Микроэволюция - 2

Факторы эволюции

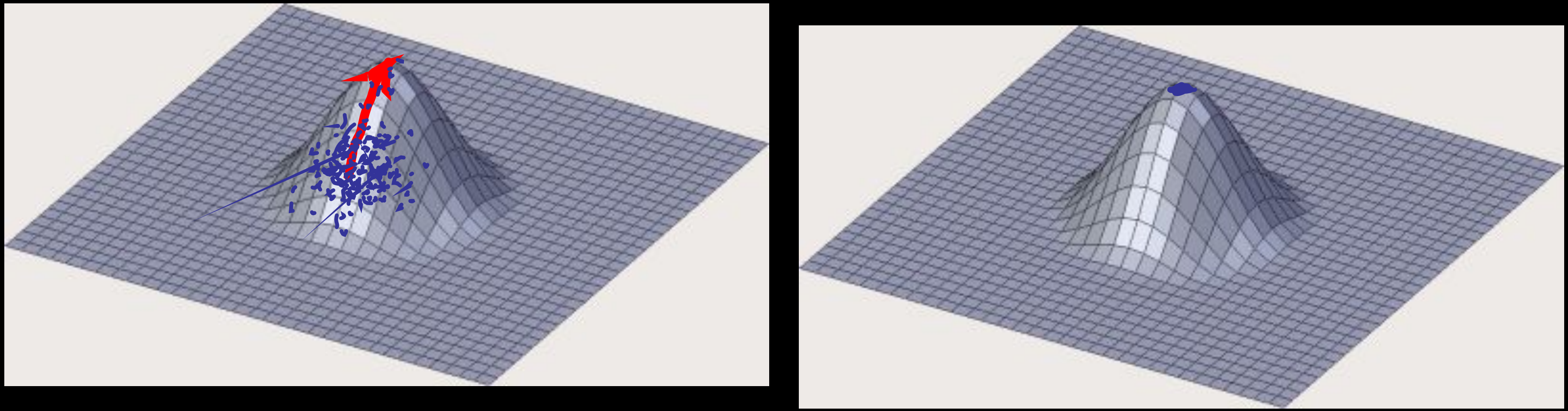
- мутации
- отбор
- половое размножение
- генетико-автоматические процессы (генетический дрейф)
- миграция

