Neutral Evolution at Two Loci

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Linkage disquilibrium (LD)

	Locus	
Gamete	1	2
1	Α	В
2	Α	В
3	Α	В
4	Α	В
5	Α	В
6	Α	b
7	а	В
8	а	В
9	а	b
10	а	b

- ▶ *B* is more common among *A*-gametes than *a*-gametes.
- ► *A* is more common among *B*-gametes than *b*-gametes.
- ► This is LD.

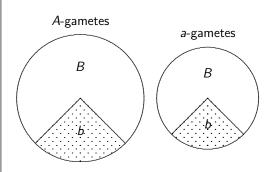
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Linkage equilibrium (LE)

Locus Gamete 1 2 1 В 2 Α В В 3 Α 4 Α В 5 Α b 6 Α b 7 В 8 В а 9 b

- ► B is equally common among A-gametes and a-gametes.
- ► A is equally common among B-gametes and b-gametes.
- ► This is LE.

Linkage Equilibrium ←⇒ shaded fractions equal



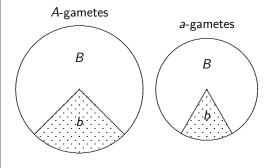
LE: Knowledge about one locus tells nothing about other.

Here, b is equally common among a-gametes and A-gametes.

(Also, a is equally common among b-gametes and B-gametes.)

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$LD \iff shaded fractions unequal$



LD: Knowledge about one locus helps predict the other.

Here, *b* is more common among *A*-gametes than among *a*-gametes.

(Also, a is more common among B-gametes than among b-gametes.)

People sometimes confuse LD with epistasis

Epistasis

In a comparison of diploid genotypes, the *phenotypic effect* of one locus depends

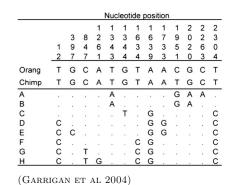
on another locus.

Linkage disequilibrium

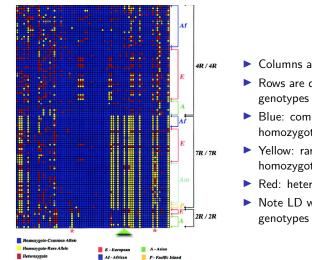
In a comparison of haploid chromosomes, the *allele frequency* at one locus depends

on another locus.

You can see LD in sequence data



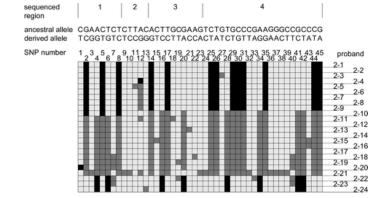
- Dots: identical to chimp sequence.
- Sites not independent.
- A at site 1343 predicts G at 1951
- This is linkage disequilibrium (LD).



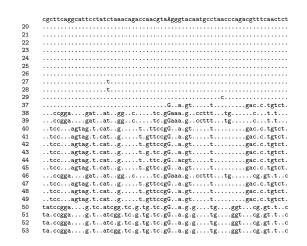
- Columns are SNPs
- Rows are diploid
- Blue: common homozygote
- Yellow: rare homozygote
- Red: heterozygote
- Note LD w/i 7R genotypes

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LD at the NF1 locus (Schmegner et al 2005)

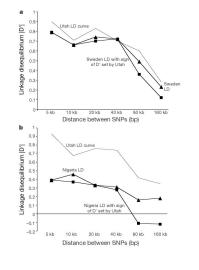


DNA sequences from region of human lactase gene



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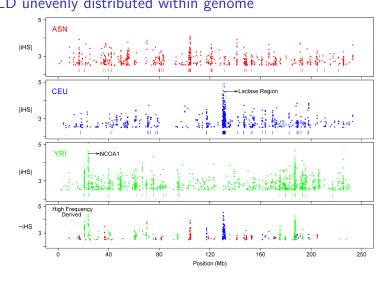
More LD in Europe than Africa



- LD declines with distance along chromosome
- More LD in Europe than Africa
- ► Why?

(Reich et al 2001)

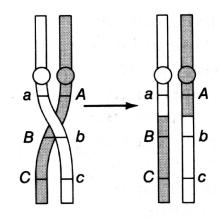
LD unevenly distributed within genome



Facts we need to understand

- ▶ LD decays w/ distance along chromosome.
- Populations differ.
- ► Unevenly distributed w/i genome

Cross-overs shuffle DNA



- occur during reproduction.
- shuffle parental chromosomes.
- sites far apart more likely to recombine
- result: "recombinant" chromosomes

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Why loci are independent on recombinants

Ingredients of a model

 x_1 = frequency of AB-gametes among parents p_A = frequency of A-gametes among parents p_B = frequency of B-gametes among parents p_B = prob of recombination between the two loci

In any generation, there are two kinds of AB gamete:

- 1. non-recombinants: these were ABs in the last generation Frequency: $(1-c)x_1$
- 2. recombinants: formed from an A gamete and a B gamete, drawn at random. Frequency: cp_Ap_B

Next step: sum these contributions.

