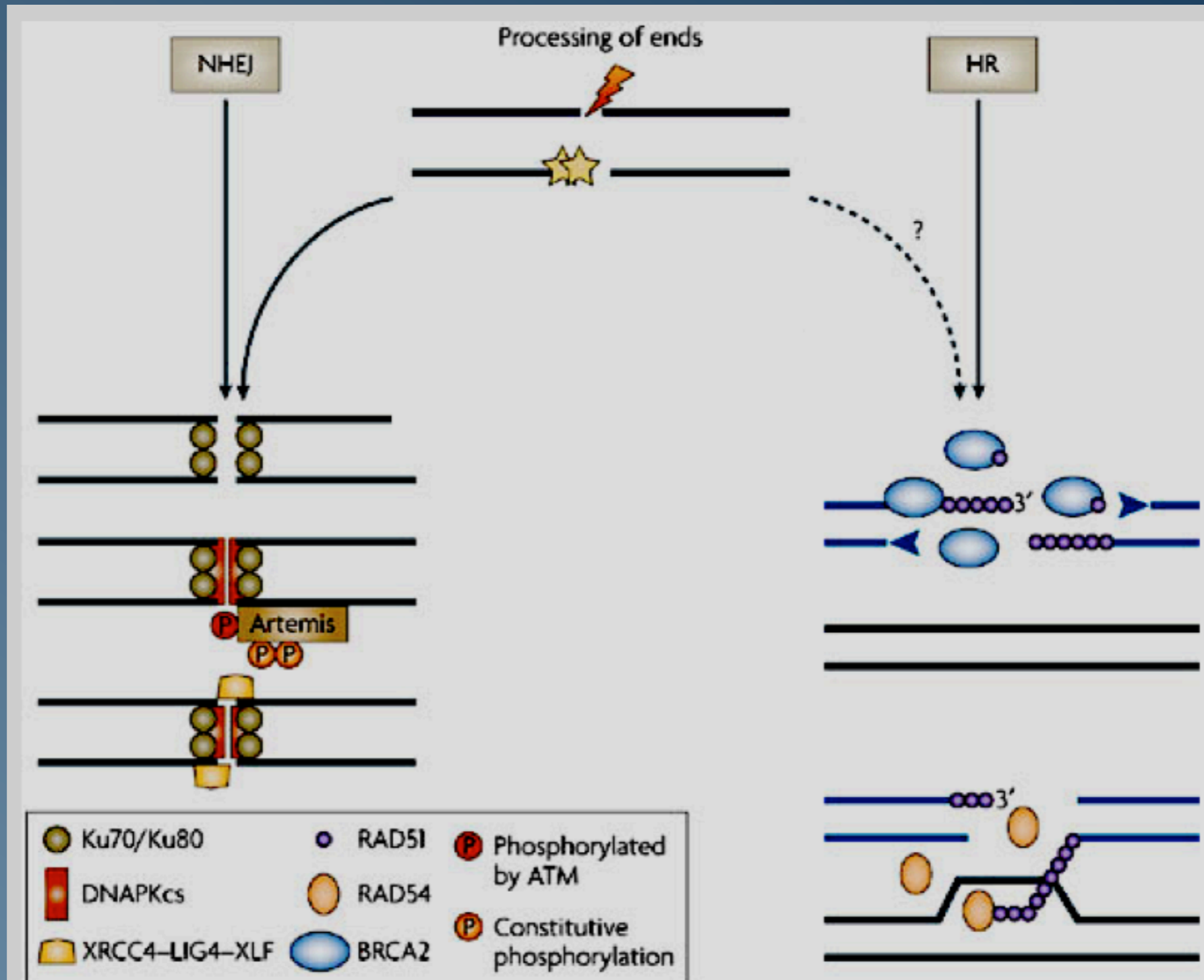


Reparación de roturas de doble cadena

