

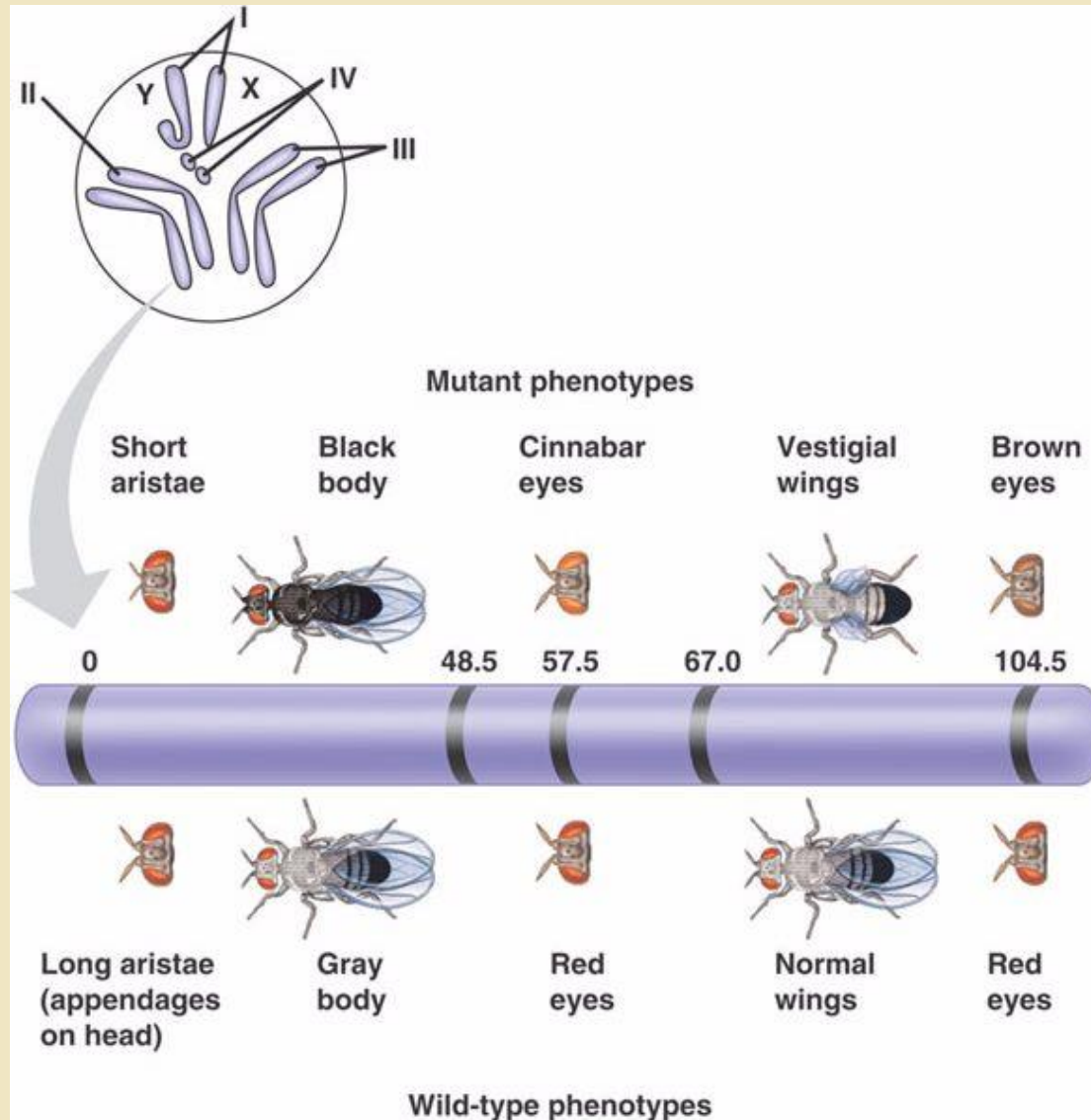
4a semana LGN 0218
Ligação e mapa genético
Material Didático, Departamento de Genética,
ESALQ/ USP

Thomas Hunt Morgan
was awarded the Nobel
Prize in 1933)



