

Микроэволюция - 2

Факторы эволюции

- мутации
- отбор
- половое размножение
- генетико-автоматические процессы (генетический дрейф)
- миграция

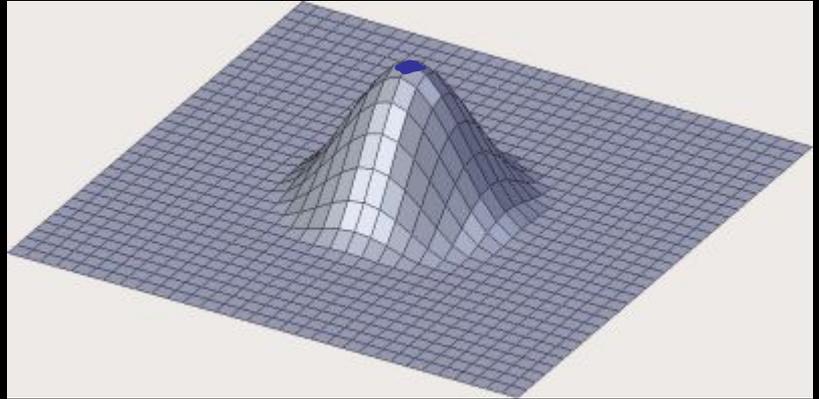
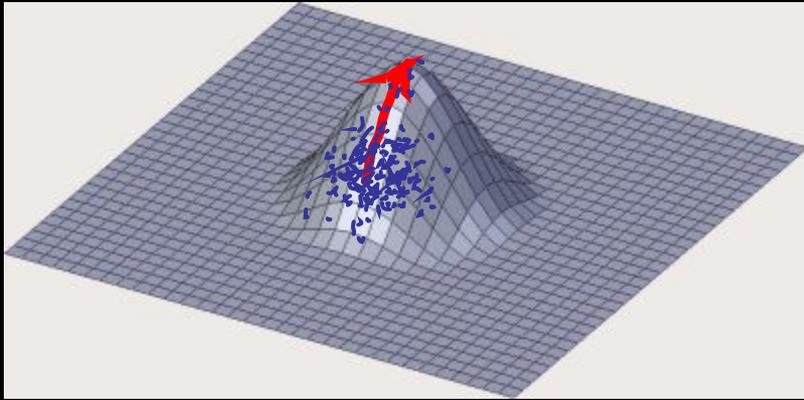
Динамика частоты аллеля в популяции

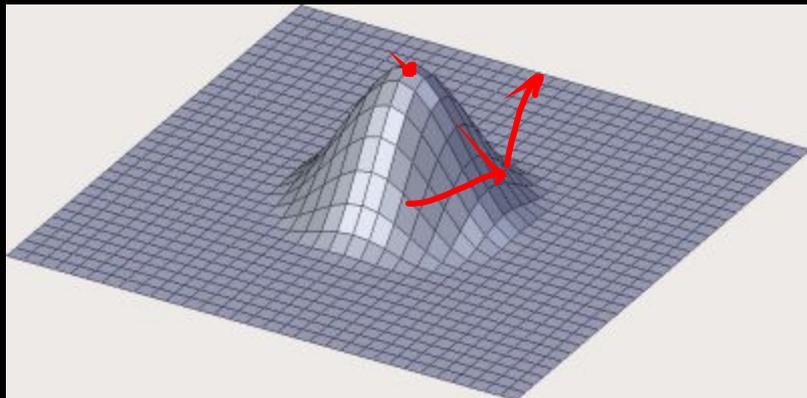
$$[a_i]_{t+1} = \frac{[a_i]_t w_i}{W_t}, \quad \text{где} \quad W_t = \sum_j [a_j]_t w_j$$

