

2008年12月9日

# 生態学 I 第8回

## 量的遺伝(3)

表現型の進化の遺伝的背景

# ダーウィンフィンチにおける自然淘汰

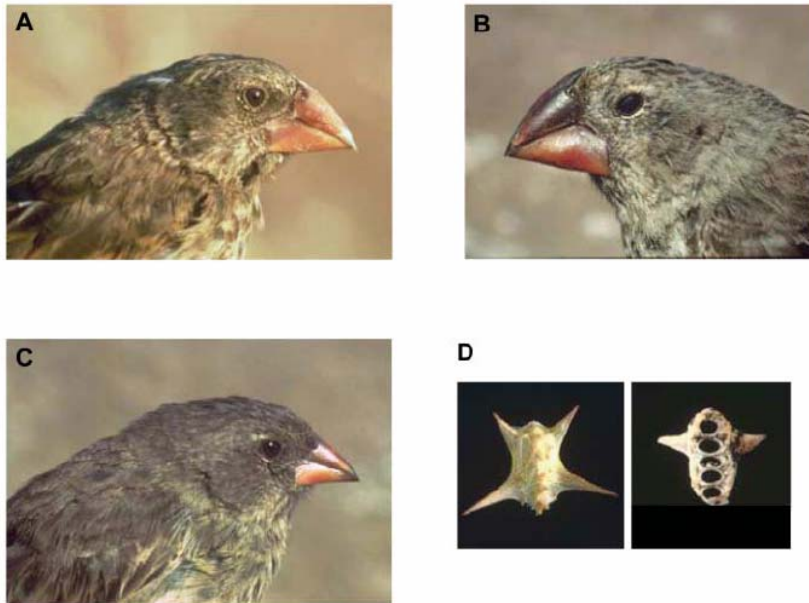


Fig. 1. Large-beaked *G. fortis* (A) and *G. magnirostris* (B) can crack or tear the woody tissues of *T. cistoides* mericarps (D), whereas small-beaked *G. fortis* (C) cannot. Five mericarps constitute a single fruit. In (D), the left-hand mericarp is intact. The right-hand mericarp, viewed from the 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]

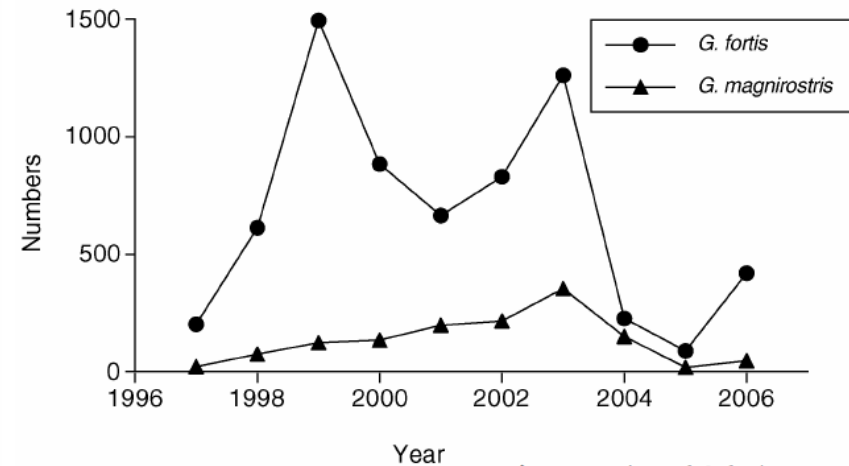


Fig. 3. Numbers of *G. fortis* and *G. magnirostris*. Breeding was extensive in 1997–1998 and 2002, and as a result finch numbers were elevated in the following years. There was no breeding in 2003 and 2004. Numbers before 1997 have been omitted because *G. magnirostris* were scarce ( $\leq 13$  pairs)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

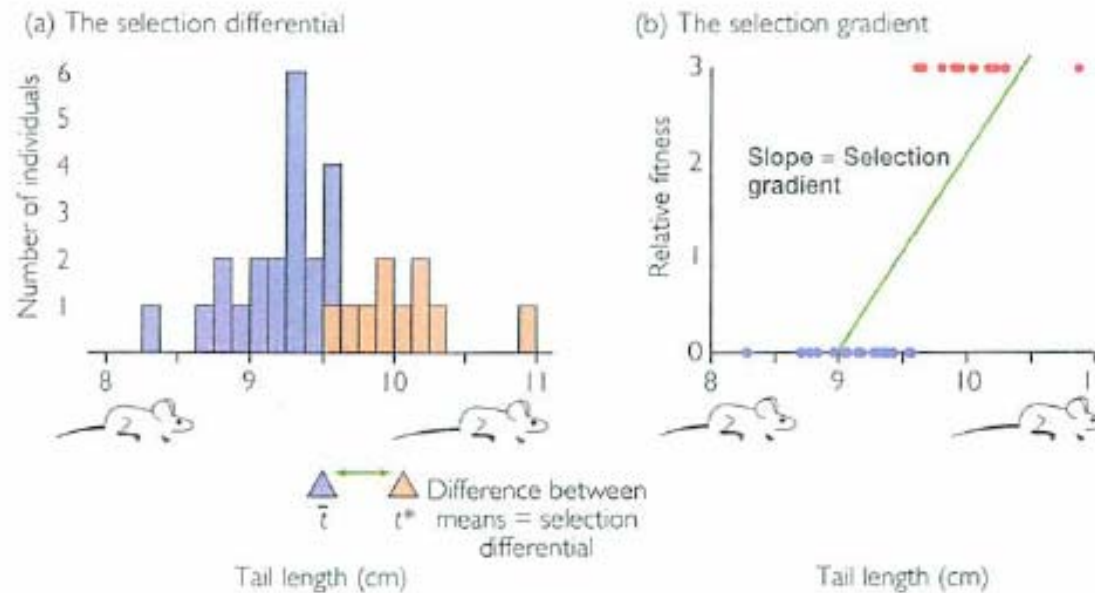
中型フィンチは嘴を小さくして生きのびていたが、飛来した大型フィンチは餌が少なくなった時点で、嘴の大きさを変化させなかったのだろうか。