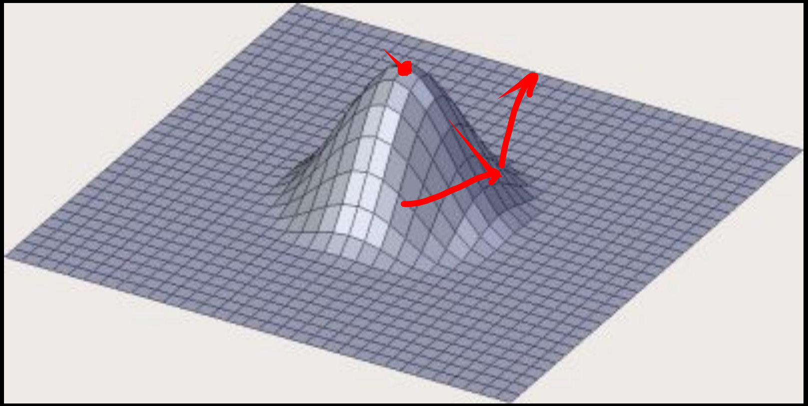
Динамика частоты аллеля в популяции

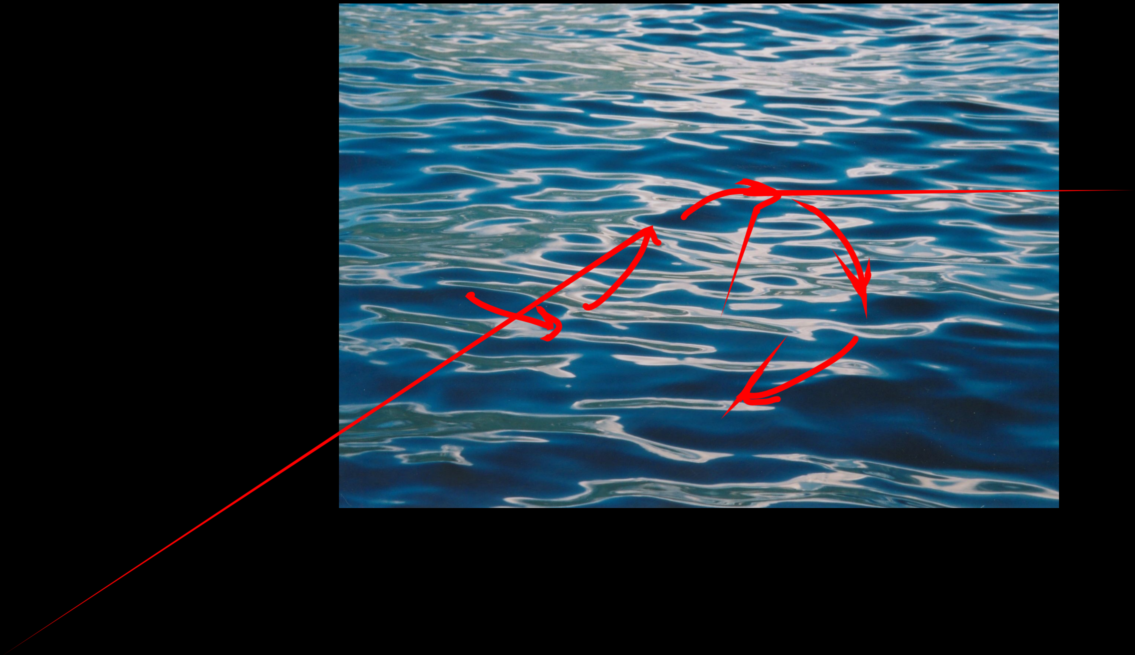
$$[a_i]_{t+1} = \frac{[a_i]_t w_i}{W_t},$$ где $$W_t = \sum_j [a_j]_t w_j$$

Фундаментальная теорема Фишера

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







Динамика частоты аллеля в популяции - 2

Динамика частоты аллеля в популяции - 2

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

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

Динамика частоты аллеля в популяции - 2

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

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

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

Типы отбора (динамика)

- положительный
- отрицательный

Типы отбора (динамика)

