

# Lecture 11: Selection on the Environmental variance

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Synbreed course  
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# Scales of Environmental sensitivity

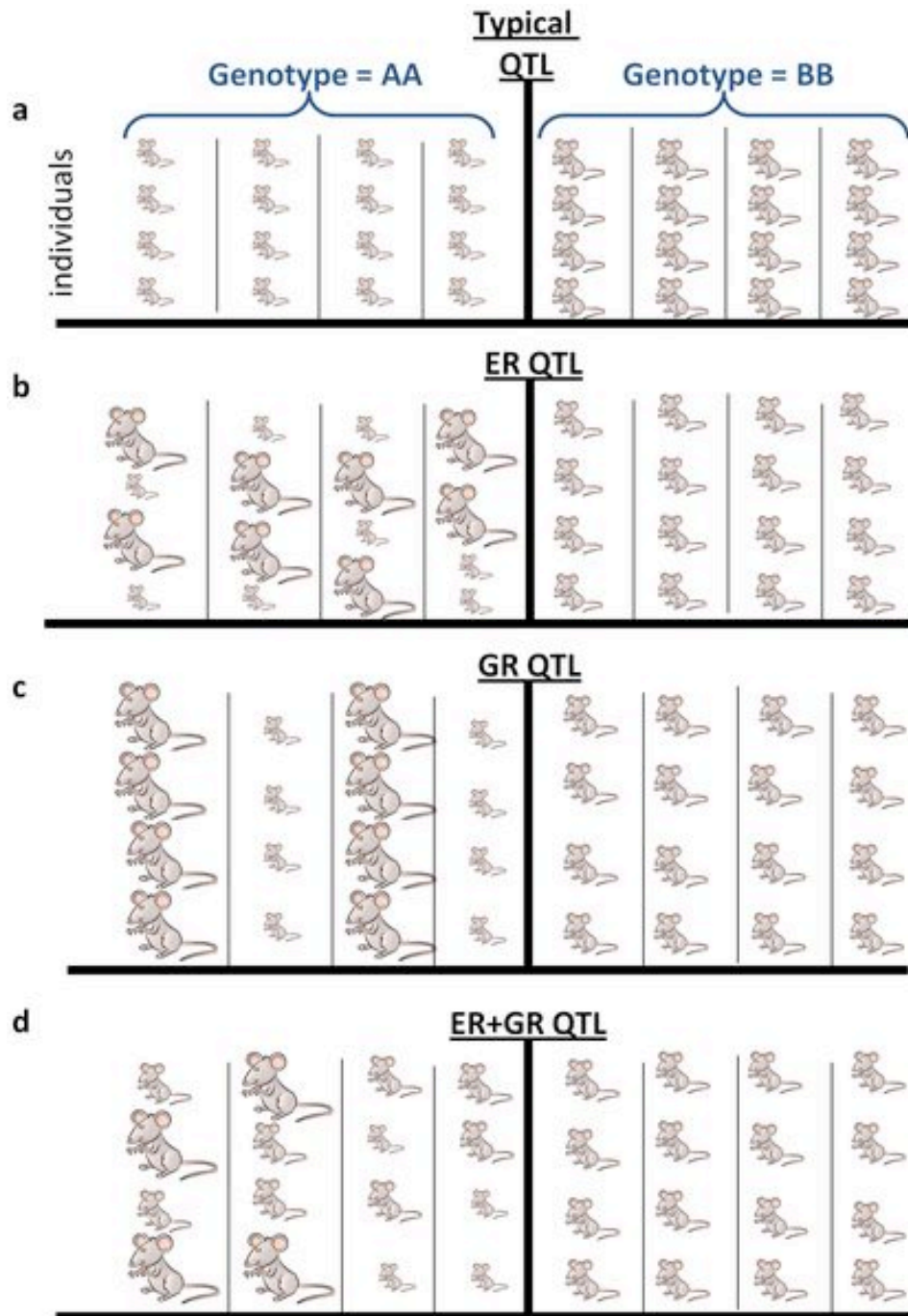
- Clones (pure lines) typically show differential (relative) performance across macroenvironments,
  - evidence of  $G \times E$
- Genotypes can also show variation in their sensitivity to microenvironmental differences,
  - Fluctuating asymmetry
  - Developmental noise