# 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

$$\text{Var}(a) = \frac{1}{N} \sum_{i=1}^N (\text{Ave}(a) - a_i)^2$$

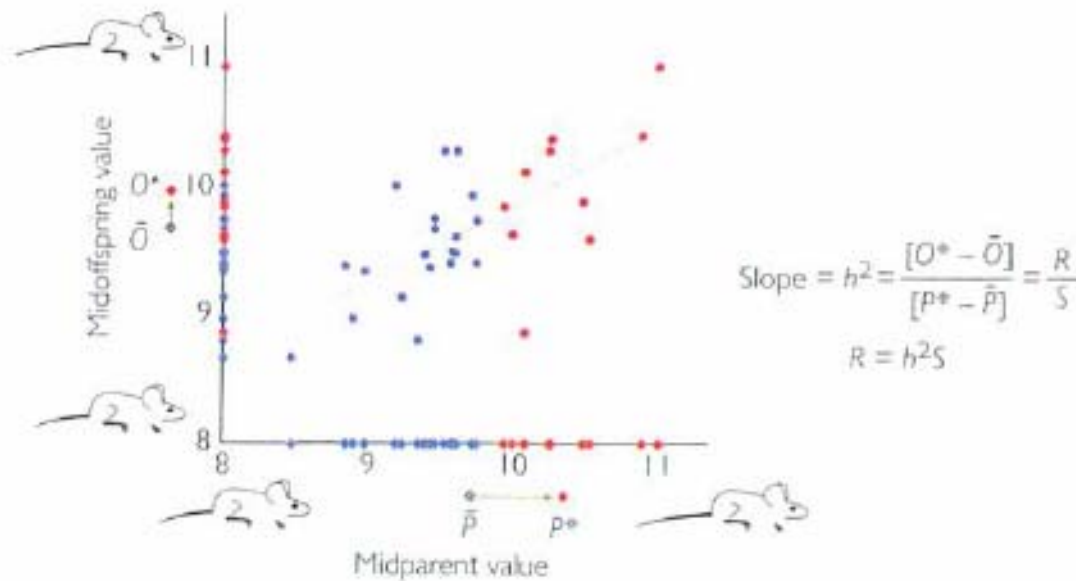
Var(a)      Ave(a)  
aの分散      aの平均値

$$\text{Cov}(x, y) = \frac{1}{N} \sum_{i=1}^N (\text{Ave}(x) - x_i) (\text{Ave}(y) - y_i)$$

