2009年11月２４日

生態学Ｉ　第６回

量的遺伝学（２）
Quantitative genetics

Quantitative phenotypic variation

- 量的な表現型変異

Evolutionary Analysis, Pearson edition, Fig 9.1

表現型分散の分割

- 全分散＝遺伝分散＋環境分散

  Var(P) = Var(G) + Var(E)

  heritability(遺伝率 h^2)＝Var(G)/Var(P)

- 表現型に関与する遺伝子がｎ個あるとき・・

  Var(P) ＝ Var(ＱＴＬ１)

  ＋Var(ＱＴＬ２)

  ＋Var(ＱＴＬ３)・・・・

  ＋Var(ＱＴＬn)

ミゾホウズキ属の姉妹種

- *Mimulus lewsii*
  - ハナバチ媒花　bee-pollinated
  - アントシアンが少ない・花弁広い pinky flower
  - 蜜量が少ない low volume of honey
  - おしべ・めしべは花弁より短い shorter stamen and pistil

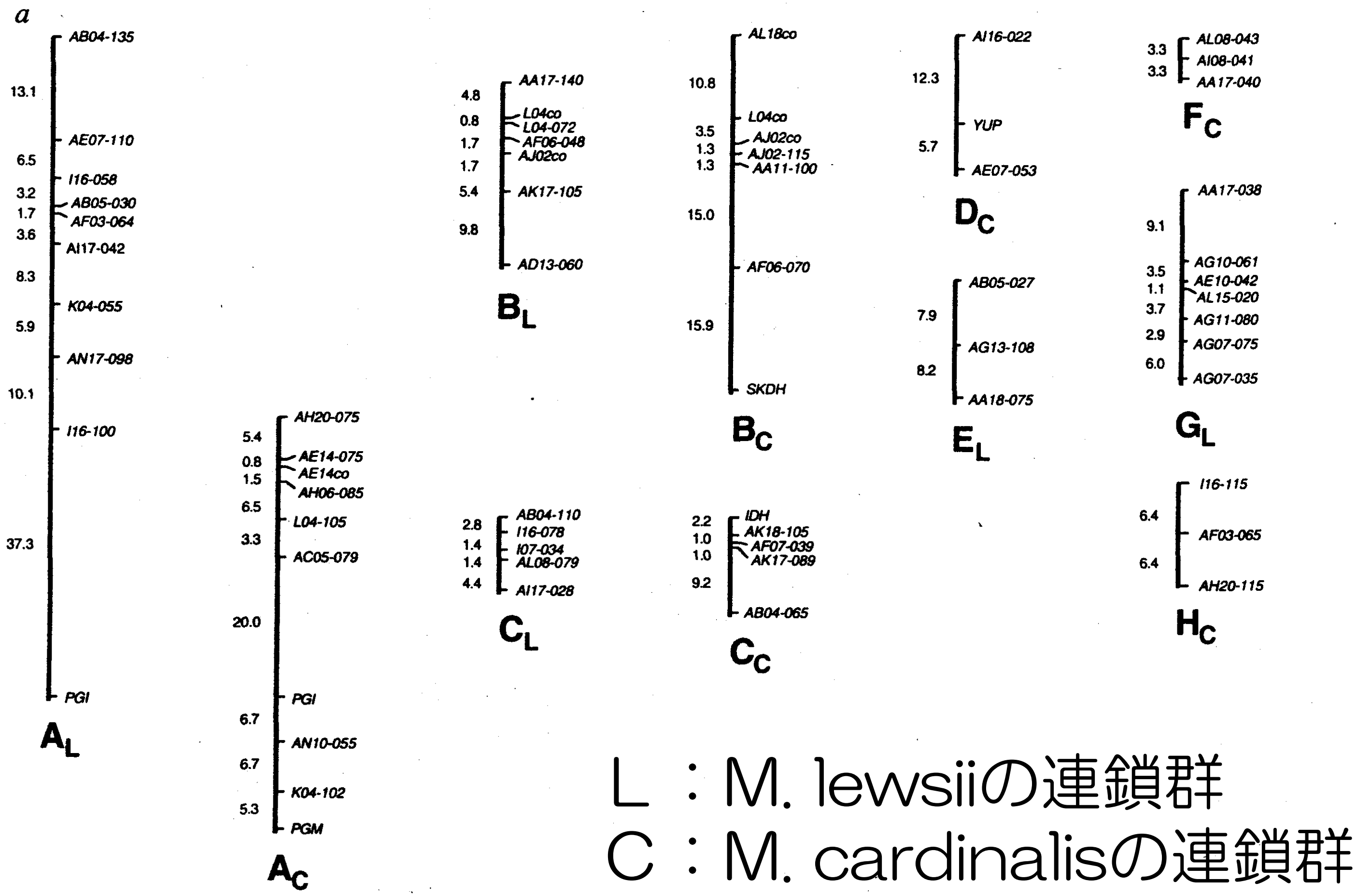
- *Mimulus cardinalis*
  - ハチドリ媒花 bird-pollinated
  - アントシアンが多い・花弁細い reddish flower
  - 蜜量が多い high volume of honey
  - おしべ・めしべが突出する longer stamen and pistil