# Environmental vs. genetic canalization

- Waddington (1942) suggested the development systems become buffered over time to be somewhat robust to environmental and/or genetic noise
- Environmental canalization
  - A genotype has robust performance over a set of microenvironments ( $G \times E$ )
- Genetic canalization
  - A particular genotype (one or several loci) has robust performance when randomized over genetic backgrounds (epistasis)

# Fraser & Schadt's experiment

- Using variation within and between a series of inbred lines, one can distinguish between genetic and environmental robustness (canalization)
- Fraser & Schadt examined mRNA levels at thousands of genes for their traits over a series of inbred lines of mice
- Environmental robustness means that the trait will have reduced within-line variation
- Genetic robustness implies that the mean trait value over lines (the between-line variance) is reduced

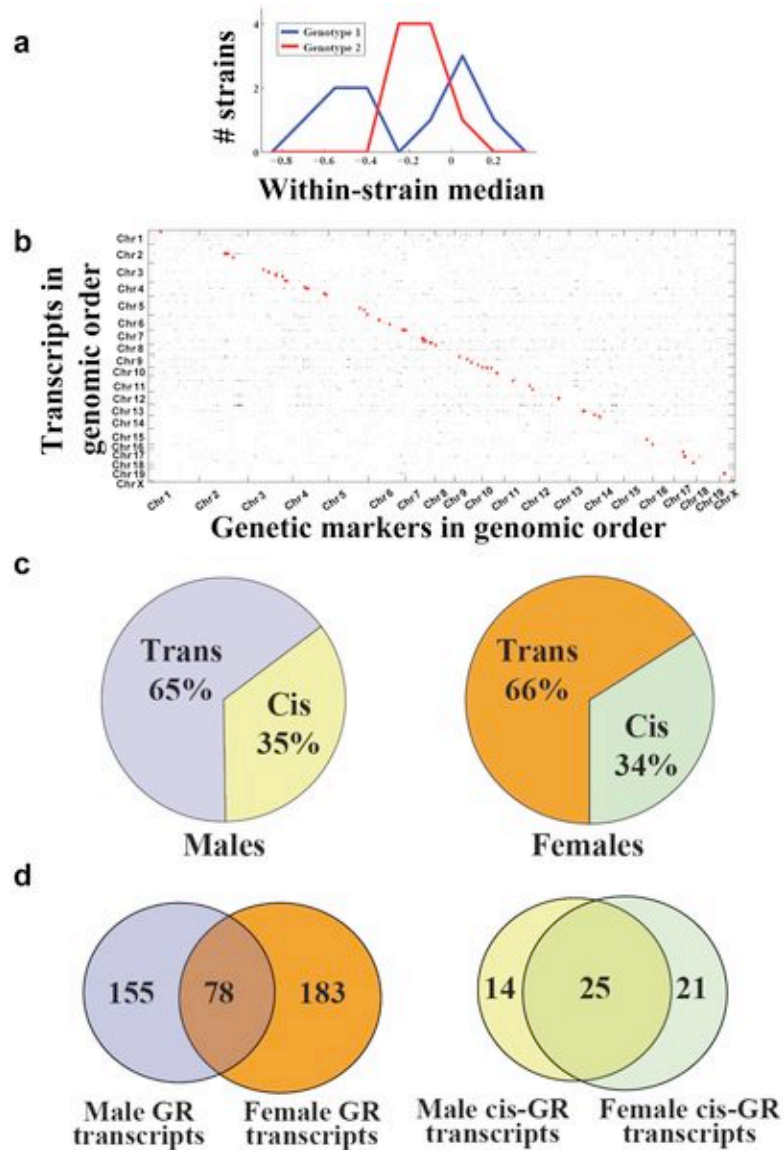


Their design: eQTLs were mapped and then examined both within (down a row) and across lines (across rows)