Cov(x, y)      Ave(x)      Ave(y)  
xとyの共分散      xの平均値      yの平均値

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

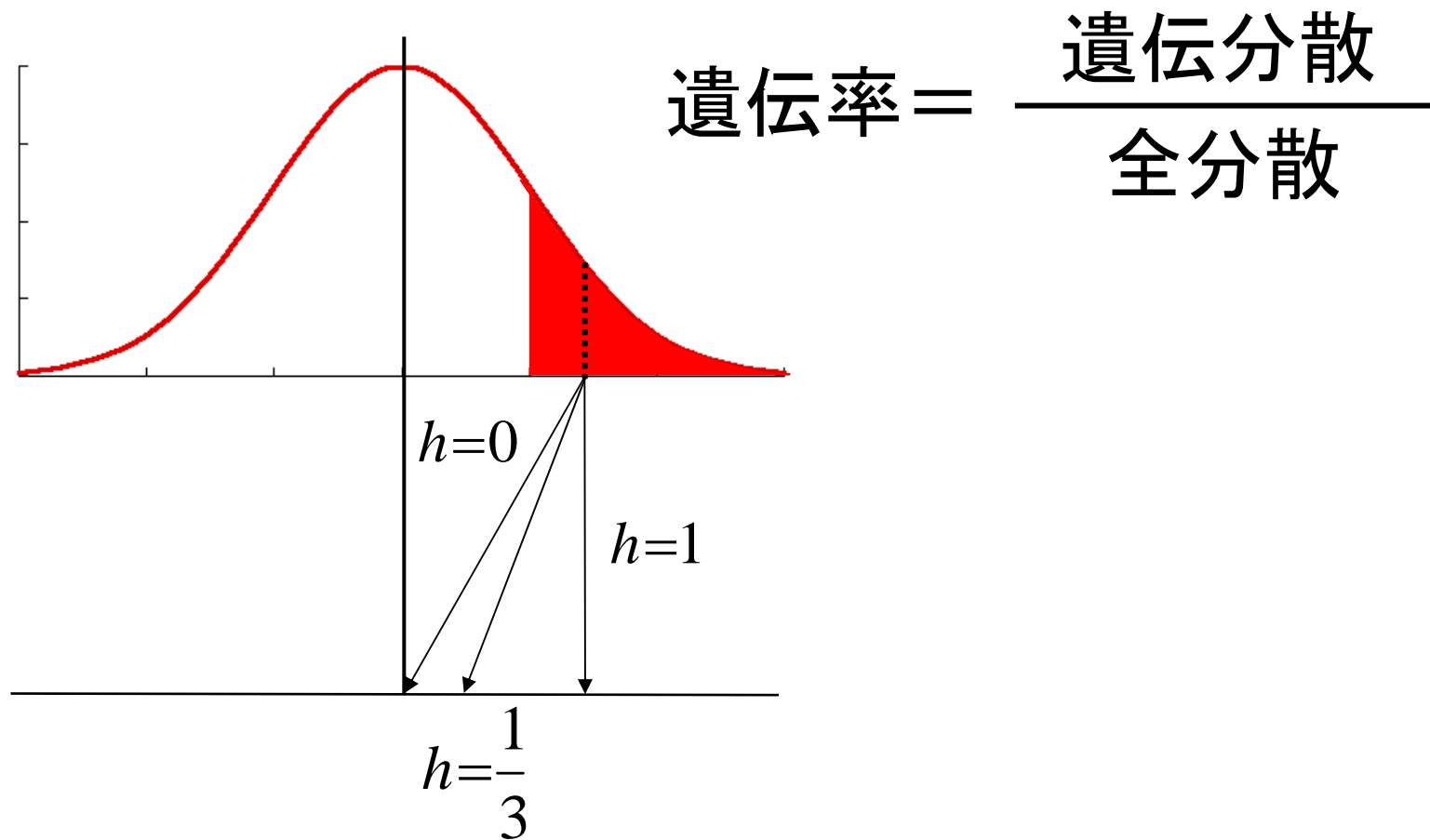
# 選択への反応と遺伝率の関係



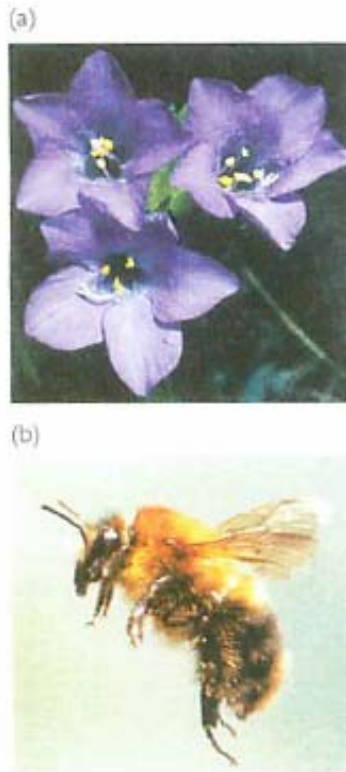
**Figure 9.18** The response to selection is equal to the heritability multiplied by the selection differential. The midoffspring and midparent values are indicated both as dots on the scatterplot and as diamonds on the y- and x-axes. The red symbols represent the 10 families with the largest midparent 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