Professora Maria Lucia Carneiro Vieira

Morgan e colaboradores atribuíram genes aos 4 cromossomos de *Drosophila*



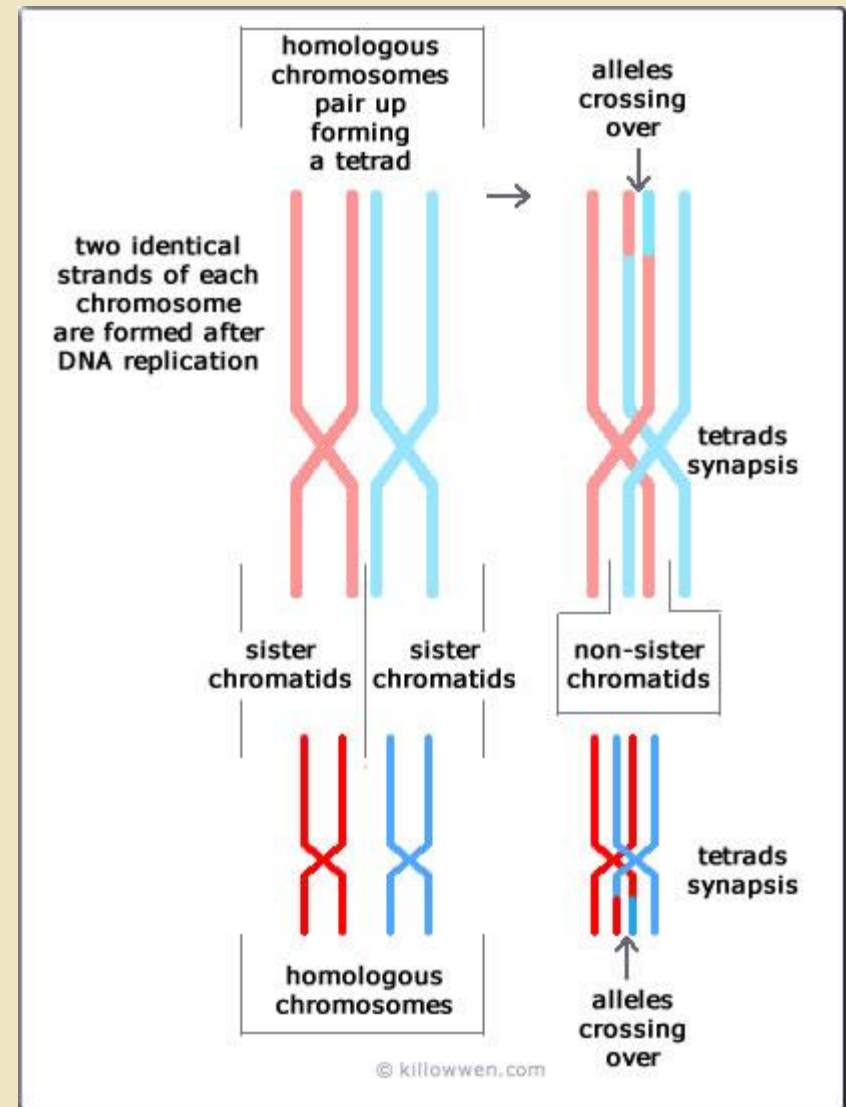
Cálculo da *fr*: no Cruzamento-Teste:

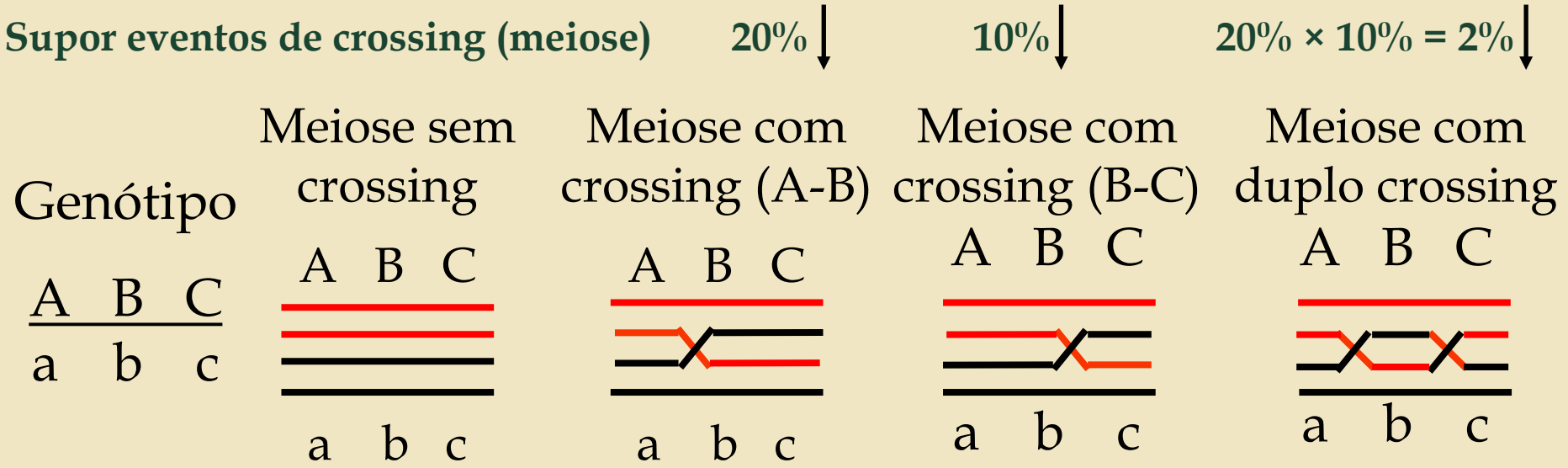
$$fr = r = \frac{\sum \text{tipos recombinantes}}{N}$$

A distância entre os genes é função da frequência de recombinação

Crossing over is the process by which the two chromosomes of a homologous pair exchange equal segments with each other. Crossing over occurs in Prophase I during meiosis I. At interphase, chromosome has replicated into two strands - the sister chromatids.

The two homologous chromosomes of a pair synapse. While the chromosomes are synapsed, breaks occur at corresponding points in two of the **non-sister** chromatids. As a result, a new combination of alleles is produced on the chromosome - this is called **recombination**.





Analise a progênie oriunda do cruzamento teste $\frac{ABC}{abc} \times \frac{abc}{abc}$

Determine a distância entre os genes A, B e C:

Progênie	Nº de indivíduos
ABC/abc	410
abc/abc	430
Abc/abc	55
aBC/abc	45
ABc/abc	24
abC/abc	26
AbC/abc	5
aBc/abc	5
Total	1.000

Distância entre A-B = $\frac{\Sigma R}{N} = \frac{55 + 45 + 5 + 5}{1.000} = 11\%$ ou 11 cM

Distância B-C = $\frac{24 + 26 + 5 + 5}{1.000} = 6\%$ = 6 cM

Distância A-C = $\frac{55 + 45 + 24 + 26}{1.000} = 15\%$ = 15 cM

- Note que a distância calculada entre os genes extremos é menor que a real
- Corrigindo: Distância AC = Distância calculada + 2 x Freq DR observada = $15\% + 2 \times [(5 + 5)/1.000 \times 100] = 15\% + 2 \times [(10/1.000) \times 100] = 15\% + (2 \times 1\%) = 17\%$ ou 17 cM
- Note que é preciso trabalhar sempre com a mesma unidade.

Diferentes linhas puras (ou homozigotos), contrastantes, que podem ser cruzadas e dar origem ao F_1 com o mesmo fenótipo, supondo tripla dominância:

$ABC/ABC \times abc/abc \rightarrow F_1: ABC/abc$

$AbC/AbC \times aBc/aBc \rightarrow F_1: AbC/aBc$

$Abc/Abc \times aBC/aBC \rightarrow F_1: Abc/aBC$

$aBC/aBC \times Abc/Abc \rightarrow F_1: aBC/Abc$

$abC/abC \times ABc/ABc \rightarrow F_1: abC/ABc$

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Qualquer um desses híbridos F_1 podem ser submetidos ao cruzamento-teste para o cálculo da distância entre os genes

Exercício:

1. Reescrevo a tabela

Progênie do cruz.-teste	No de indivíduos	Progênie do cruz.-teste	No de indivíduos
+++ / abc	330	+++ / abc	330
abc / abc	320	abc / abc	320
+b+ / abc	64	+b+ / abc	64
a++ / abc	10	a+c / abc	66
a+c / abc	66	++c / abc	100
++c / abc	100	ab+ / abc	95
+bc / abc	15	+bc / abc	15
ab+ / abc	95	a++ / abc	10
Total	1.000	Total	1.000

2. Identifico as classes com maior número de indivíduos (são os parentais)

+++ (330)

abc (320)