Mimulus lewsii x M. cardinalis

Ｆ２世代における形質の分離

Schemske & Bradshaw (1999) PNAS 96: 11910-11915

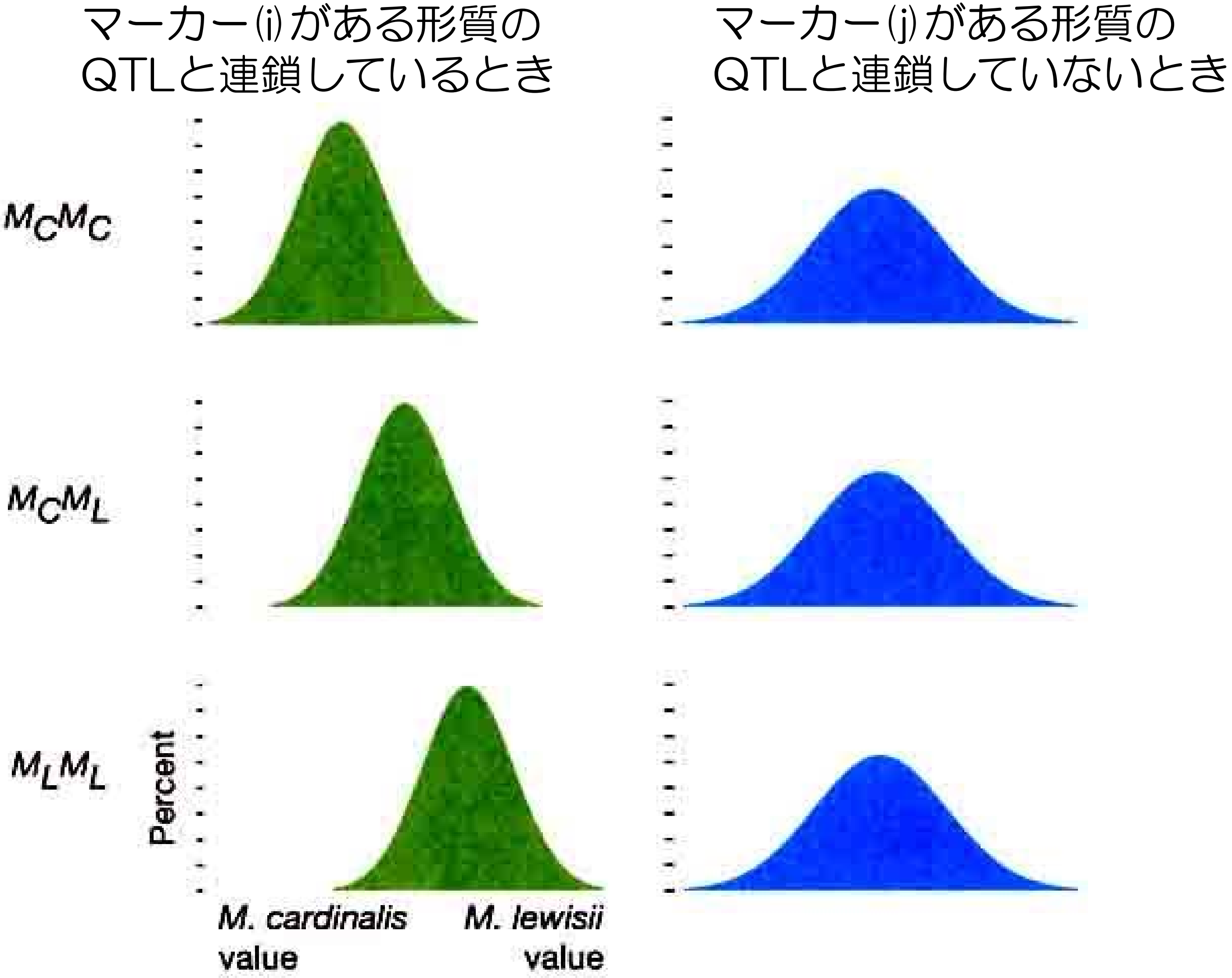
マーカー遺伝子多型の連鎖地図



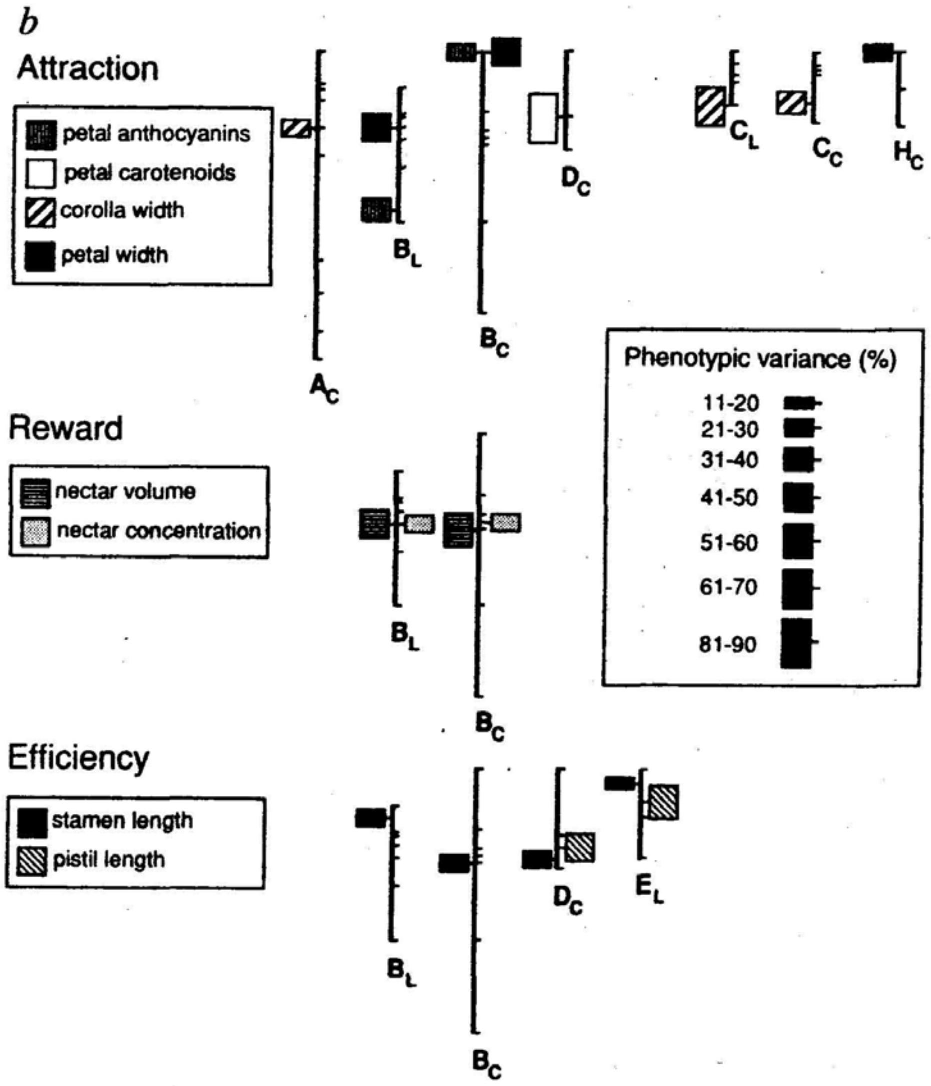
L：M. lewsiiの連鎖群
C：M. cardinalisの連鎖群

Bradshaw & Schemske: Nature

マーカー遺伝子型と量的形質の関係



*Mimulus*の花形質のＱＴＬ



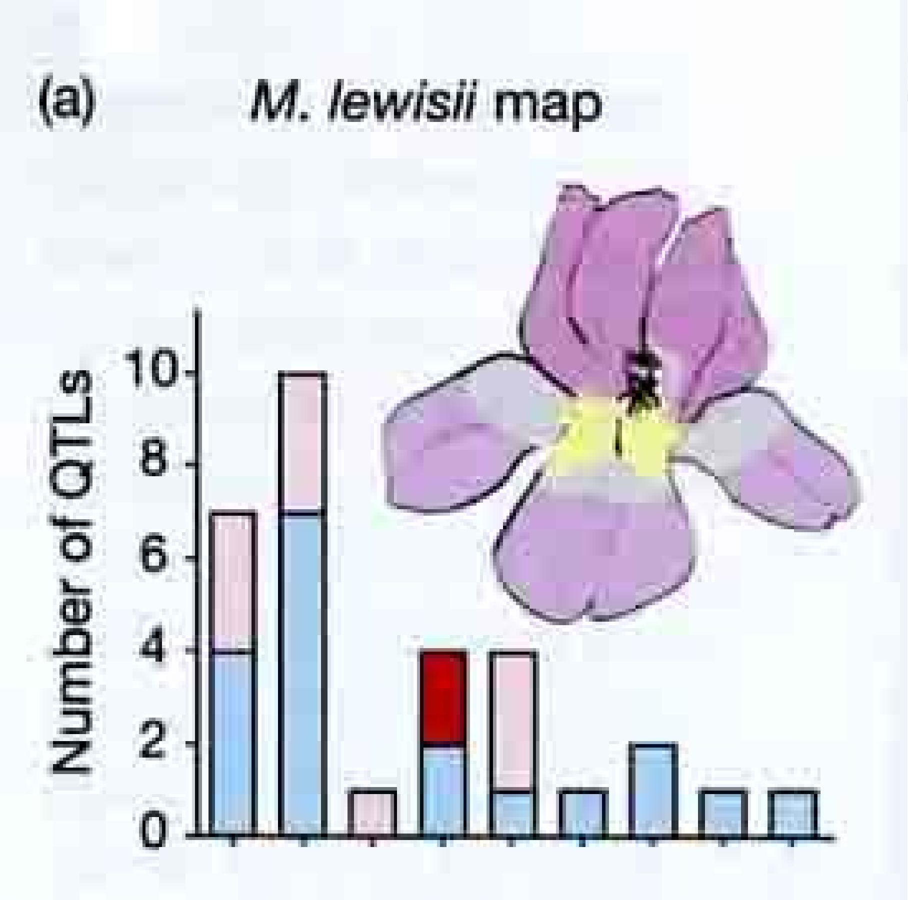
誘引

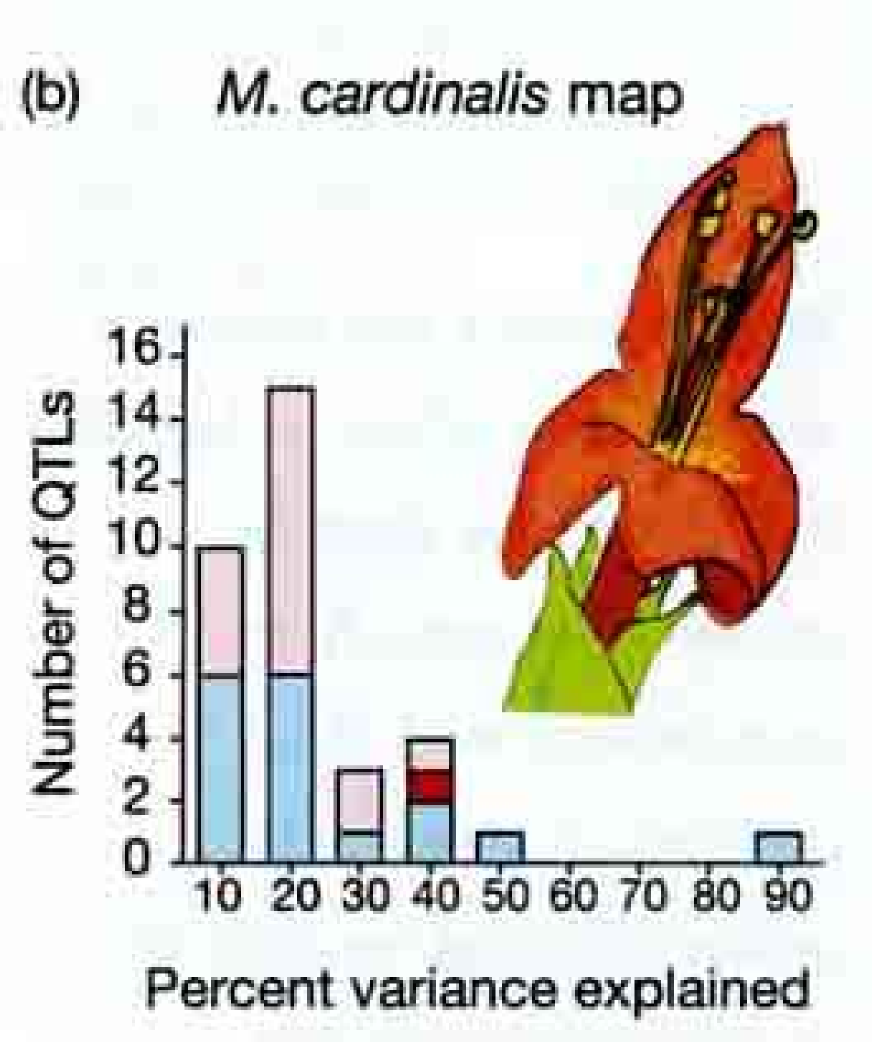
報酬

送粉
効率

各ＱＴＬで説明できる
表現型分散（%）

ＱＴＬの表現型効果の分布





🟦 誘引 🟥 報酬 🟪 送粉効率

ダーウィンフィンチにおける自然淘汰

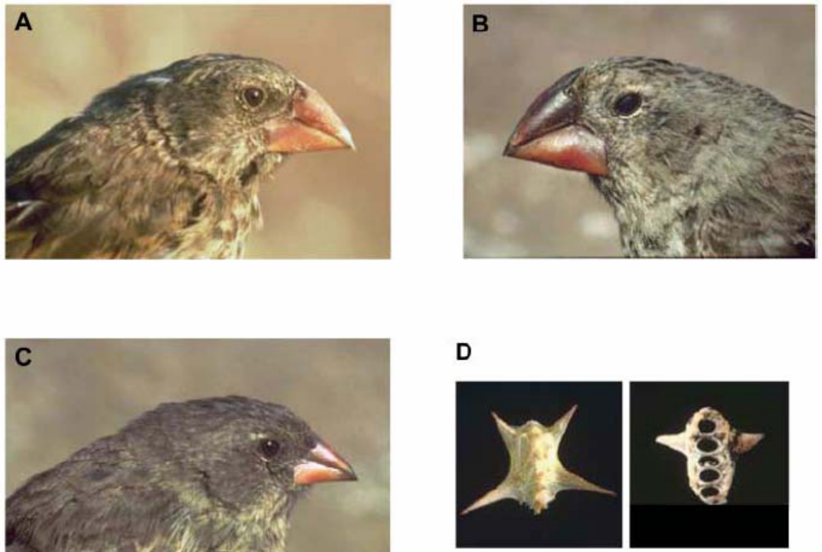


