

Lecture 6. Directional diploid selection. Overdominance.

2.4 Directional diploid selection

Directional selection favoring allele A

$$w_{AA} = 1, w_{Aa} = 1 - hs, w_{aa} = 1 - s$$

diploid selection coefficient $s > 0$

Degree of dominance or heterozygous effect h

$h = 0$: harmful allele a is recessive in fitness

$h = 1$: harmful allele a is dominant in fitness

$0 < h < 1$: incomplete dominance

$h = 0.5$: additive selection

$$\Delta p = spq(ph + q(1 - h)), \text{ if } s \approx 0$$

Allele fixation dynamics

Directional selection eventually fixes the favored allele

Fig. 6.3, p. 225: three different curves of allele fixation

$$h = 0, \Delta p = spq^2 \quad \ln\left(\frac{p_t}{q_t}\right) + \frac{1}{q_t} = \ln\left(\frac{p_0}{q_0}\right) + \frac{1}{q_0} + st$$

$$h = 0.5, \Delta p = \frac{s}{2}pq \quad \ln\left(\frac{p_t}{q_t}\right) = \ln\left(\frac{p_0}{q_0}\right) + \frac{st}{2}$$

$$h = 1, \Delta p = sp^2q \quad \ln\left(\frac{p_t}{q_t}\right) - \frac{1}{p_t} = \ln\left(\frac{p_0}{q_0}\right) - \frac{1}{p_0} + st$$

Rare diseases: natural selection eliminates

dominant diseases more effectively than recessive ones

Additive selection is similar to haploid selection

with haploid selection coefficient $\frac{s}{2}$

Ex 6: industrial melanism

melanic allele A , wildtype allele a

Fig 3.4, p. 86: if no lichens, then A is a favored dominant

melanic moth frequency: 1% in 1848, 95% in 1898

1 generation = 1 year

Selection coefficient estimation

$$p_0^2 + 2p_0q_0 \approx 0.01, p_0 \approx 0.005 \quad \ln\left(\frac{p_0}{q_0}\right) + \frac{1}{q_0} \approx -4.29$$

$$1 - q_{50}^2 \approx 0.95, p_{50} \approx 0.776 \quad \ln\left(\frac{p_{50}}{q_{50}}\right) + \frac{1}{q_{50}} \approx 5.72$$

Solve equation

$$5.72 = -4.29 + 50s \text{ to find } s = 0.20$$

2.5 Overdominance

Overdominance favors heterozygotes

$$w_{Aa} = 1, w_{AA} = 1 - s_1, w_{aa} = 1 - s_2$$

$$\Delta p = \frac{pq}{\bar{w}}(qs_2 - ps_1), \bar{w} = 1 - p^2s_1 - q^2s_2$$

Equilibrium frequencies $\hat{p} = \frac{s_2}{s_1+s_2}, \hat{q} = \frac{s_1}{s_1+s_2}$
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Fig 6.4, p.229: equilibrium frequency \hat{p} maximizes \bar{w}

if $p = \hat{p}$, then $\frac{d\bar{w}}{dp} = 2\hat{q}s_2 - 2\hat{p}s_1 = 0, \bar{w}_{\max} = 1 - \frac{s_1s_2}{s_1+s_2}$

Segregational load $L = 1 - \bar{w}_{\max} = \frac{s_1s_2}{s_1+s_2}$
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Due to gene segregation \bar{w} is always less than theoretical maximal genotype fitness $w_{Aa} = 1$

Equilibrium genotype frequencies

$$D = \frac{1-s_1}{\bar{w}} \cdot \hat{p}^2, H = \frac{2}{\bar{w}} \cdot \hat{p}\hat{q}, R = \frac{1-s_2}{\bar{w}} \cdot \hat{q}^2$$

excess of heterozygotes $F = 1 - \frac{1}{\bar{w}} = -\frac{s_1s_2}{s_1+s_2 - s_1s_2}$

Ex 8: sickle-cell anemia

Fig 6.5, p. 231: regions in Africa with incidences of malaria and sickle-cell anemia

Gene coding for β chain of hemoglobin

A = normal allele, S = anemia allele

Relative fitnesses in Africa regions with malaria

$$w_{AS} = 1, w_{AA} = 0.9 \text{ (malaria)}, w_{SS} = 0.2 \text{ (anemia)}$$

Selection coefficients and equilibrium frequencies

$$s_1 = 0.1, s_2 = 0.8, \hat{p} = \frac{8}{9} = 0.89, \hat{q} = \frac{1}{9} = 0.11$$

$\hat{q} = 0.11$ is close to the average q across West Africa
considerable variation in q among local populations

Ex 9: multiple alleles selection

West Africa: S is prevalent, it is found a rare allele C

genotype	AA	AS	SS	AC	SC	CC
premalarial environment	1.0	1.0	0.2	1.0	0.7	1.0
malarial environment w	0.9	1.0	0.2	0.9	0.7	1.3

Historical stable equilibrium $A : S = 8 : 1, \bar{w} = 0.911$

genotype ratio for new allele $AC : SC : CC = 8 : 1 : 0$

marginal $w_C = 0.9 \cdot \frac{8}{9} + 0.7 \cdot \frac{1}{9} = 0.878$ less than \bar{w}

Fig 6.11, p. 252: fixation of C starts from $p_C = 0.073$

Literature:

1. D.L.Hartl, A.G.Clarc. Principle of population genetics. Sinauer Associates, 2007.

2. R.Nielson, M. Statkin. An introduction to population genetics: theory and applications, Sinauer Associates. 2013.