3. Identifico as classes com menor número de indivíduos (DRs)

+bc (15)

a++ (10)

Progênie do cruz.-teste	No de indivíduos
+++ / abc	330
abc / abc	320
+b+ / abc	64
a+c / abc	66
++c / abc	100
ab+ / abc	95
+bc / abc	15
a++ / abc	10
Total	1.000

4. Comparo os genótipos (parentais com DRs) e identifico o gene diferente entre as classes. O gene a, portanto, é o gene que está no centro do mapa

➤ A ordem correta é bac ou cab (tanto faz)

5. Construo o genótipo do $F_1 = +++/bac$

6. Calculo as distâncias entre $b \text{ — } a$, $a \text{ — } c$, e $b \text{ — } c$

$$b \text{ — } a = 64 + 66 + 15 + 10 = 155/1.000 = 15,5 \text{ cM}$$

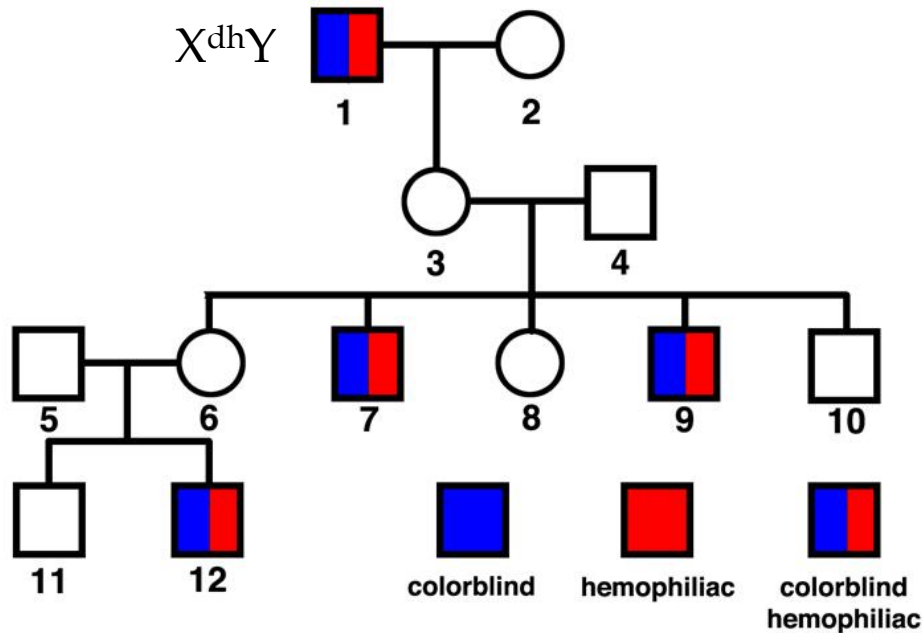
$$a \text{ — } c = 100 + 95 + 15 + 10 = 220/1.000 = 22 \text{ cM}$$

$$b \text{ — } c = 64 + 66 + 100 + 95 = 325/1.000 = 32,5 \text{ cM}$$

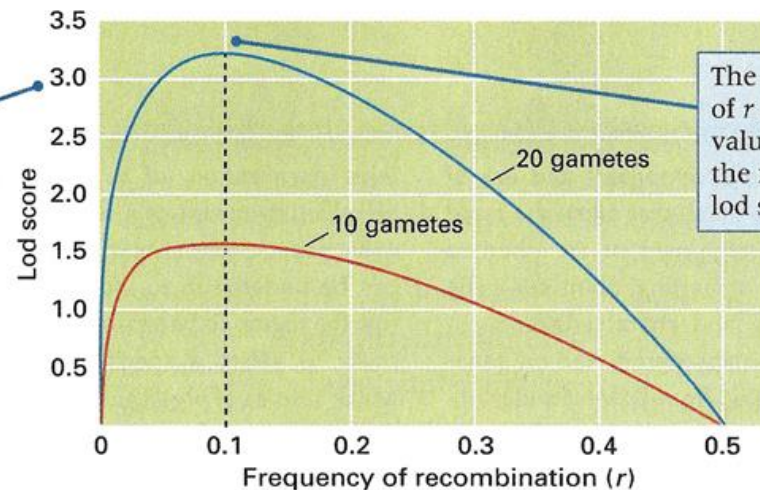
$$\text{Corrigindo: } 32,5 + 2 \times \text{FDR obs.} = 32,5 + [2 \times (10+15/1.000)] \\ = 32,5 + 2 \times [(25/1.000) \times 100] = 32,5\% + 2 \times 2,5\% = 37,5 \text{ cM}$$



Hemophilia and color blindness



In human genetics, a lod score ≥ 3 is regarded as statistically significant.