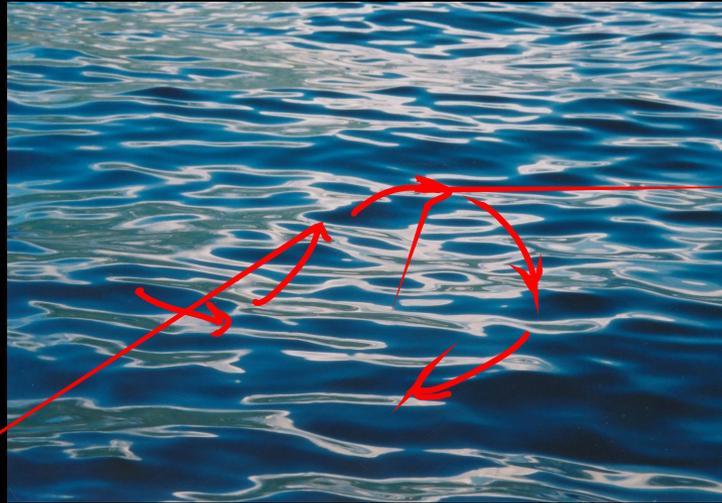
Фундаментальная теорема Фишера

$$\Delta W = \frac{1}{W} \text{Var}\{w_j\}$$









Динамика частоты аллеля в популяции - 2

Динамика частоты аллеля в популяции - 2

$$\frac{dp}{dt} = sp(1-p)$$

$$p = \frac{C_0 e^{st}}{1 + C_0 e^{st}} \quad , \quad \text{где} \quad C_0 = \frac{p_0}{1 - p_0}$$

Динамика частоты аллеля в популяции - 2

$$\frac{dp}{dt} = sp(1-p)$$

$$p = \frac{C_0 e^{st}}{1 + C_0 e^{st}} \quad , \quad \text{где} \quad C_0 = \frac{p_0}{1 - p_0}$$

$$t = \frac{1}{s} \ln \frac{(1 - p_0)p}{p_0(1 - p)}$$

Типы отбора (динамика)

- положительный
- отрицательный

Типы отбора (динамика)

- положительный
- отрицательный

- балансирующий

Nucleotide polymorphism at the alcohol dehydrogenase locus of *Drosophila melanogaster*

Martin Kreitman

Museum of Comparative Zoology, Harvard University, Cambridge, Massachusetts 02138, USA

The sequencing of eleven cloned *Drosophila melanogaster* alcohol dehydrogenase (*Adh*) genes from five natural populations has revealed a large number of previously hidden polymorphisms. Only one of the 43 polymorphisms results in an amino acid change, the one responsible for the two electrophoretic variants (fast *Adh-f* and slow *Adh-s*) found

Table 1

Reference sequence	5' Flanking sequence	Adult leader (exon 1)	Intron 1 (Adult intron, larval non-coding)	Larval leader	Translated region of exon 2	Intron 2	Exon 3	Intron 3	Translated region of exon 4	3'-Untranslated region	3' Flanking sequence
	C C G		C A A T A T G G G ∇1 C ∇2 G	C	T	A C	C C C C	G G A A T	C T C C A * C T A G	A ∇3 C	A G C ∇4 C ∇5 T ∆6
Strain											
Wa-S A T	T T . A	C A . T A	A C ∆
Fl-1S	. . C		T T . A	C A . T A	A C ∆
Af-S A T ∇ . 1 A .
Fr-S	G T A	-1 .	T A
Fl-2s	. . .		A G . . . A . T C	A	G	G T	C 3
Ja-S	. . C		G T . T . C A	C 4 T . . .
Fl-P	. . C		G G T C T C C .	C 4
Fr-P	T G C		A G . . . A . T C ∇ G ∇ .	.	G G T C T C C .	C 4 G
Wa-P	T G C		A G . . . A . T C ∇ G ∇ .	.	G G T C T C C .	C 4 G
Af-P	T G C		A G . . . A . T C ∇ G ∇ .	.	G G T C T C C .	C 5 G
Ja-P	T G C		A G G G G A . . . ∇ . . T	.	G A .	. . G G T C T C C .	C 4 -1 . .
No. of polymorphic sites	3	0	11	1	1	2	4	5	9	2	5
Average no. of Nucleotides compared	63	87	620	70	99	65	405	70	204	178	767
% Sites polymorphic	4.7	0	1.8	1.4	1.0	3.1	1.0	7.1	3.5	1.1	0.6

One *Adh-f*, and either one or two *Adh-s* electrophoretic alleles were randomly chosen from isochromosomal lines derived from each of five population samples. S, *Adh-s* alleles; F, *Adh-f* alleles. Collection sites and year collected: Fl, West Palm Beach, Florida, 1979; Wa, Seattle, Washington, 1979; Af, Burundi, Africa, 1977; Fr, Bully, France, 1977; Is, Ishigaki, Japan, 1978. The reference nucleotide sequence is the most common *Adh-s* nucleotide at each of the polymorphic sites. Differences are shown in the body of the table. ∇/∆: insertion/deletion polymorphisms. The numbers in columns ∇3 and ∇5 are the differences in homopolynucleotide run lengths compared with the consensus sequence. *: Thr-Lys amino acid replacement polymorphism. All other polymorphisms are either silent or noncoding.