Fig. 1. Large-beaked *G. fortis* (**A**) and *G. magnirostris* (**B**) can crack or tear the woody tissues of *T. cistoides* mericarps (**D**), whereas small-beaked *G. fortis* (**C**) cannot. Five mericarps constitute a single fruit. In (D), the left-hand mericarp is intact. The right-hand mericarp, viewed from the other (mesial) side, has been exploited by a finch, exposing five locules from which seeds have been extracted. Mericarps are ~8 mm long and are shown at twice the magnification of the finches. [Photos are by the authors]

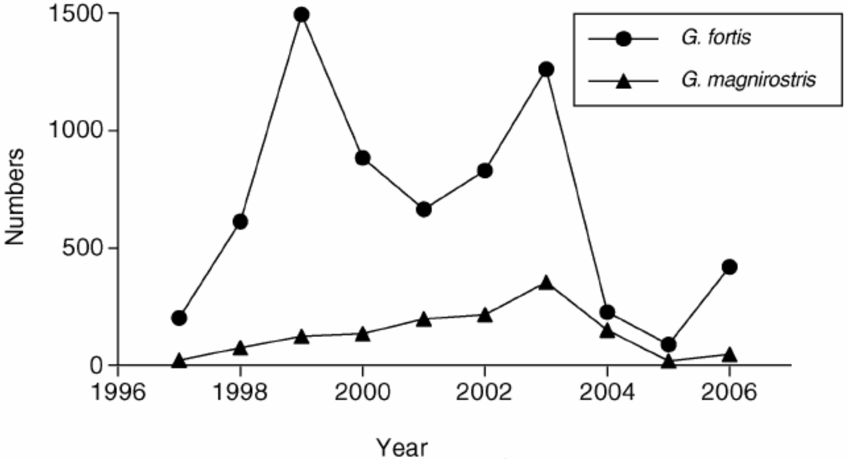