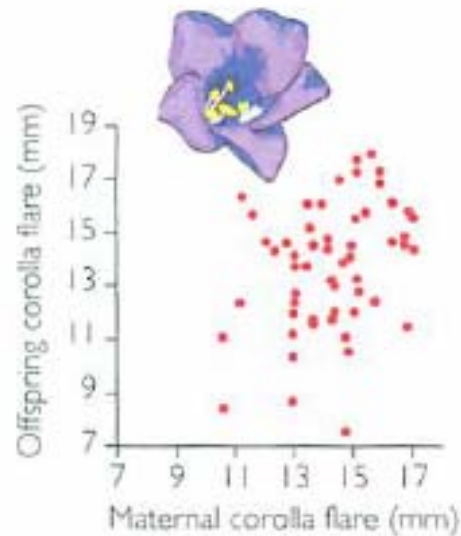
- 全分散 = 遺伝分散 + 環境分散



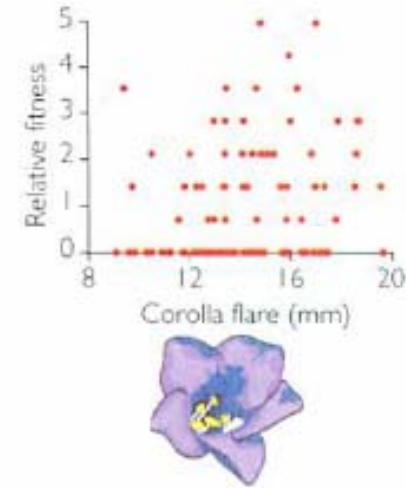
# 花サイズの遺伝率と選択勾配



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



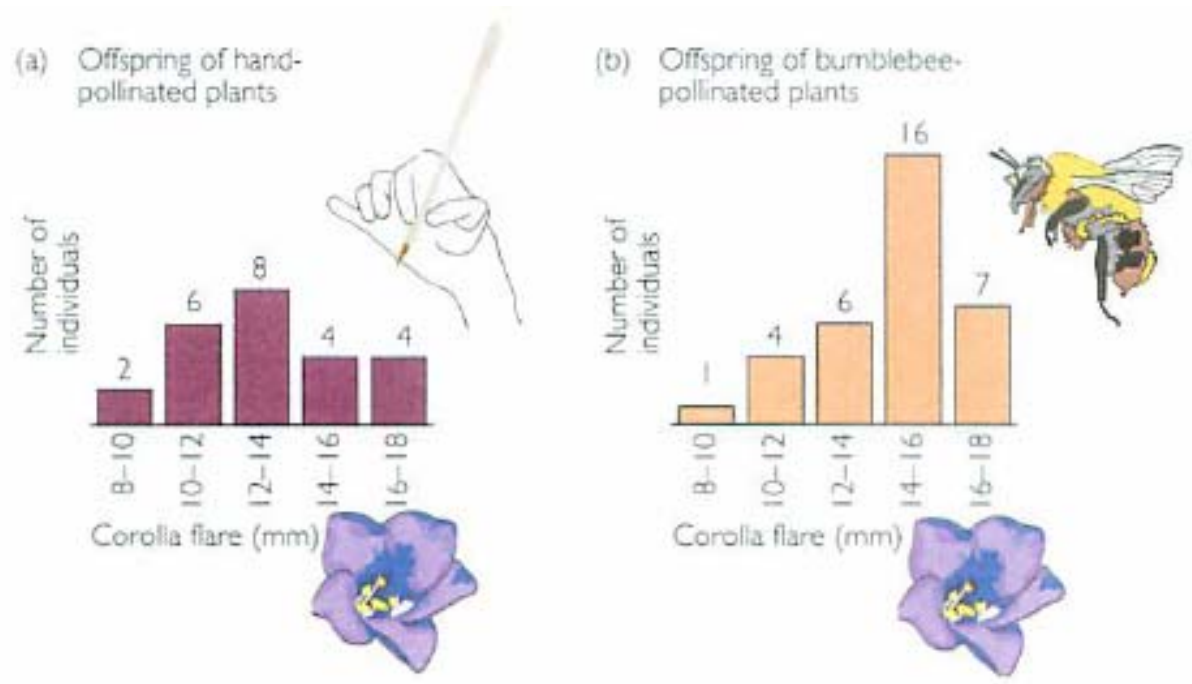
**Figure 9.20** Estimating the heritability of flower size (corolla flare) in alpine sky pilots. This scatterplot shows offspring corolla flare as a function of maternal plant corolla flare for 58 sky pilots. The slope of the best-fit line is 0.5. Redrawn from Galen (1996).



**Figure 9.21** Estimating the selection gradient in alpine sky pilots 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).