- положительный
- отрицательный

- балансирующий

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

Martin Kreitman

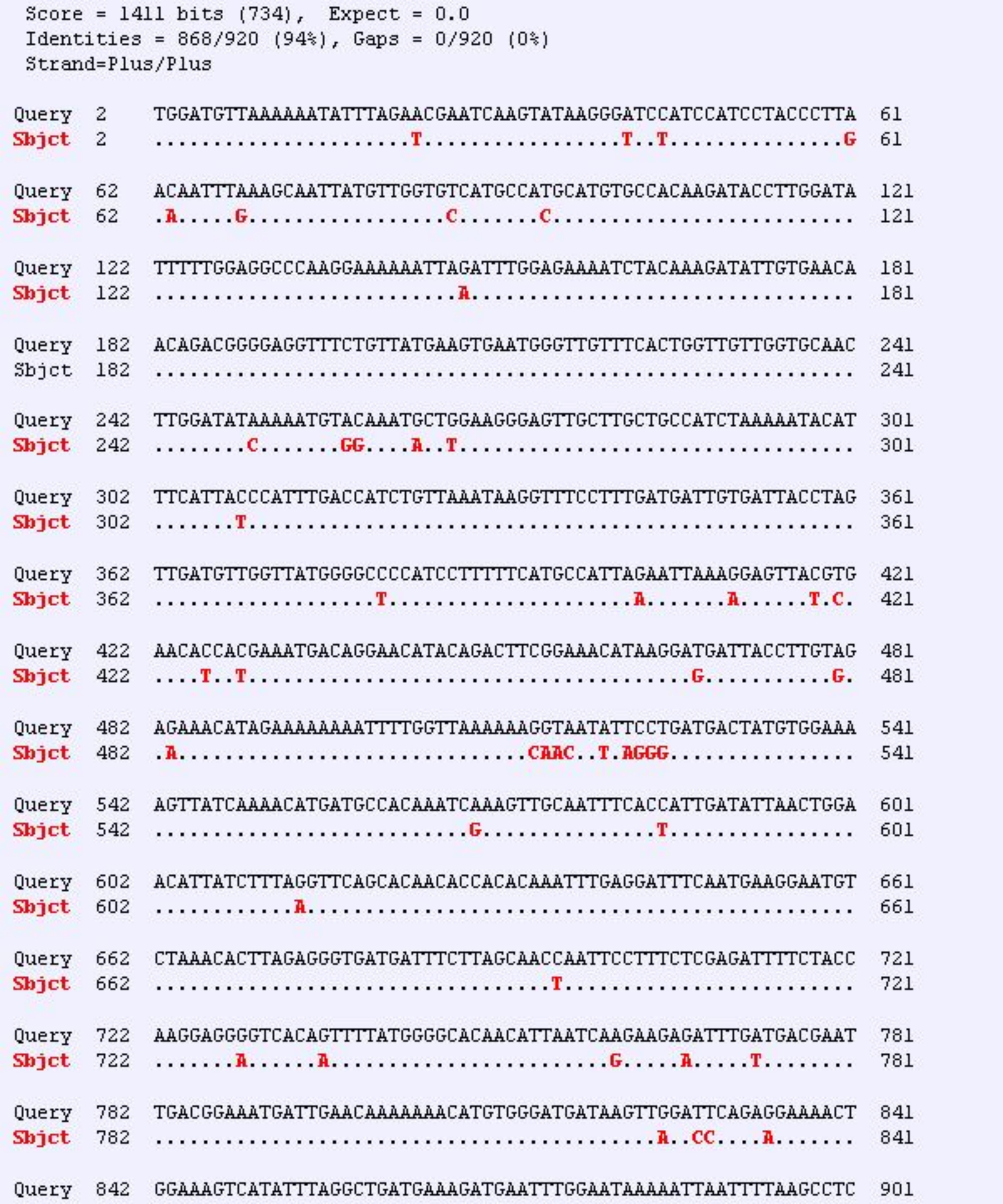
Museum of Comparative Zoology, Harvard University, Cambridge, Massachusetts 02138, USA

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 Δ6
Strain											
Wa-S	. . .		. . . . . A T	.	.	. .	T T . A	C A . T A	A C	. . .	. . . . Δ
Fl-1S	. . C		. . . .	.	.	. .	T T . A	C A . T A	A C	. . .	. . . . Δ
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-F	. . C		. . . .	.	G	. .	. . . .	. . . . .	. . G T C T C C .	C 4 .	. . . .
Fr-F	T G C		A G . . . A . T C ∇ G ∇ .	.	G	. .	. . . .	. . . . .	. . G T C T C C .	C 4 G	. . . .
Wa-F	T G C		A G . . . A . T C ∇ G ∇ .	.	G	. .	. . . .	. . . . .	. . G T C T C C .	C 4 G	. . . .
Af-F	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. ∇/Δ: 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  2    ......................T.................T..T...............G  61

Query  62   ACAATTTAAAGCAATTATGTTGGTGTCATGCCATGCATGTGCCACAAGATACCTTGGATA  121
Sbjct  62   .A.....G.................C.......C..........................  121

Query  122  TTTTTGGAGGCCCAAGGAAAAAATTAGATTTGGAGAAAATCTACAAAGATATTGTGAACA  181
Sbjct  122  ..........................A.................................  181