Fig. 3. Numbers of *G. fortis* and *G. magnirostris*. Breeding was extensive in 1997–1998 and 2002, and as a result finch numbers were elevated in the following years. There was no breeding in 2003 and 2004. Numbers before 1997 have been omitted because *G. magnirostris* were scarce (≤13 pairs) (*25*).

Grant and Grant (2006) Science

中型フィンチにおける選択差

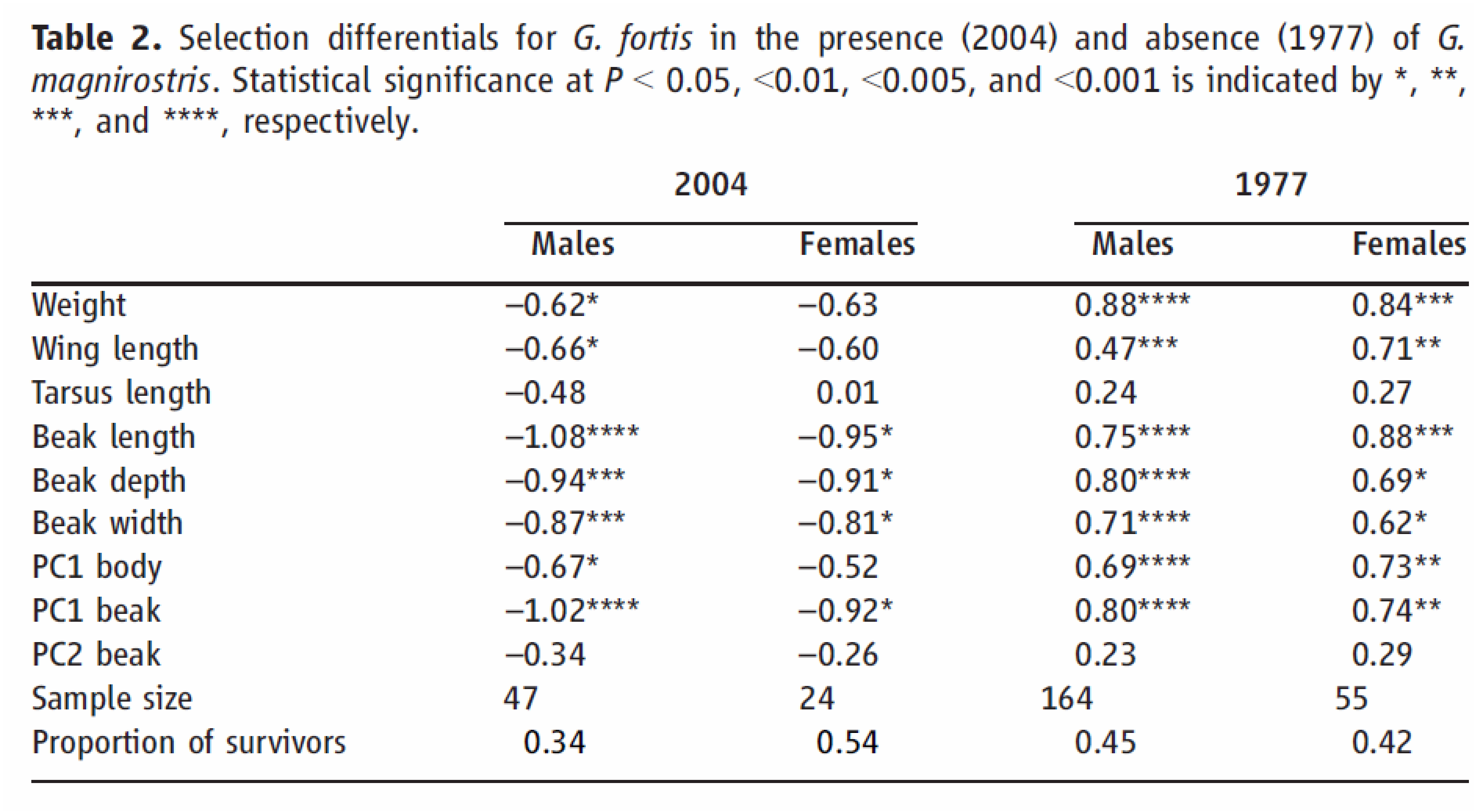


Table 2. Selection differentials for *G. fortis* in the presence (2004) and absence (1977) of *G. magnirostris*. Statistical significance at $P < 0.05$, <0.01, <0.005, and <0.001 is indicated by *, **, ***, and ****, respectively.