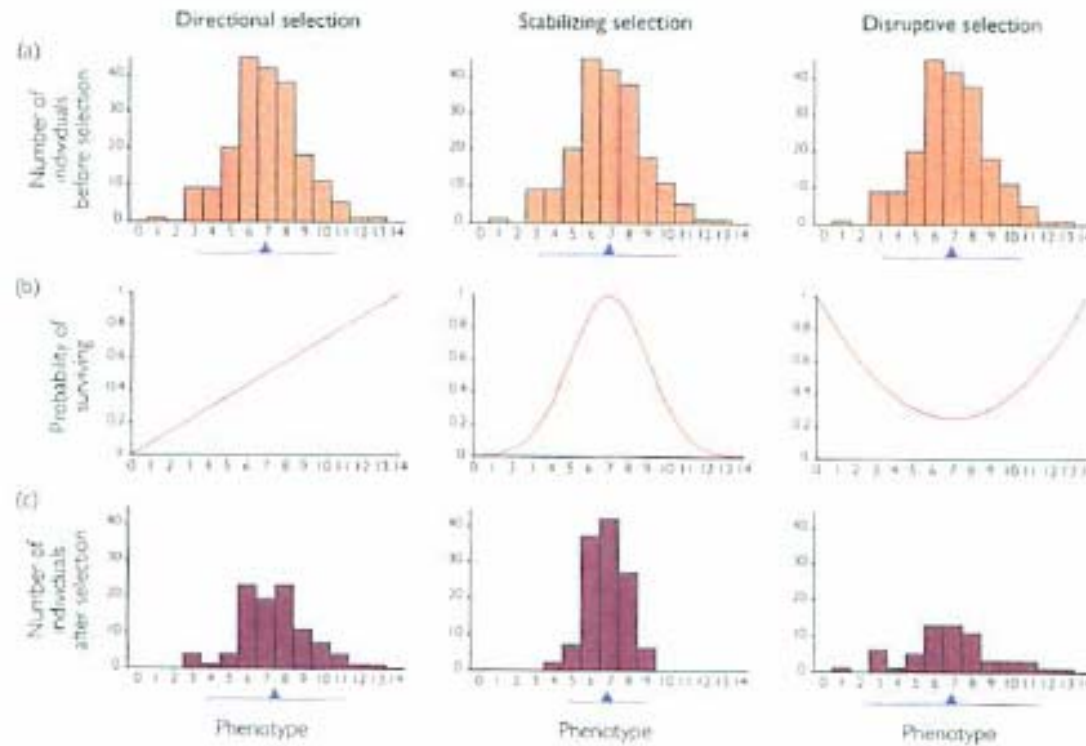
# 3つの選択モード

方向性選択

安定化選択

分断化選択

選択前



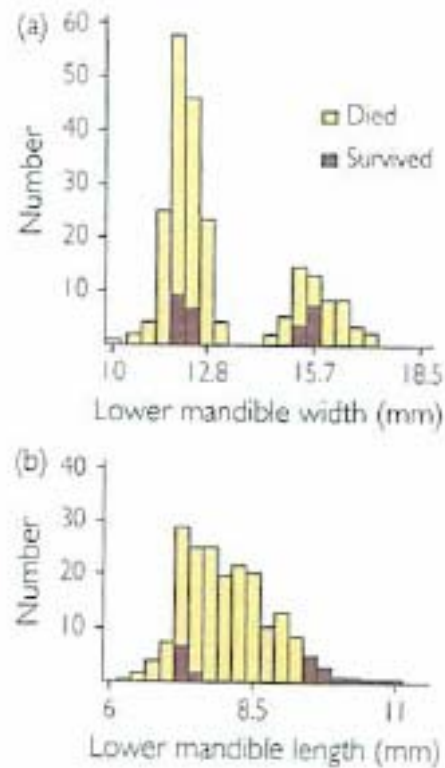
生存率

選択後

# 嘴の大きさに対する分断化選択

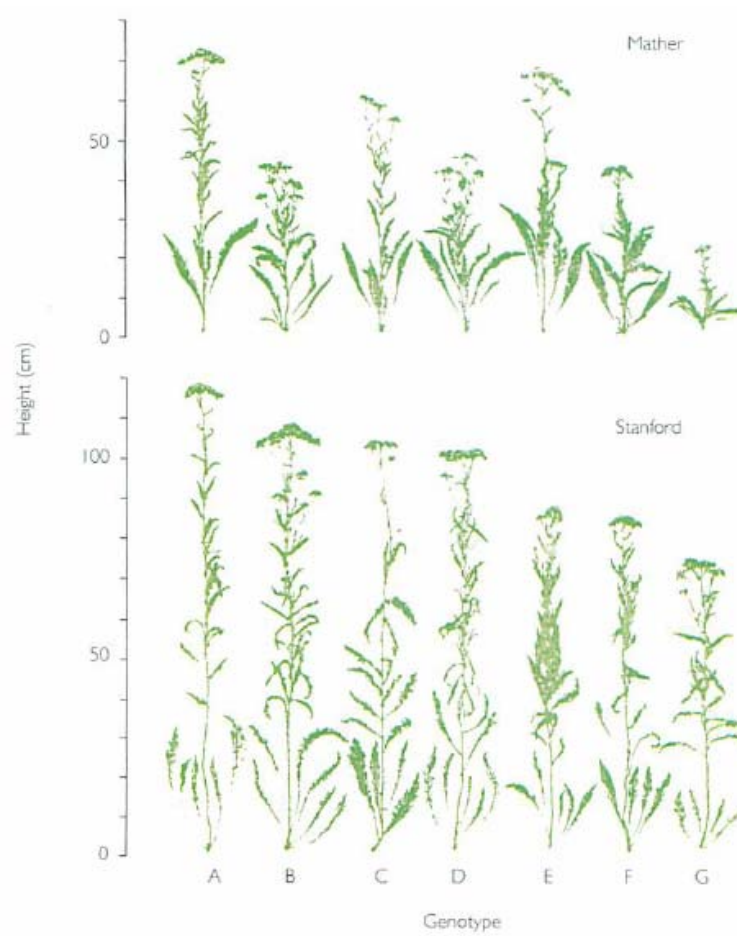


アカクロタネワリキンパラ



**Figure 9.37** 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).

# エコタイプ(生態型)



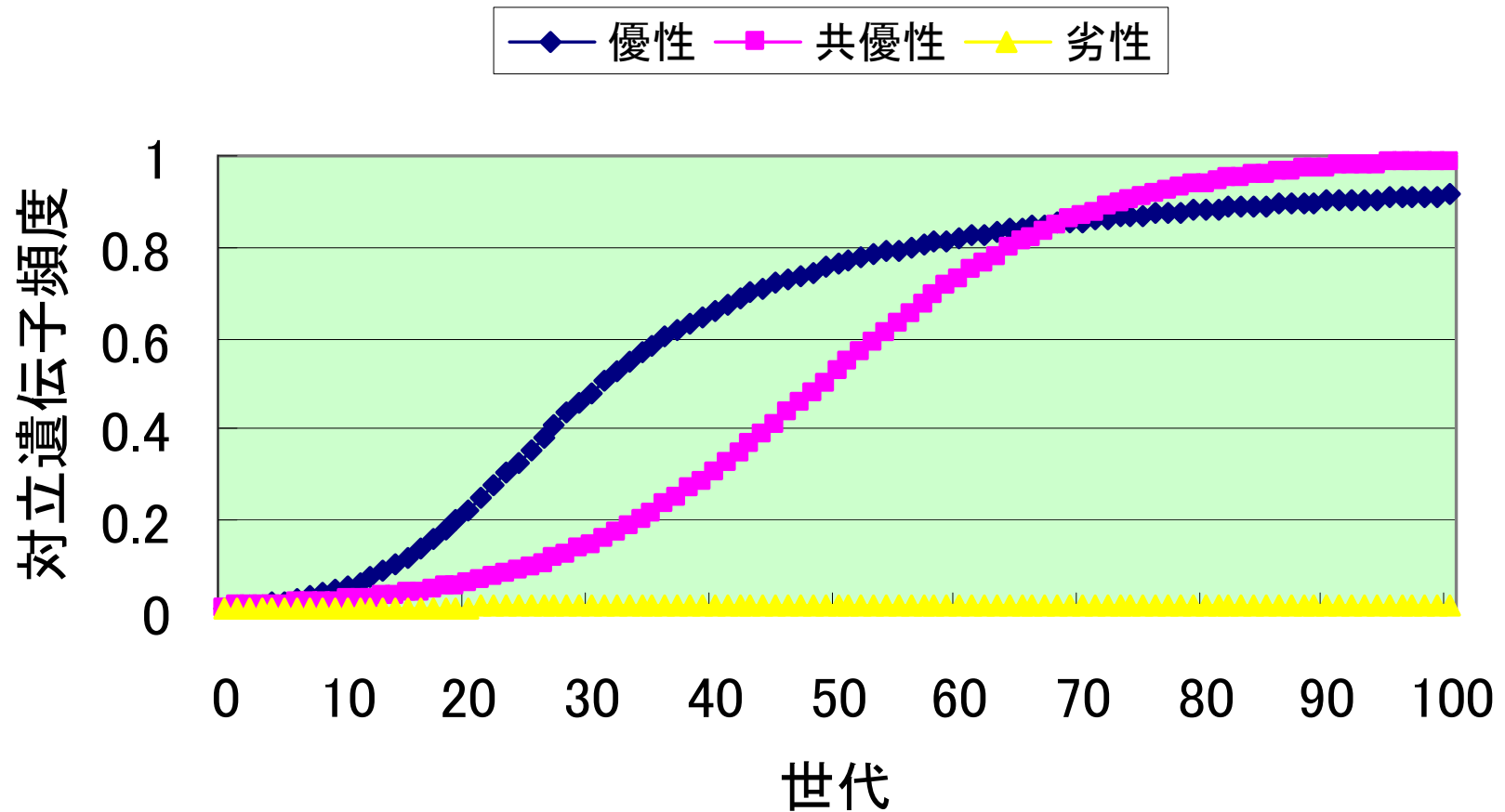
**Figure 9.28** High heritability within populations tells us nothing about the cause of differences between populations. We know the variation in height among the plants within each of these populations is entirely due to differences in their genes, because the plants grew in experimental common gardens 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？