The estimate of r is the value yielding the maximum lod score.

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Sex-reversal, autosomal
 Hyperglycinemia, nonketotic
 Suppression of tumorigenicity, pancreas
 Diaphyseal medullary stenosis
 Melanoma
 Trichoepithelioma, multiple familial
 Immotile cilia syndrome
 Cartilage-hair hypoplasia
 X-ray repair
 Fanconi anemia, complementation group G
 Sialuria
 Hyperoxaluria, primary, type II
 Cardiomyopathy
 Deafness, autosomal recessive
 Choreoacanthocytosis
 Prostate-specific gene
 Bamforth-Lazarus syndrome
 Tyrosine kinase-like orphan receptor
 Brachydactyly, type B1
 Nephronophthisis (infantile)
 Neuropathy, sensory and autonomic, type 1
 Fructose intolerance
 Basal cell carcinoma, sporadic
 Muscular dystrophy, Fukuyama congenital
 Basal cell nevus syndrome
 Dysautonomia (Riley-Day syndrome)
 Esophageal cancer
 Endotoxin hyporesponsiveness
 Amyotrophic lateral sclerosis, juvenile dominant
 Berardinelli-Seip congenital lipodystrophy
 Dystonia, torsion, autosomal dominant
 Lethal congenital contracture syndrome
 Leukemia, acute undifferentiated
 Tuberous sclerosis
 Hemolytic anemia
 Telangiectasia, hereditary hemorrhagic
 Ehlers-Danlos syndrome, types I and II
 Joubert syndrome
 Leukemia, T-cell acute lymphoblastic

136 million base pairs



Ovarian cancer
 Albinism, brown and rufous
 Interferon, alpha, deficiency
 Leukemia
 Cyclin-dependent kinase inhibitor
 Venous malformations, multiple cutaneous and mucosal
 Arthrogryposis multiplex congenita, distal, type 1
 Galactosemia
 Acromesomelic dysplasia, Maroteaux type
 Myopathy, inclusion body, autosomal recessive
 Hypomagnesemia with secondary hypocalcemia
 Friedrich ataxia
 Geniospasm
 Bleeding diathesis
 Hemophagocytic lymphohistiocytosis, familial
 Chondrosarcoma, extraskeletal myxoid
 Pseudohermaphroditism, male, with gynecomastia
 Tangier disease
 HDL deficiency, familial
 Fanconi anemia, type C
 Xeroderma pigmentosum
 Epithelioma, self-healing, squamous
 Leukemia, T-cell acute lymphoblastic
 Muscular dystrophy, limb-girdle, type 2H
 Bladder cancer
 Sex reversal, XY, with adrenal failure
 Leukemia transcription factor, pre-B-cell
 Porphyria, acute hepatic
 Lead poisoning, susceptibility to
 Citrullinemia
 Dopamine-beta-hydroxylase deficiency
 Amyloidosis, Finnish type
 Microcephaly, primary autosomal recessive
 Leigh syndrome
 Leukemia
 Nail-patella syndrome
 Prostaglandin D2 synthase (brain)
 Pituitary hormone deficiency

Exercício: Observe o mapa do cromossomo II de *Drosophila*.

Calcule o quanto se espera de cada classe fenotípica na progênie de um cruzamento-teste entre moscas com corpo cinza (+), olhos vermelhos (+) e asas normais (+) e moscas com corpo negro (*b*), olhos cinnabar (*c*) e asas vestigiais (*vg*).

Importante: suponha que apenas 50% dos DR esperados ocorreram (ou seja, houve uma interferência de 50% na probabilidade teórica de ocorrência de duplo crossing-over).

Genetic Map Based on Recombination Frequencies in <i>Drosophila</i>				
MUTANT			WILD TYPE	
Short aristae	0		Long aristae	
Black body	48.5		Gray body	
Cinnabar eyes	57.5		Red eyes	
Vestigial wings	65.5		Normal wings	
Brown eyes	104.5		Red eyes	
Values in centimorgan (cM) map units; recombination frequency of 0.01 = 1 cM				