	2004		1977	
	Males	**Females**	**Males**	**Females**
Weight	–0.62*	–0.63	0.88****	0.84***
Wing length	–0.66*	–0.60	0.47***	0.71**
Tarsus length	–0.48	0.01	0.24	0.27
Beak length	–1.08****	–0.95*	0.75****	0.88***
Beak depth	–0.94***	–0.91*	0.80****	0.69*
Beak width	–0.87***	–0.81*	0.71****	0.62*
PC1 body	–0.67*	–0.52	0.69****	0.73**
PC1 beak	–1.02****	–0.92*	0.80****	0.74**
PC2 beak	–0.34	–0.26	0.23	0.29
Sample size	47	24	164	55
Proportion of survivors	0.34	0.54	0.45	0.42

選択差と選択勾配

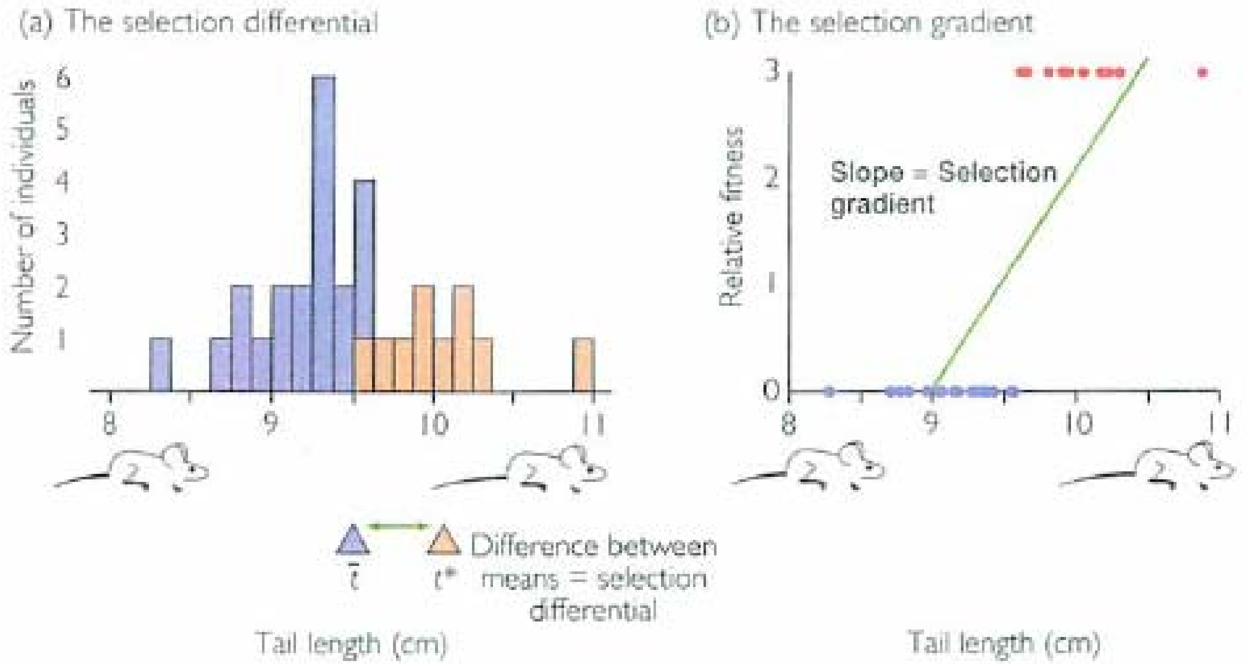


Figure 9.17 **Measuring the strength of selection** (a) The histogram shows the variation in tail length in a fictional population of lab mice. The red bars represent the mice chosen as breeders for the next generation. The gray triangle indicates the average tail length for the entire population; the red triangle indicates the average tail length for the breeders. The difference between these two averages is the selection differential. (b) A scatterplot for the same fictional population of mice showing relative fitness (see text) as a function of tail length. Red dots represent mice chosen as breeders for the next generation. The scatterplot includes the best-fit line (green). The slope of the best-fit line is the selection gradient.

分散・共分散と回帰係数

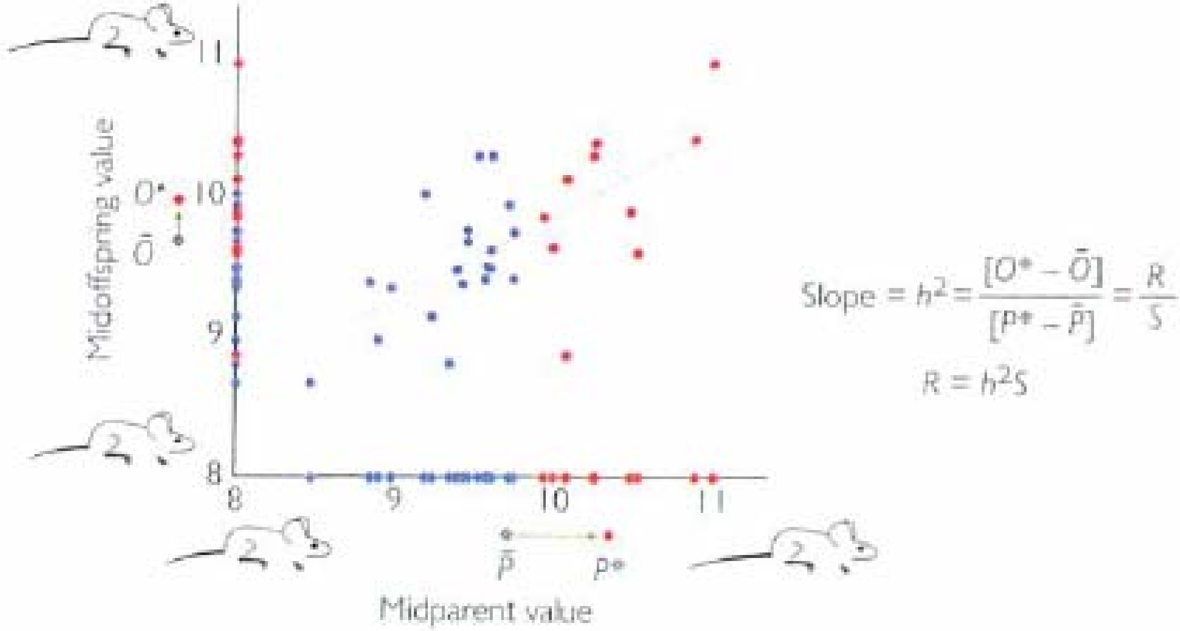
$$\underbrace{\mathrm{Var}\,(a)}_{\text{aの分散}} = \frac{1}{N}\sum_{i=1}^{N}\left(\underbrace{\mathrm{Ave}(a)}_{\text{aの平均値}} - a_i\right)^2$$