Score = 1411 bits (734), Expect = 0.0
Identities = 868/920 (94%), Gaps = 0/920 (0%)
Strand=Plus/Plus

Query	2	TGGATGTTAAAAAATATTTAGAACGAATCAAGTATAAGGGATCCATCCATCCTACCCTTA	61
Sbjct	2T.....T..T.....G	61
Query	62	ACAATTTAAAGCAATTATGTTGGTGTGCATGCCATGCATGTGCCACAAGATACCTTGGATA	121
Sbjct	62	.A.....G.....C.....C.....	121
Query	122	TTTTTGGAGGCCCAAGGAAAAAATTAGATTTGGAGAAAAATCTACAAAGATATTGTGAACA	181
Sbjct	122A.....	181
Query	182	ACAGACGGGGAGGTTTCTGTTATGAAAGTGAATGGGTTGTTTCACTGGTTGTTGGTGCAAC	241
Sbjct	182	241
Query	242	TTGGATATAAAAAATGTACAAATGCTGGAAGGGAGTTGCTTGCTGCCATCTAAAAATACAT	301
Sbjct	242C.....GG....A..T.....	301
Query	302	TTCATTACCCATTTGACCATCTGTAAATAAGGTTTCCTTTGATGATTGTGATTACCTAG	361
Sbjct	302T.....	361
Query	362	TTGATGTTGGTTATGGGGCCCCATCCTTTTTTCATGCCATTAGAATTAAGGAGTTACGTG	421
Sbjct	362T.....A.....A.....T.C.	421
Query	422	AACACCACGAAATGACAGGAACATACAGACTTCGGAAACATAAGGATGATTACCTTGTAG	481
Sbjct	422T..T.....G.....G.....	481
Query	482	AGAAACATAGAAAAAATTTTGGTTAAAAAAGGTAATATTCCTGATGACTATGTGGAAA	541
Sbjct	482	.A.....CRAC..T..AGGG.....	541
Query	542	AGTTATCAAAACATGATGCCACAAATCAAAGTTGCAATTTACCATTGATATTAAGTGA	601
Sbjct	542G.....T.....	601
Query	602	ACATTATCTTTAGGTTTACAGCACAAACACCACACAAATTTGAGGATTTCAATGAAGGAATGT	661
Sbjct	602A.....	661
Query	662	CTAAACACTTAGAGGGTGATGATTCTTAGCAACCAATTCTTTCTCGAGATTTTCTACC	721
Sbjct	662T.....	721
Query	722	AAGGAGGGGTCACAGTTTTATGGGGCACAACATTAATCAAGAAGAGATTTGATGACGAAT	781
Sbjct	722A.....A.....G.....A.....T.....	781
Query	782	TGACGGAAATGATTGAACAAAAAACATGTGGGATGATAAGTTGGATTTCAGAGGAAAACT	841
Sbjct	782A..CC....A.....	841
Query	842	GGAAAGTCATATTTAGGCTGATGAAAGATGAATTTGGAATAAAAAATTAATTTTAAGCCTC	901

Ciona savignyi – мама и папа



Score = 607 bits (1565), Expect = 5e-172
Identities = 282/306 (92%), Positives = 299/306 (97%), Gaps = 0/306 (0%)

Query	2	DVKKYLERIKYKGSIHPTLMNLKQLCWCHAMHVPQDTLDFGGPRKKLDLEKIYKDIVNM	61
Sbjct	2 D E T H	61
Query	62	RRGGFCYEVNGLFHLLVQLGYKNVQMLEGSCLLPSKNTFHYPPFDHLLMKVSFDDCDYLV	121
Sbjct	62 Q .. EI	121
Query	122	DVGYGAPSFPMPLKELREHHEMTGTYRLRKHKDDYLVEKHRKKILVKKGNIPDDYVEK	181
Sbjct	122 K .. C E QHLG	181
Query	182	LSKHDTNQSCNFTIDINWNIIFRFSTTPHKFEDFNEGMSKHLEGDDFLATNSFLEIFYQ	241
Sbjct	182 R K	241
Query	242	GGVTVLWGTTLIKKRFDDELTEMIEQKNMWDDKLDSEENWKVIFRLMKDEFGIKINFKPH	301
Sbjct	242 I R.K.V P D	301
Query	302	LMSKNL	307
Sbjct	302	.V.R..	307