Query  182  ACAGACGGGGAGGTTTCTGTTATGAAGTGAATGGGTTGTTTCACTGGTTGTTGGTGCAAC  241
Sbjct  182  ............................................................  241

Query  242  TTGGATATAAAAATGTACAAATGCTGGAAGGGAGTTGCTTGCTGCCATCTAAAAATACAT  301
Sbjct  242  ........C.......GG....A..T..................................  301

Query  302  TTCATTACCCATTTGACCATCTGTTAAATAAGGTTTCCTTTGATGATTGTGATTACCTAG  361
Sbjct  302  .......T....................................................  361

Query  362  TTGATGTTGGTTATGGGGCCCCATCCTTTTTCATGCCATTAGAATTAAAGGAGTTACGTG  421
Sbjct  362  ...................T.....................A.......A......T.C.  421

Query  422  AACACCACGAAATGACAGGAACATACAGACTTCGGAAACATAAGGATGATTACCTTGTAG  481
Sbjct  422  ....T..T......................................G...........G.  481

Query  482  AGAAACATAGAAAAAAAATTTTGGTTAAAAAAGGTAATATTCCTGATGACTATGTGGAAA  541
Sbjct  482  .A..............................CAAC..T.AGGG................  541

Query  542  AGTTATCAAAACATGATGCCACAAATCAAAGTTGCAATTTCACCATTGATATTAACTGGA  601
Sbjct  542  ...........................G...............T................  601

Query  602  ACATTATCTTTAGGTTCAGCACAACACCACACAAATTTGAGGATTTCAATGAAGGAATGT  661
Sbjct  602  ............A...............................................  661

Query  662  CTAAACACTTAGAGGGTGATGATTTCTTAGCAACCAATTCCTTTCTCGAGATTTTCTACC  721
Sbjct  662  ..................................T.........................  721

Query  722  AAGGAGGGGTCACAGTTTTATGGGGCACAACATTAATCAAGAAGAGATTTGATGACGAAT  781
Sbjct  722  .......A......A........................G.....A.....T........  781

Query  782  TGACGGAAATGATTGAACAAAAAAACATGTGGATGATAAGTTGGATTCAGAGGAAAACT  841
Sbjct  782  ...........................................A..CC....A.......  841

Query  842  GGAAAGTCATATTTAGGCTGATGAAAGATGAATTTGGAATAAAAATTAATTTTAAGCCTC  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    DVKKYLERIKYKGSIHPTLNNLKQLCWCHAMHVPQDTLDIFGGPRKKLDLEKIYKDIVNN  61
Sbjct  2    ......D............E..........T.................N...........  61

Query  62   RRGGFCYEVNGLFHWLLVQLGYKNVQMLEGSCLLPSKNTFHYPFDHLLNKVSFDDCDYLV  121
Sbjct  62   ......................Q..EI.................................  121

Query  122  DVGYGAPSFFMPLELKELREHHEMTGTYRLRKHKDDYLVEKHRKKILVKKGNIPDDYVEK  181
Sbjct  122  .............K....C...............E...............QHLG......  181