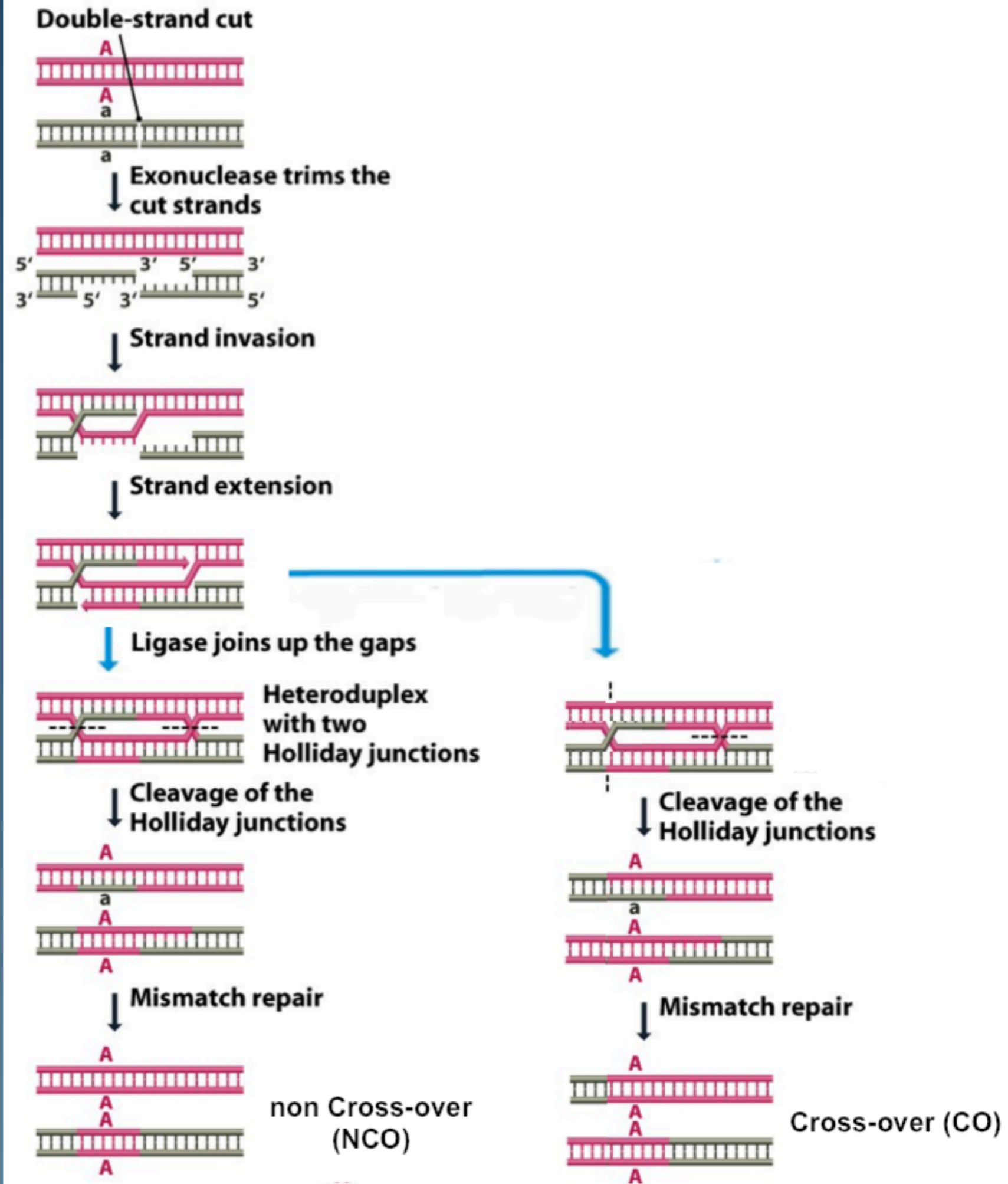
Unión de sitios no homólogos.