Ciona savignyi – мама и папа

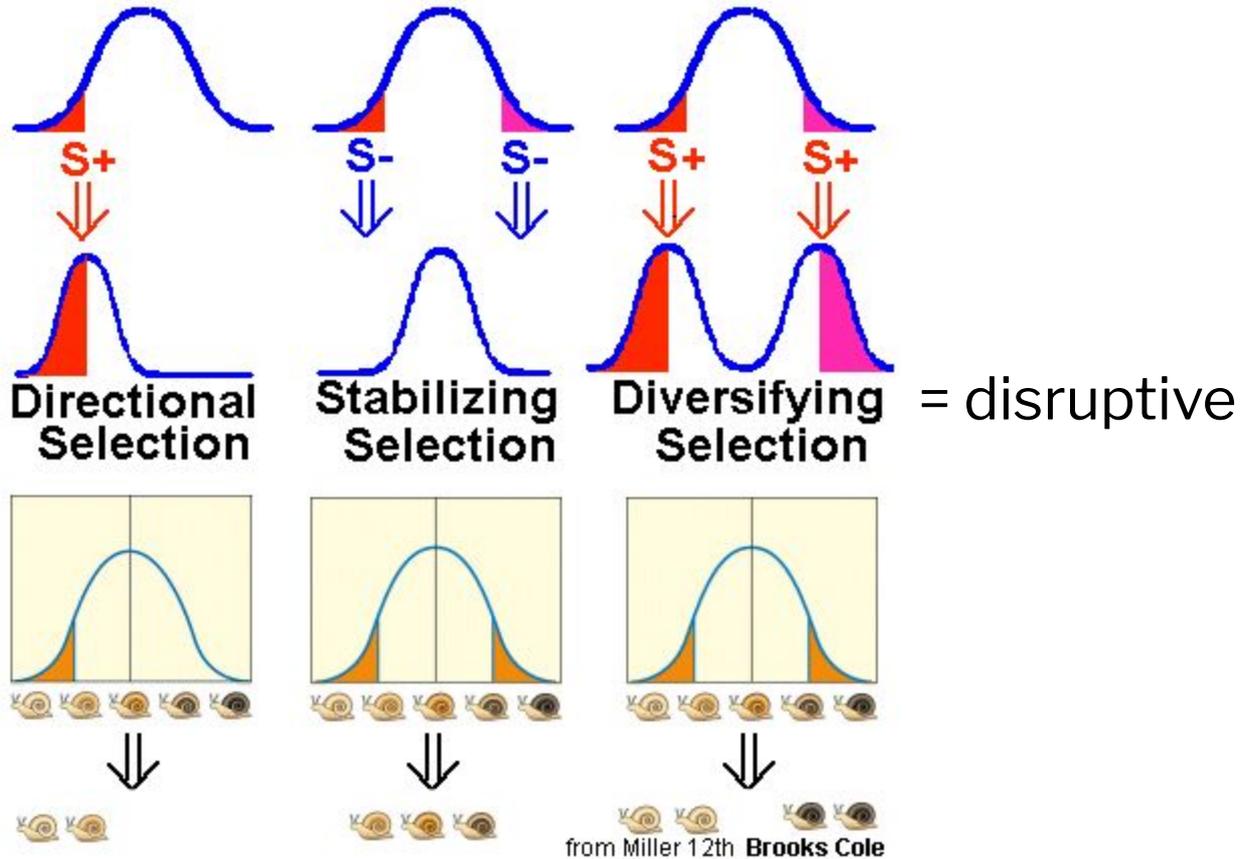


Типы отбора (динамика)