Query  182  LSKHDATNQSCNFTIDINWNIIFRFSTTPHKFEDFNEGMSKHLEGDDFLATNSFLEIFYQ  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
```

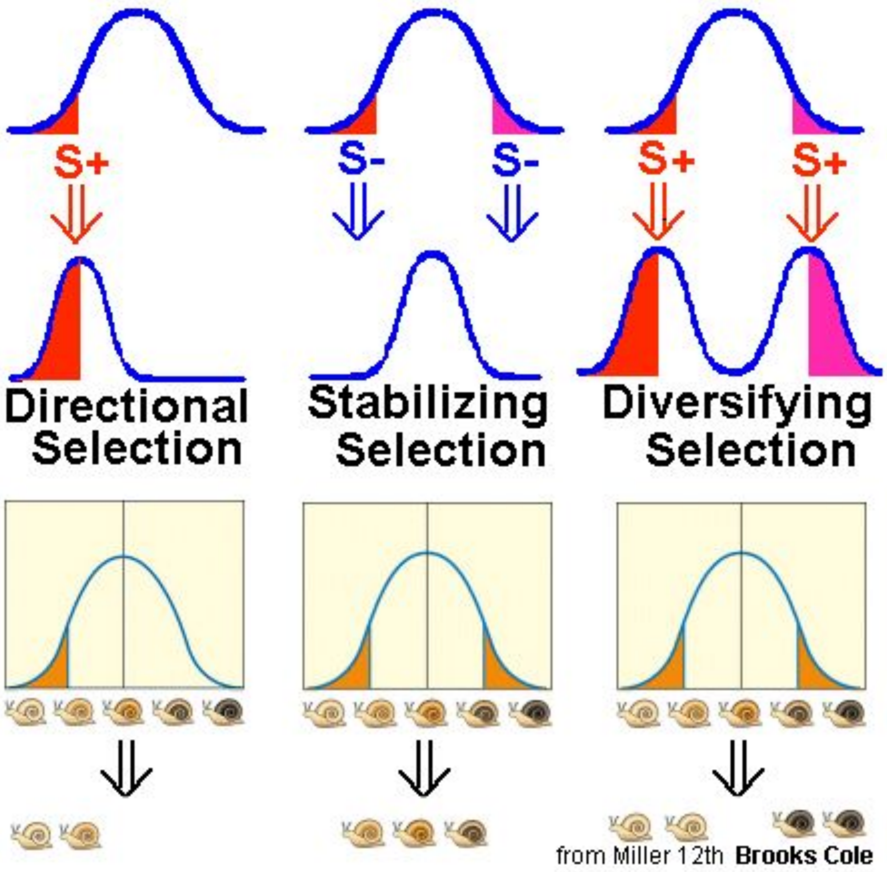
Ciona savignyi – мама и папа

Типы отбора (динамика)

- положительный
- отрицательный

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

Типы отбора (колич. признак)

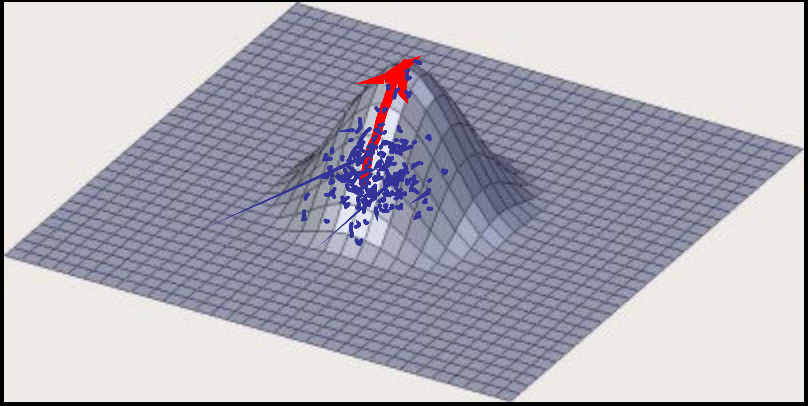


from Miller 12th **Brooks Cole**

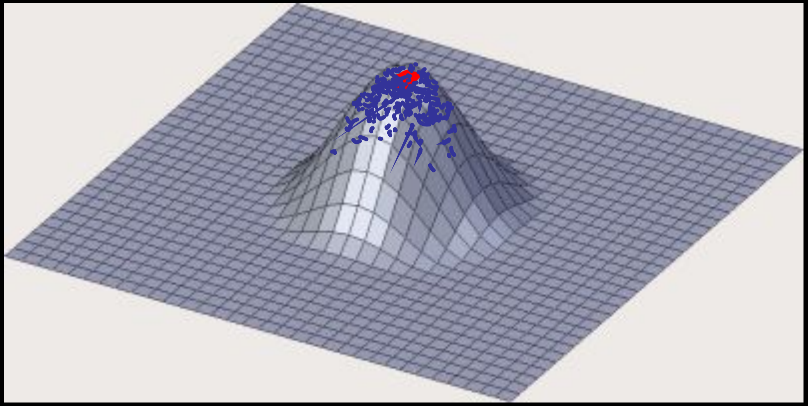
= disruptive

Типы отбора (колич. признак)