# 優性度と自然淘汰の関係

$q(0)=0.01, s=0.2$ のとき

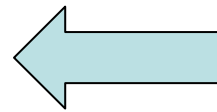


# 弱有害変異の平衡頻度

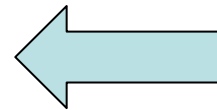
$$p = \sqrt{\frac{\mu}{s}}$$

# 寿命が延びると有害変異が増える？

$$p = \sqrt{\frac{\mu}{s}}$$



突然変異率：  
寿命が延びることで増加



淘汰の強さ：  
寿命が延びることで減少



# 生活習慣病の遺伝子

- 糖尿病
- 肥満
- 高血圧
- 高尿酸血症（痛風など）
- 脂質異常症（高コレステロール血症） など

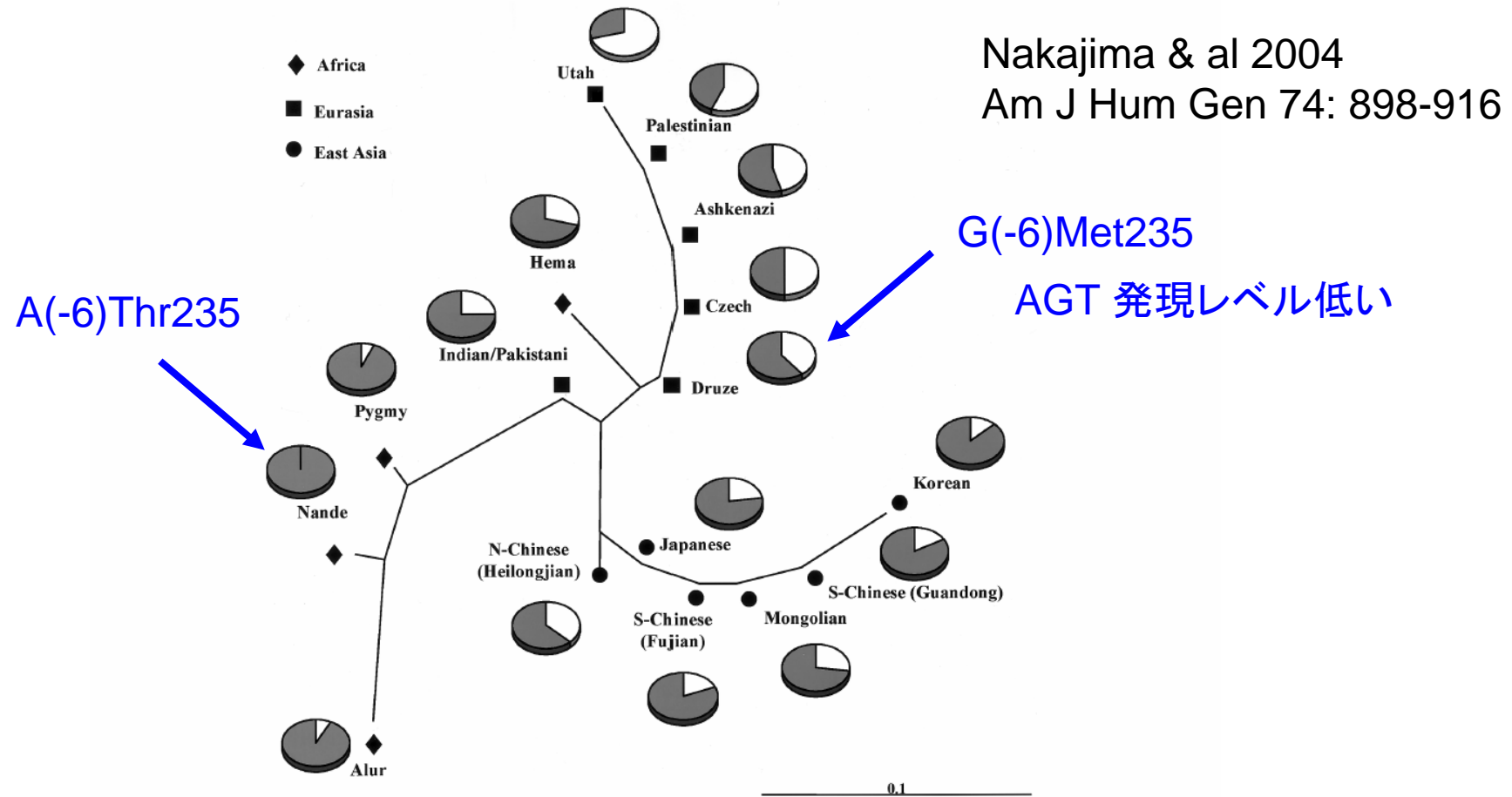


ヒトの進化過程では有利な遺伝子  
（儉約遺伝子）だった可能性あり

# Angiotensinogen 遺伝子の変異

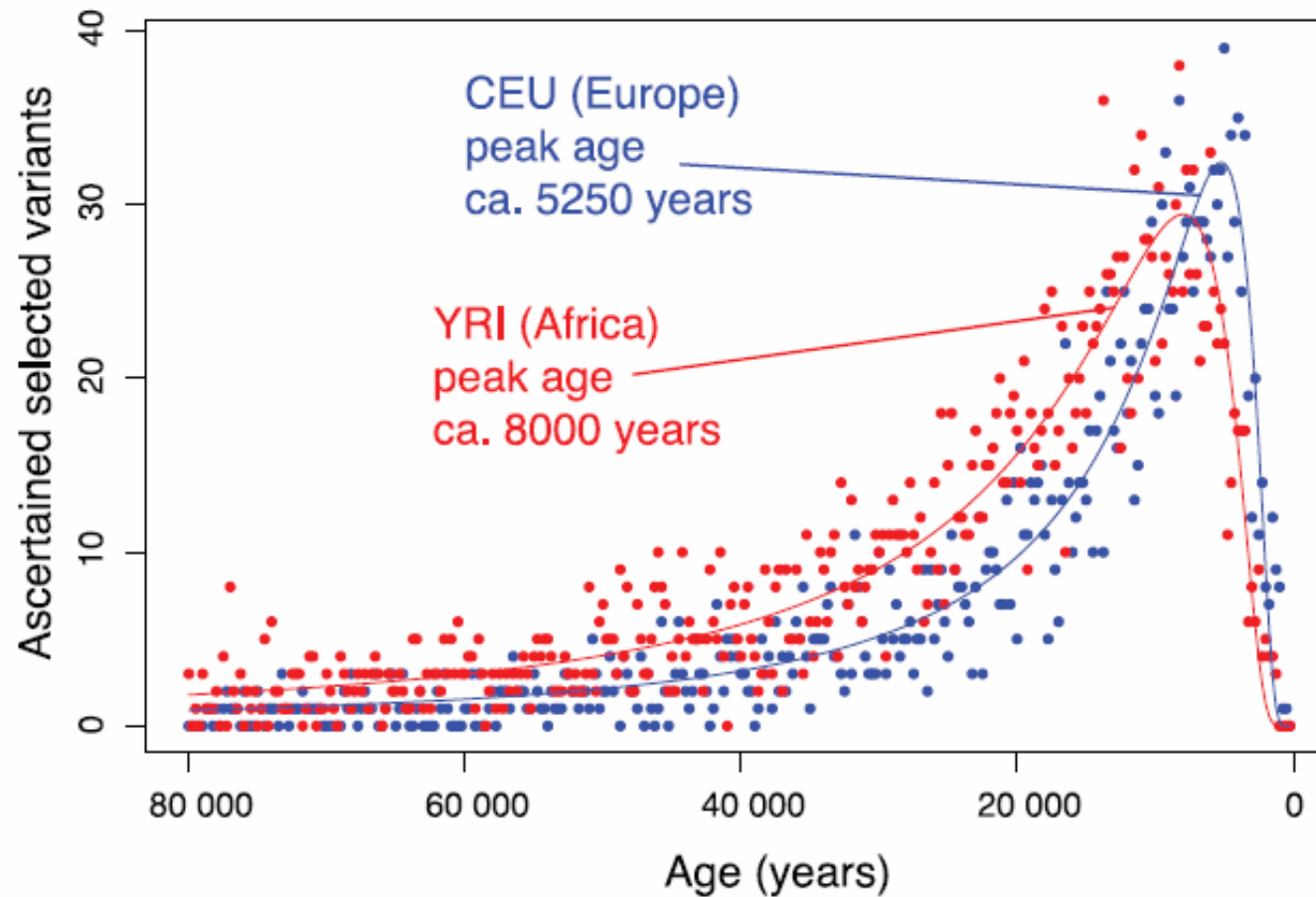
Nakajima et al.: Natural Selection in *AGT*

909



**Figure 3** Neighbor-joining tree based on Nei's distance among seven populations. The shaded portion of each circle indicates the frequency of the A(-6)/T235 allele.