- положительный
- отрицательный

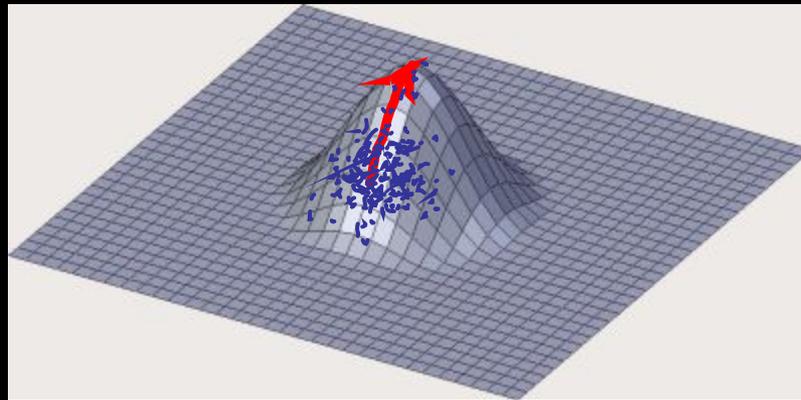
- балансирующий
 - преимущество гетерозигот
 - частотно-зависимый
 - примеры: серповидно-клет. анемия, МНС

Типы отбора (колич. признак)

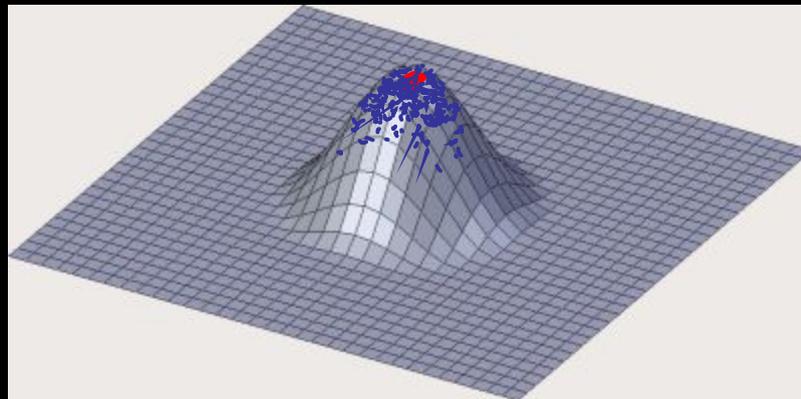


Типы отбора (колич. признак)

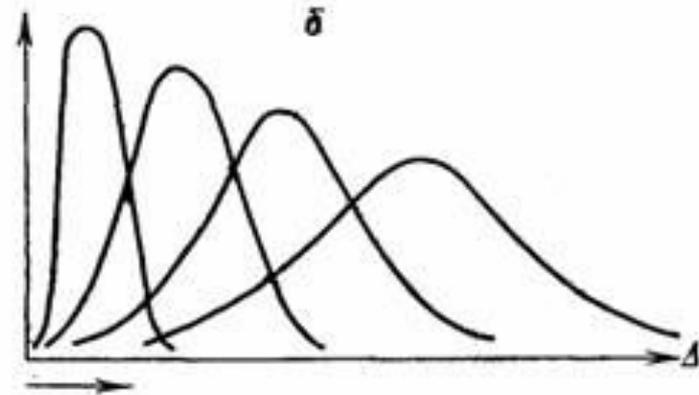
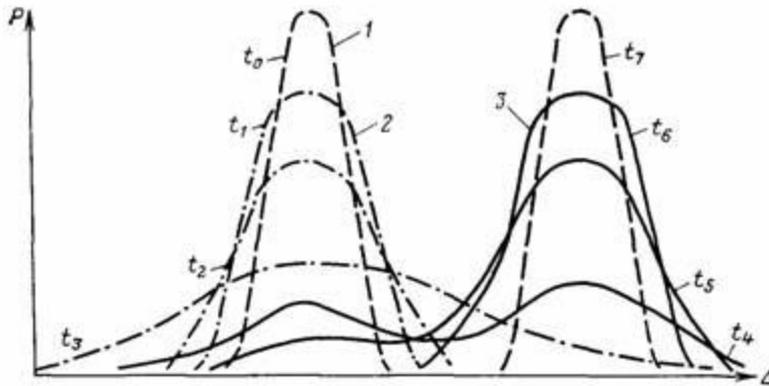
- направленный (directional)



- стабилизирующий (stabilizing)



Типы отбора (колич. признак)



Раутиан А.С. Современная палеонтология. М.: Недра, 1988. Т.2. С. 76-118

<http://macroevolution.narod.ru/rautian.htm>

Факторы эволюции

- мутации
- отбор
- половое размножение
- генетико-автоматические процессы (генетический дрейф)
- миграция