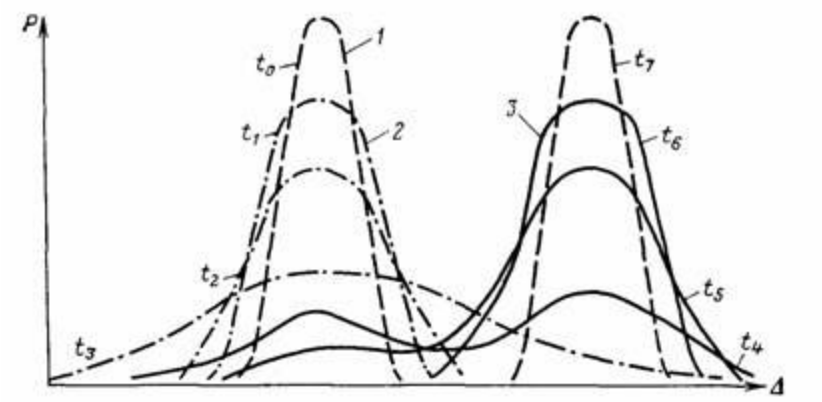
- направленный (directional)

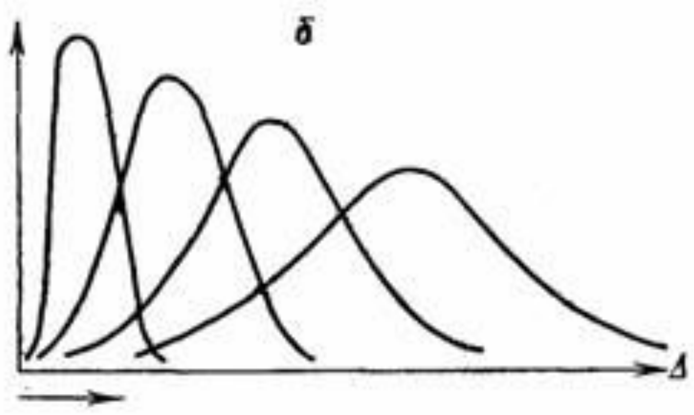


- стабилизирующий (stabilizing)



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
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- генетико-автоматические процессы (генетический дрейф)
- миграция

Мутационно-селективное равновесие

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

Мутационно-селективное равновесие

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

При $\mu < s << 1$ $\quad q = \mu / s$