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Model with random mating, no selection

 x_1 = frequency of AB-gametes among parents p_A = frequency of A-gametes among parents p_B = frequency of B-gametes among parents c = prob of recombination between the two loci

Change in frequency of AB-gametes during one generation:

$$x'_1 = \overbrace{(1-c)x_1}^{\text{nonrecombinants}} + \overbrace{cp_Ap_B}^{\text{recombinants}}$$

$$= x_1 - c(x_1 - p_Ap_B)$$

$$= x_1 - cD$$

Several equivalent definitions of D

The previous slide defined *D*, a measure of LD:

Gamete Definition $AB D = x_1 - p_A p_B$ $Ab -D = x_2 - p_A p_b$ $aB -D = x_3 - p_a p_B$ $ab D = x_4 - p_a p_b$

If the association between A and B is positive, then that between A and b must be negative. A more convenient formula:

$$D = x_1 x_4 - x_2 x_3$$

They all give the same answer.

Calculating D

	Locus	
Gamete	1	2
1	Α	В
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$$D = x_1x_4 - x_2x_3$$

$$= \frac{5}{10} \cdot \frac{2}{10} - \frac{1}{10} \cdot \frac{2}{10}$$

$$= \frac{2}{25}$$

All four gametes, still no selection

Gamete Recurrence
AB
$$x'_1 = x_1 - cD$$

Ab $x'_2 = x_2 + cD$
aB $x'_3 = x_3 + cD$
ab $x'_4 = x_4 - cD$

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How recombination affects D

After one generation,

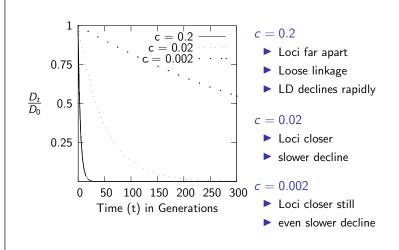
$$D' = x'_1x'_4 - x'_2x'_3$$

= $(x_1 - cD)(x_4 - cD) - (x_2 + cD)(x_3 + cD)$
= $(1 - c)D$

D declines each generation by a factor of 1-c. After t generations,

$$D_t = D_0(1-c)^t$$

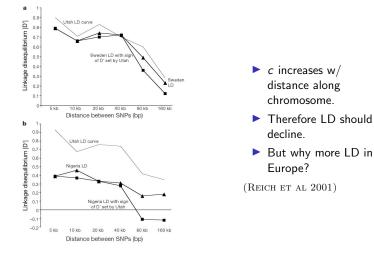
D declines gradually toward zero



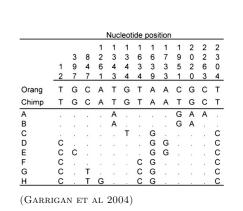
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Is this theory enough to explain the data?

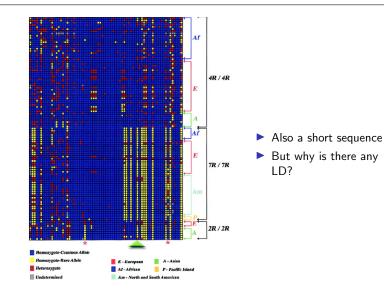
More LD in Europe than Africa



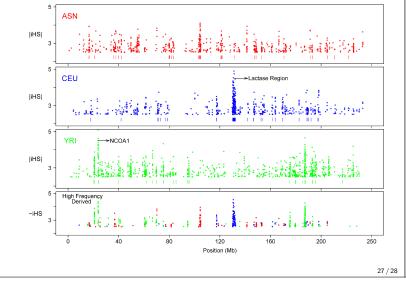
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- ► Short DNA sequence.
- ► tight linkage: c is small
- ► LD decays very slowly
- But why is it not zero?



Why is LD unevenly distributed?



Summary

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- ▶ Our theory explains why *D* declines w/ distance along chromosome.
- ▶ If loci are far apart on chromosome, *c* is high and *D* declines rapidly.
- ▶ It tells us nothing about the forces that generate LD.
- ▶ Nothing about population differences.
- Nothing about variation across the genome.