$$\underbrace{\mathrm{Cov}\,(x,\ y)}_{\text{xとyの共分散}} = \frac{1}{N}\sum_{i=1}^{N}\left(\underbrace{\mathrm{Ave}(x)}_{\text{xの平均値}} - x_i\right)\left(\underbrace{\mathrm{Ave}(y)}_{\text{yの平均値}} - y_i\right)$$

$$\text{回帰係数} = \frac{\mathrm{Cov}(x,\ y)}{\mathrm{Var}(x)}$$

$$\text{Selection gradient} = \frac{\text{Selection differential}}{\mathrm{Var}(x)}$$

選択への反応と遺伝率の関係



$$\text{Slope} = h^2 = \frac{[O^* - \bar{O}]}{[P^* - \bar{P}]} = \frac{R}{S}$$

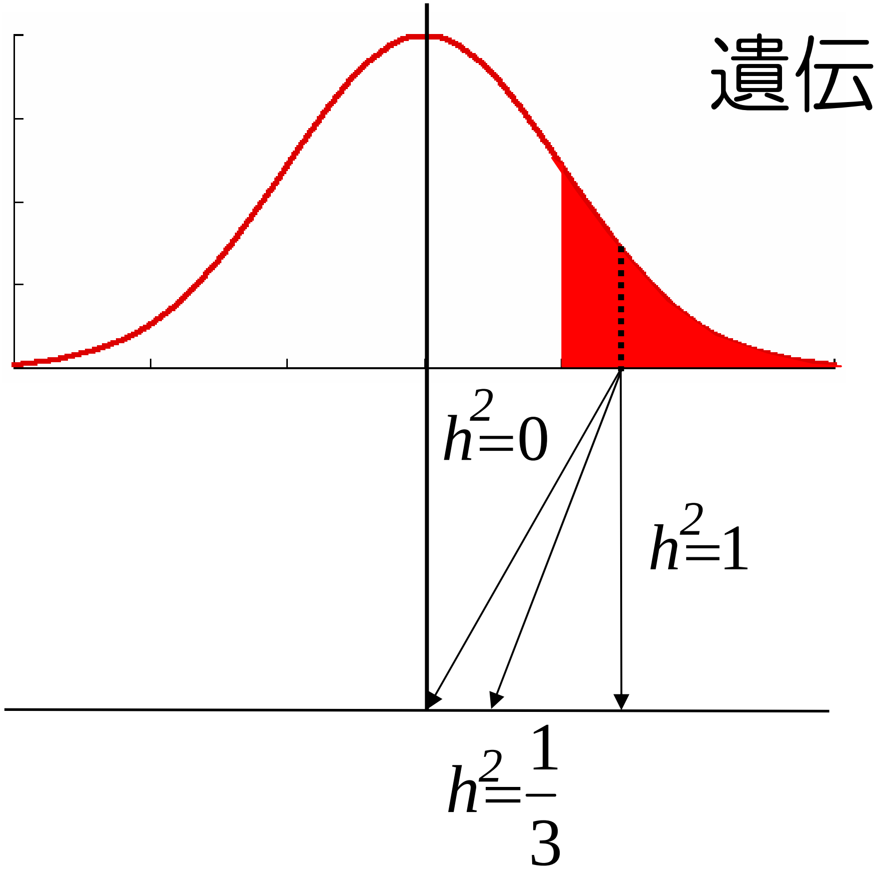
$$R = h^2 S$$

Figure 9.18 **The response to selection is equal to the heritability multiplied by the selection differential** The midoffspring and midparent values are indicated both as dots on the scatterplot and as diamonds on the y- and x-axes. The red symbols represent the 10 families with the largest midparent values. $\bar{P}$ is the average midparent value for the entire population; P^* is the average midparent value of the families with the largest midparent values. $\bar{O}$ is the average midoffspring value for the entire population; O^* is the average midoffspring value for the families with the largest midparent values. After Falconer (1989).

遺伝率と選択への反応

- Var(P)＝Var(G)＋Var(E)

$$遺伝率\ h^2 \equiv \frac{\mathrm{Var(G)}}{\mathrm{Var(P)}}$$



選択への反応の測定

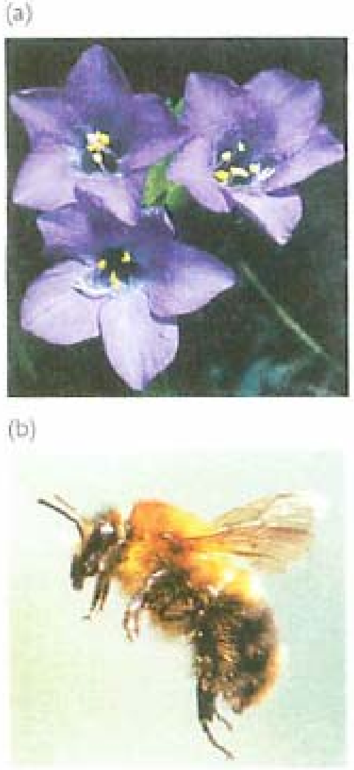


Figure 9.19 **An alpine skypilot and a bumblebee** (a) Alpine skypilot (*Polemonium viscosum*). (b) Bumblebee (*Bombus* sp.).