Факторы эволюции

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- миграция

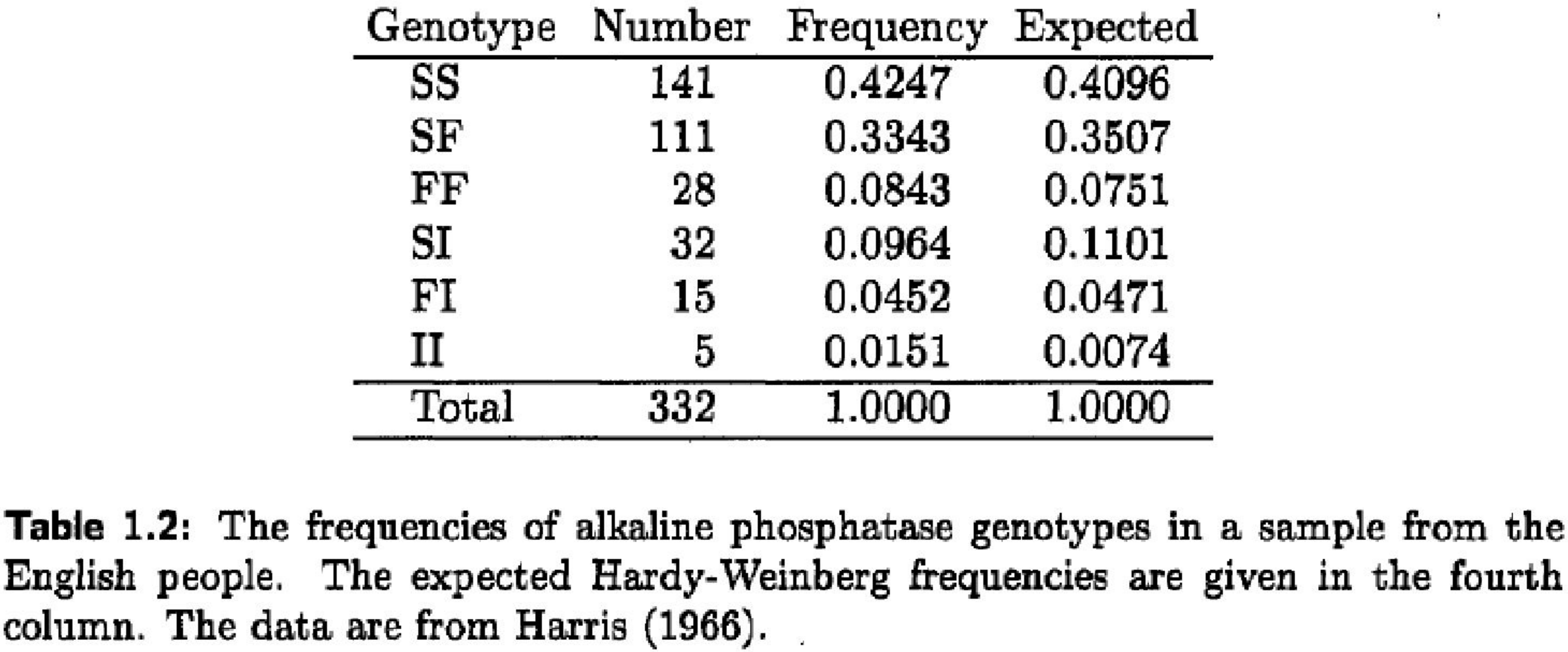
Половое размножение

- сегрегация (расщепление)
- рекомбинация
- выбор партнера

Сегрегация

Теорема Харди-Вайнберга:

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



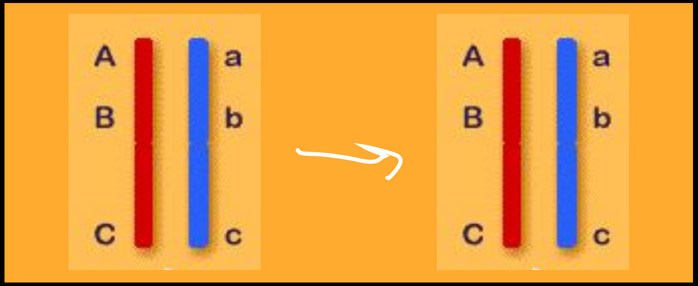
Genotype	Number	Frequency	Expected
SS	141	0.4247	0.4096
SF	111	0.3343	0.3507
FF	28	0.0843	0.0751
SI	32	0.0964	0.1101
FI	15	0.0452	0.0471
II	5	0.0151	0.0074
Total	332	1.0000	1.0000