Мутационно-селективное равновесие

$$-vq + \mu p - \frac{sp(1-p)}{sp+1} = 0$$

Мутационно-селективное равновесие

$$-vq + \mu p - \frac{sp(1-p)}{sp+1} = 0$$

При $\mu < s \ll 1$ $q = \mu / s$

Факторы эволюции

- мутации
- отбор
- половое размножение
- генетико-автоматические процессы (генетический дрейф)
- миграция

Половое размножение

- сегрегация (расщепление)
- рекомбинация
- выбор партнера

Сегрегация

Теорема Харди-Вайнберга:

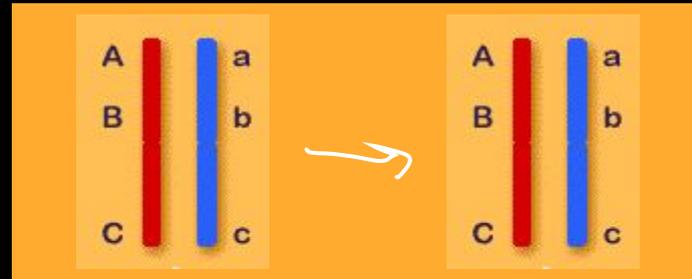
$$[AA]_{t+1} = [A]_t^2$$

Genotype	Number	Frequency	Expected
SS	141	0.4247	0.4096
SF	111	0.3343	0.3507
FF	28	0.0843	0.0751
SI	32	0.0964	0.1101
FI	15	0.0452	0.0471
II	5	0.0151	0.0074
Total	332	1.0000	1.0000

Table 1.2: The frequencies of alkaline phosphatase genotypes in a sample from the English people. The expected Hardy-Weinberg frequencies are given in the fourth column. The data are from Harris (1966).

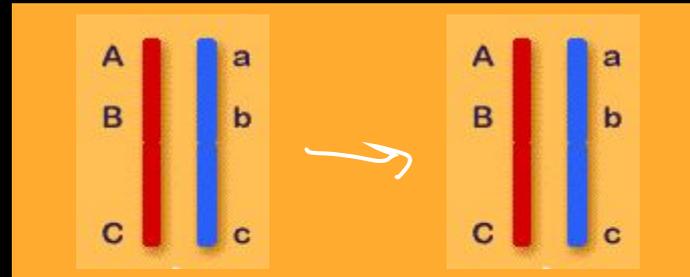
Рекомбинация

без:

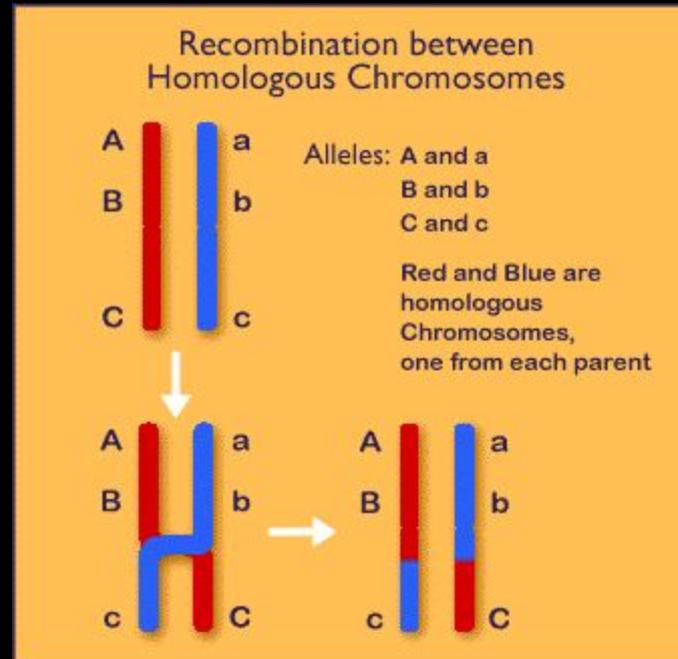


Рекомбинация

без:



с:



Выбор партнера

- инбридинг
- ассортативное скрещивание

К след. лекции:

A limited role for balancing selection

Saurabh Asthana, Steffen Schmidt and Shamil Sunyaev

Genetics Division, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Harvard Medical School
New Research Building, 77 Ave Louis Pasteur, Boston, MA 02115, USA

**(статья, оставшаяся
с прошлого раза)**