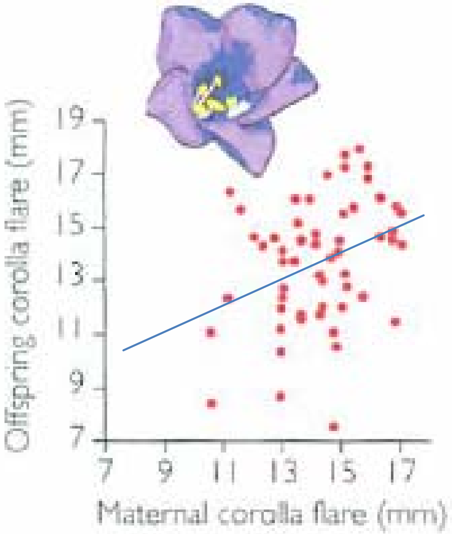


Figure 9.20 **Estimating the heritability of flower size (corolla flare) in alpine skypilots** This scatterplot shows offspring corolla flare as a function of maternal plant corolla flare for 58 skypilots. The slope of the best-fit line is 0.5. Redrawn from Galen (1996).

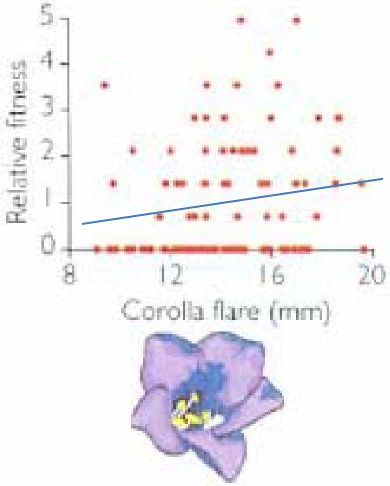


Figure 9.21 **Estimating the selection gradient in alpine skypilots pollinated by bumblebees** This scatterplot shows relative fitness (number of surviving 6-year-old offspring divided by average number of surviving 6-year-old offspring) as a function of maternal flower size (corolla flare). The slope of the best-fit line is 0.13. Prepared with data provided by Candace Galen.

選択への反応の測定

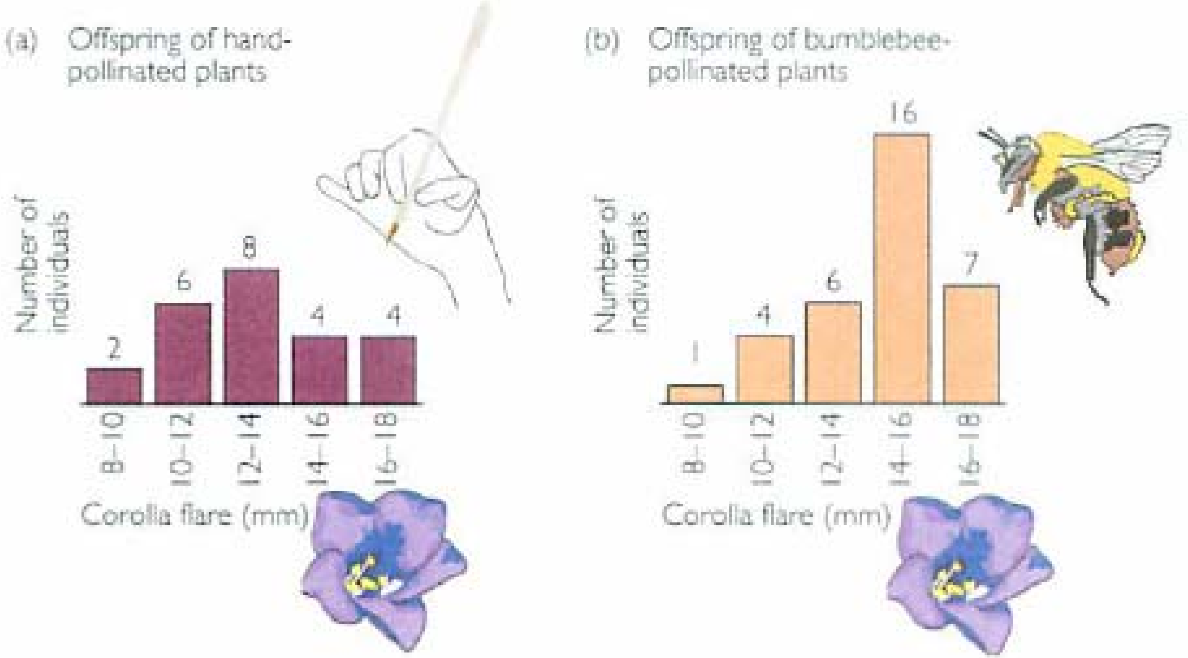


Figure 9.22 **Measuring the evolutionary response to selection in alpine skypilots** These histograms show the distribution of flower size (corolla flare) in the offspring of hand-pollinated skypilots (a; average = 13.1 mm) and bumblebee-pollinated skypilots (b; average = 14.4 mm). Redrawn from Galen (1996).