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).

Gillespie *Population genetics: a concise guide*

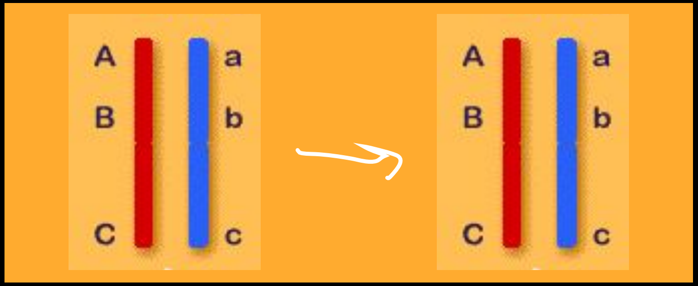
Рекомбинация

без:

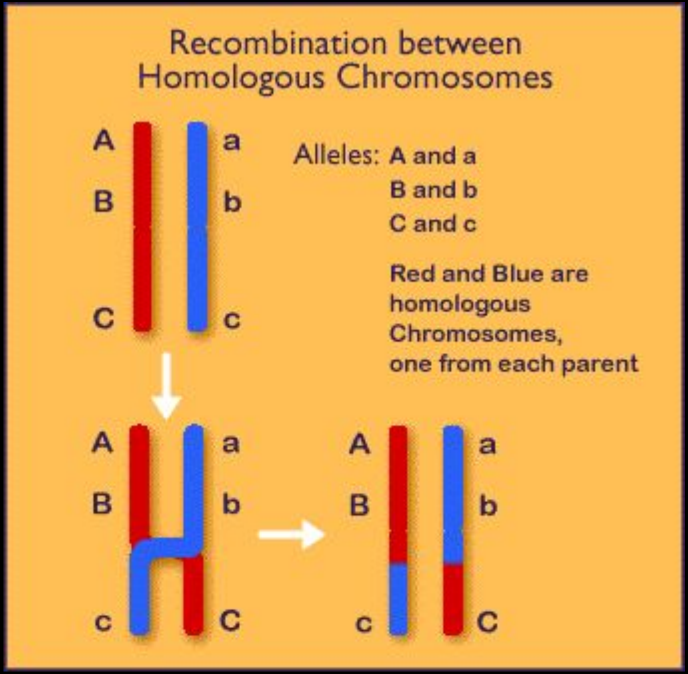


Рекомбинация

без:



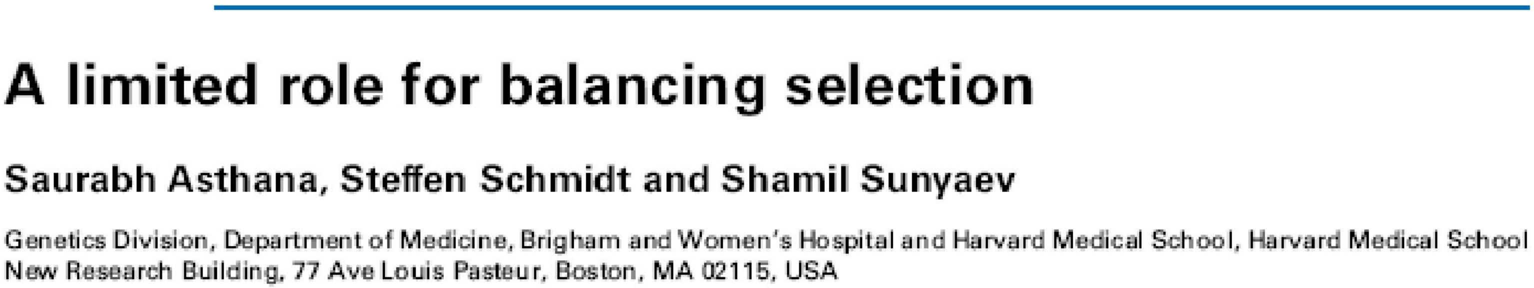
с:



Выбор партнера

- инбридинг
- ассортативное скрещивание

К след. лекции:



A limited role for balancing selection

Saurabh Asthana, Steffen Schmidt and Shamil Sunyaev

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(статья, оставшаяся
с прошлого раза)