Suele llevar a deleciones e inserciones

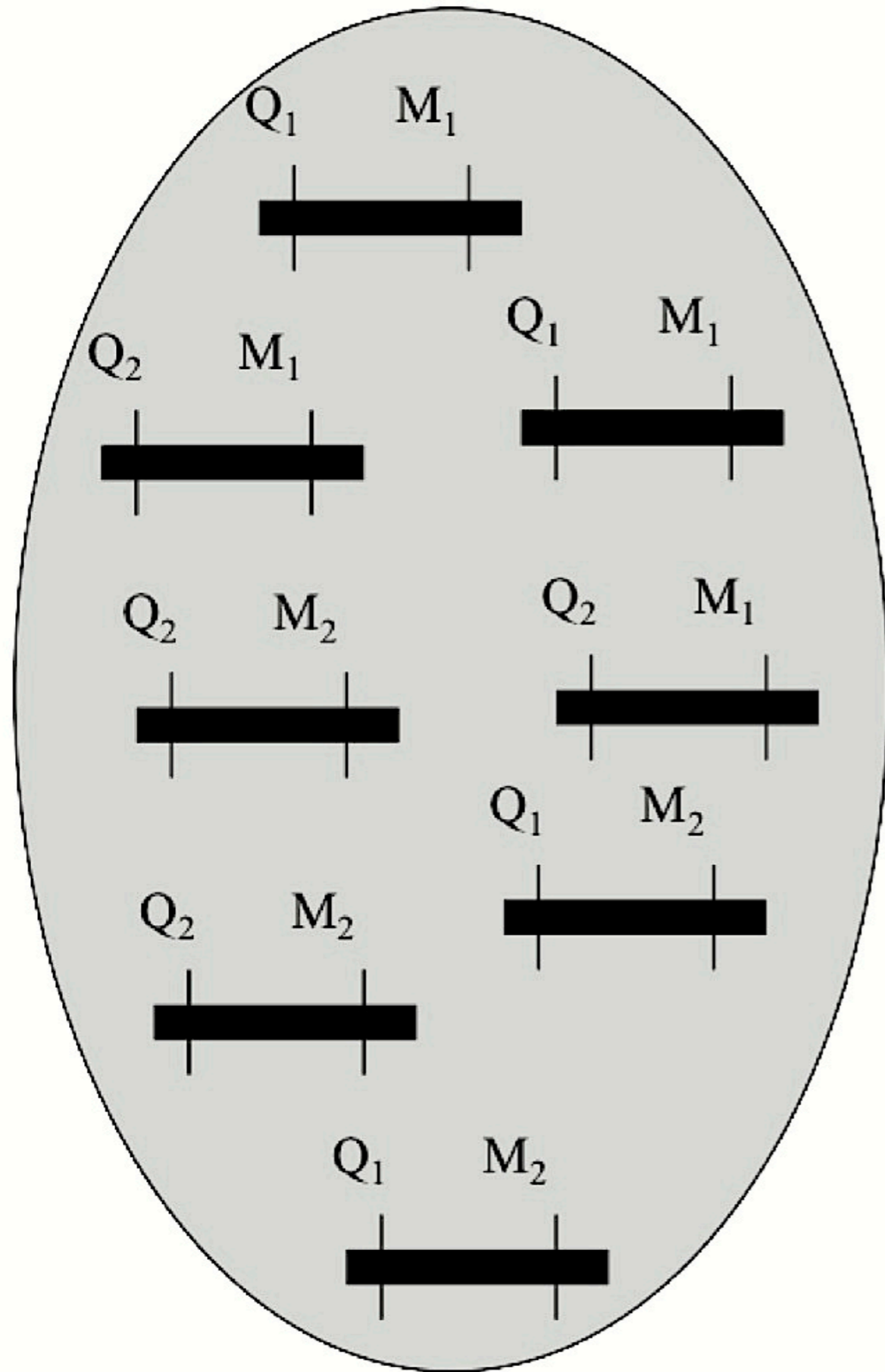
Recombinación homóloga



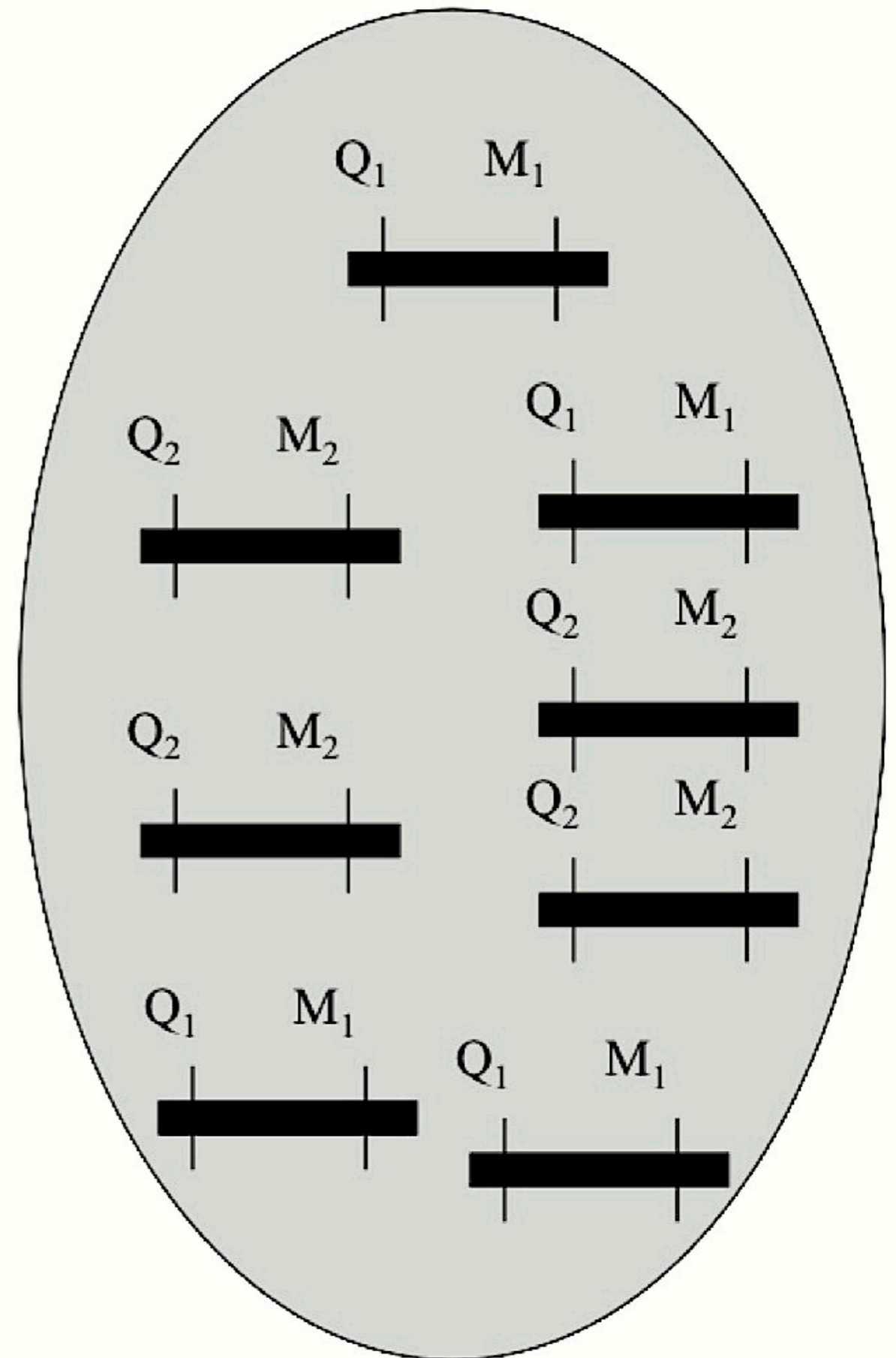
Modelo de rotura de doble cadena



Linkage equilibrium



Linkage disequilibrium



Desequilibrio de ligamiento entre pares de snp próximos:

		NUMEROS ABSOLUTOS					PROPORCIONES		
		Locus 1					Locus 1		
		alelo 1	alelo 2				alelo 1	alelo 2	
Locus 2	alelo 1	n11 = 150	n21 = 15	165	Locus 2	alelo 1	x11 = 0,389	x21 = 0,039	q1 = 0,428
	alelo 2	n12 = 0	n22 = 221	221		alelo 2	x12 = 0	x22 = 0,572	q2 = 0,572
		150	236	T = 386			p1 = 0,389	p2 = 0,611	1