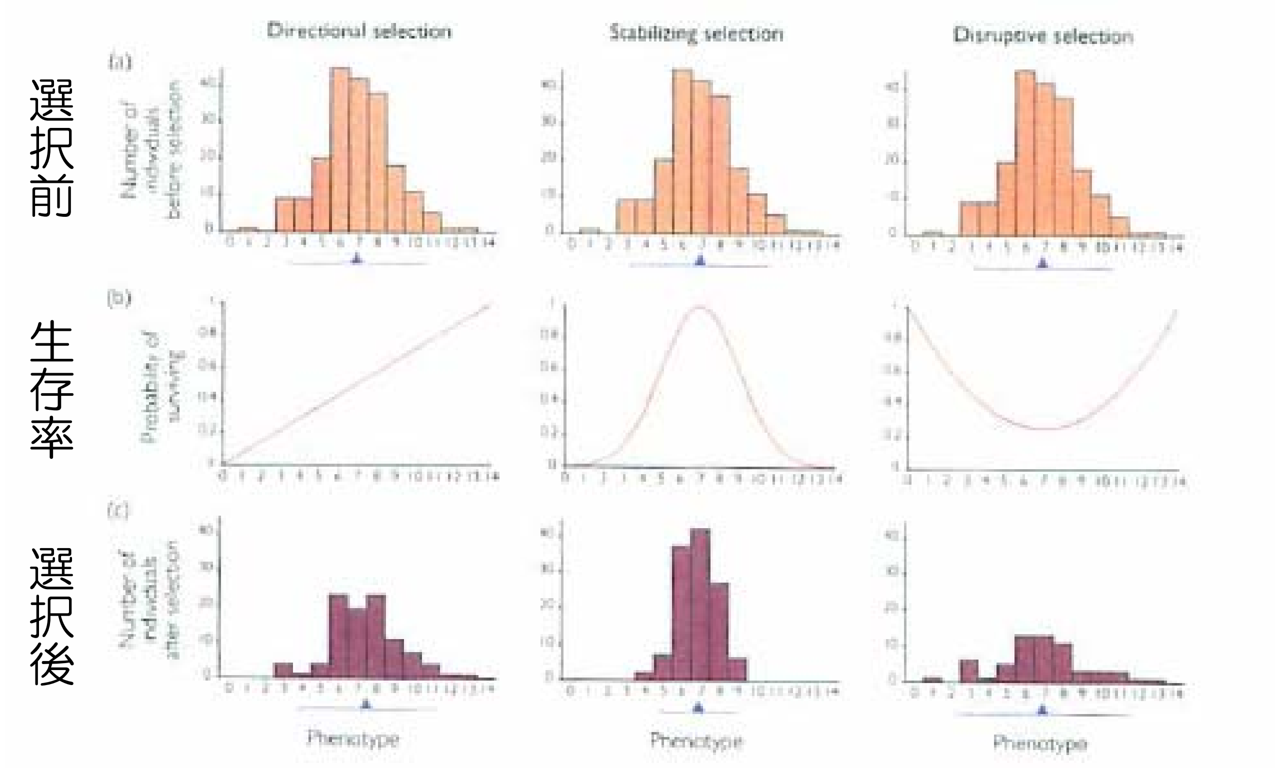
３つの選択モード

方向性選択　安定化選択　分断化選択

選択前

生存率

選択後



嘴の大きさに対する分断化選択

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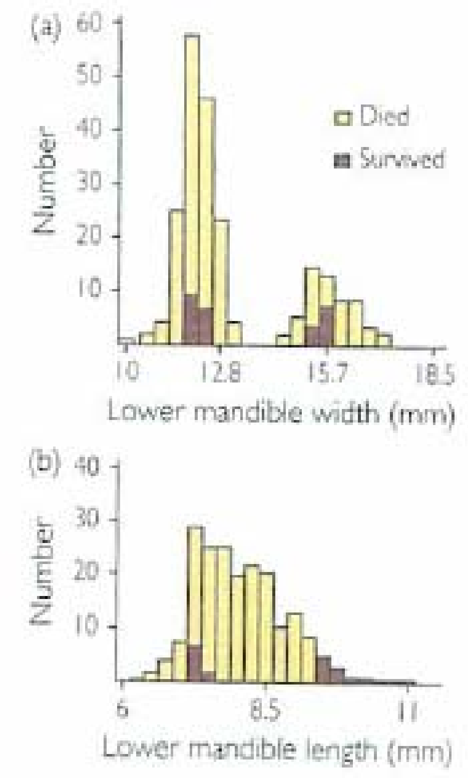

Figure 9.27 **Disruptive selection on bill size in the black-bellied seedcracker (*Pyrenestes o. ostrinus*)** Each graph shows the distribution of lower bill widths (a) or lengths (b) in a population of black-bellied seedcrackers, an African finch. The light-colored portion of each bar represents juveniles that did not survive to adulthood; the dark-colored portion represents juveniles that did survive. The survivors were those individuals with bills that were either relatively large or relatively small. Rerendered from Bates Smith (1993).

環境要因の大きさ

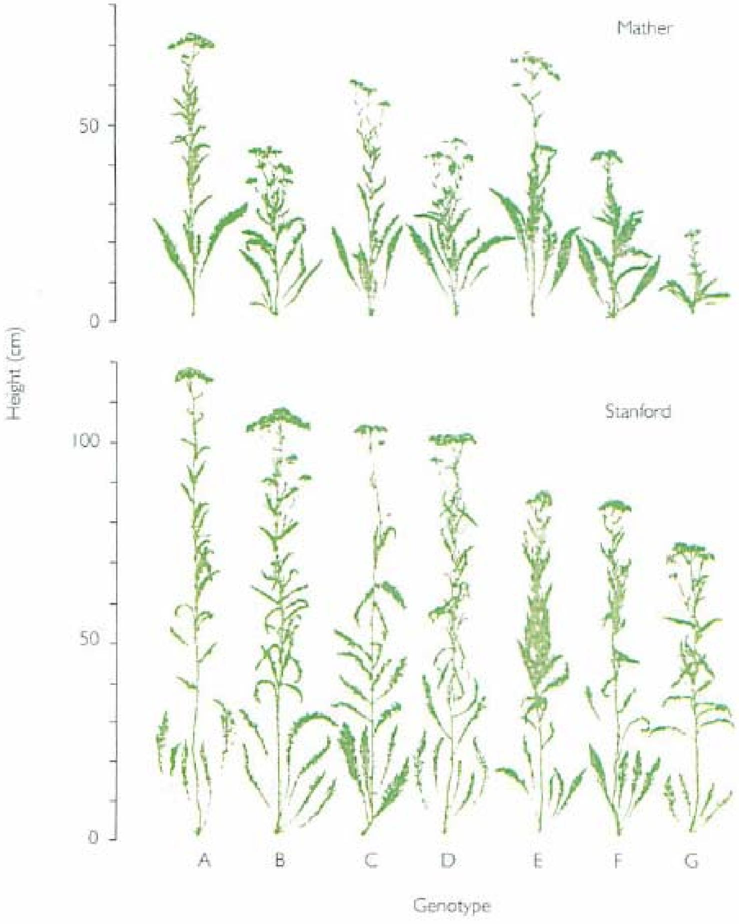

Figure 9.28 High heritability within populations tells us nothing about the cause of differences between populations We know the variation in height among the plants within each of these populations is entirely due to differences in their genes, because the plants grew in experimental common gardens where all experienced the same environment. The plants in the Stanford population are taller, on average, than the plants in the Mather population. Does this mean that the Stanford population is genetically superior to the Mather population? No: We know these two populations are genetically identical because they were grown from cuttings of the same seven plants. Reprinted from Clausen, Keck, and Hiesey (1948).

Question

- 集団内で草丈に遺伝的変異があるのはなぜだろうか？