# 正の選択を受けた対立遺伝子の年齢

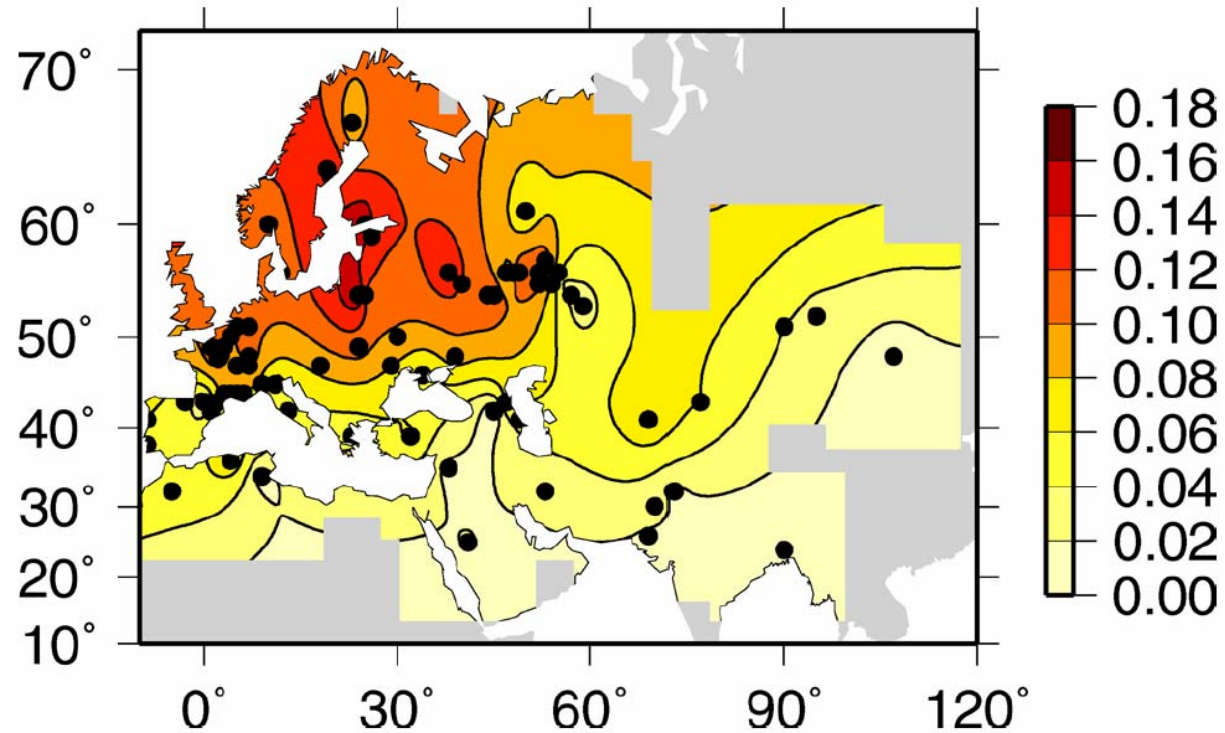


Hawks et al. (2007) Recent acceleration of human adaptive evolution. PNAS 104.

# ヒトにおける淘汰圧

- ヨーロッパに北上した集団における環境適応
  - 皮膚: Ding Y-C, et al. (2002) PNAS 99:309–314.
  - 寒冷適応: Wang E et al. (2004) Am. J. Hum. Genet. 74:931-944.
  - 食事: Akey JM et al. (2004) PLoS Biol 2:e286.
- 農耕の発達にともなう淘汰圧
  - 病気: Wang ET et al. (2006) PNAS 103: 135-140.
  - 食事の変化: Bersaglieri T et al. (2004) Am. J. Hum. Genet. 74:1111-1120
- 文化の発達(後期更新世)
  - 死亡率は低下したが、繁殖における分散が拡大
  - コミュニケーション、社会的相互作用、創造性への淘汰

# HIV抵抗性対立遺伝子頻度の変異

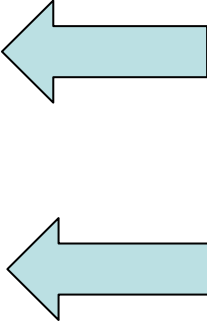


**Figure 1.** Shaded Contour Map of  $\Delta 32$  Allele Frequency Data

The sampling locations are marked by black points. The interpolation is masked in regions where data are unavailable.

DOI: 10.1371/journal.pbio.0030339.g001

# 弱有害変異の平衡頻度

$$p = \sqrt{\frac{\mu}{s}}$$


多くの機能的遺伝子では  
ほとんど無視できるレベル

突然変異率：  
寿命が延びることで増加

淘汰の強さ：  
寿命が延びることで減少

ほぼ中立であり、決定論的  
なこの公式はあてはまらない

ヒト集団はおそらく平衡状態ではない。淘汰圧は変動している。  
環境や他の遺伝子との相互作用が、重要な場合が少なくない。

# まとめ：変異を保つ仕組み

- 中立なプロセス
  - 中立な突然変異の新生と消失のバランス
- 自然選択
  - 弱有害突然変異の新生と除去のバランス
  - 選択圧の変動
  - 個体数の増加