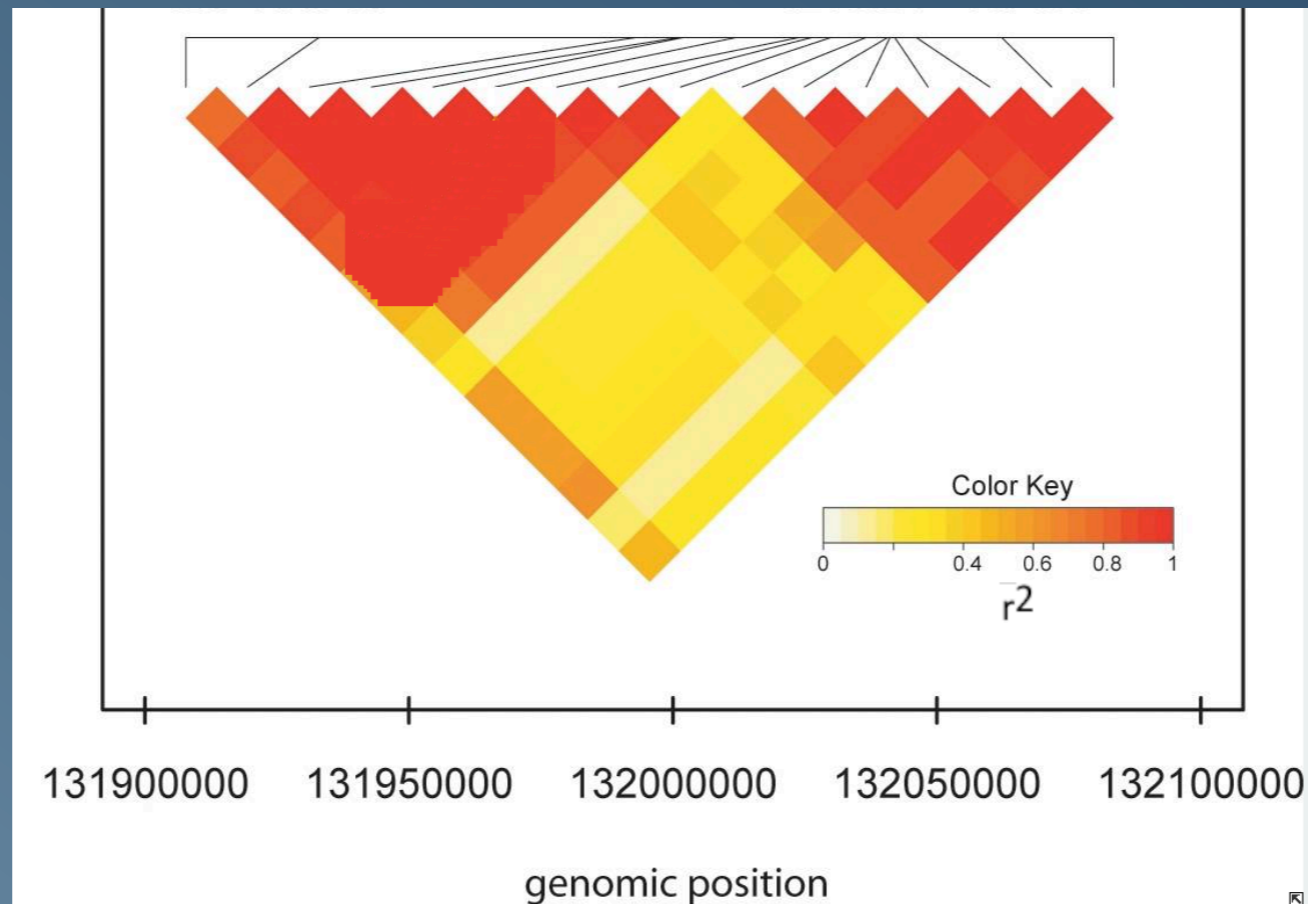
n21=número de genomas con el alelo 2 del Locus 1 y el alelo 1 del Locus 2

$\chi^2(1gl) = 328,6 \gg 3,84$ (altamente significativo)

$x21 = n21 / T$

$D = (x11 * x22) - (x21 * x12) = 0,223$

$r^2 = D^2 / (p1 * p2 * q1 * q2) = 0,855$



Frecuencias de recombinación entre snp obtenidas de espermatozoides individuales