Environmental robustness (ER) QTLs: within-line variation, no between-line

Genetic robustness (GR) QTLs: Between-line variation, no within-line

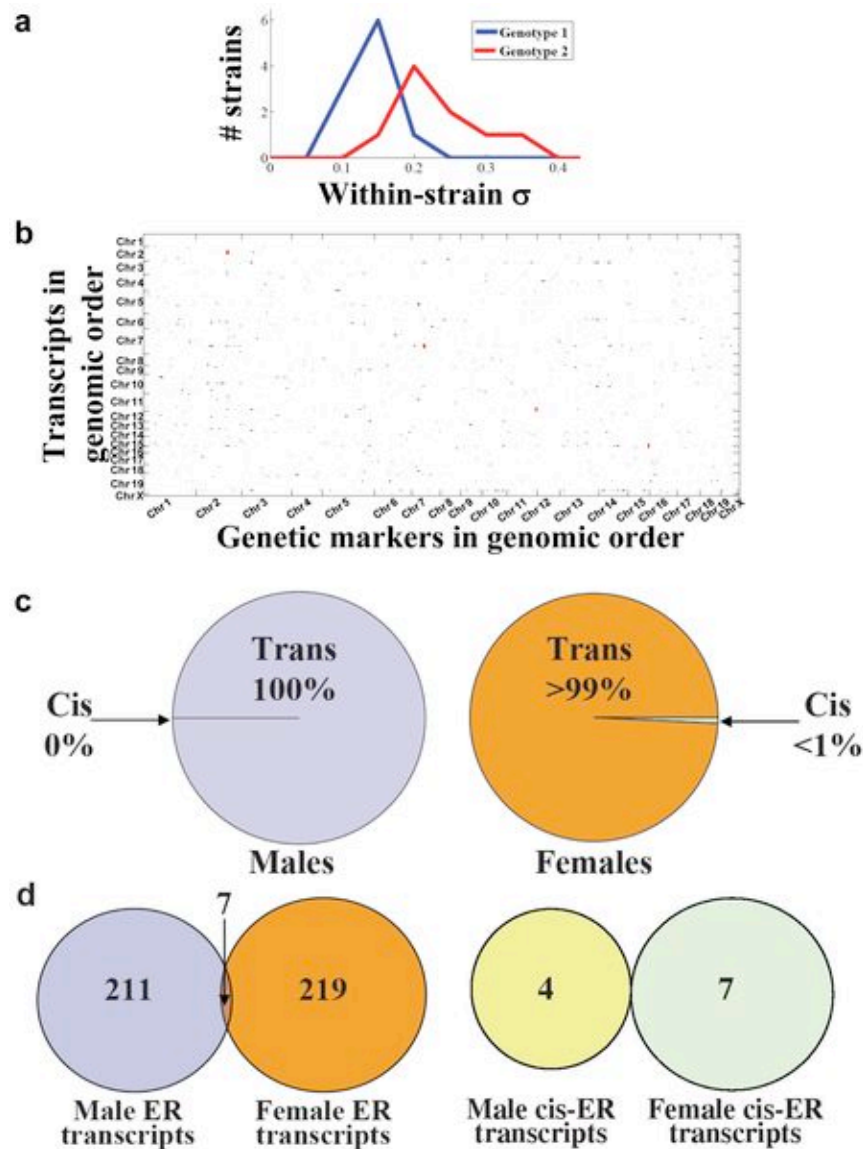
Figure 2. Genetic robustness QTLs in mouse.



GR QTLs tend to be mainly trans-acting, modest sex-specific overlap.

When present, due to Cis-acting factors

Figure 3. Environmental robustness QTLs in mouse.



ER QTLs trans-acting, No sex-specific overlap.

No overlap between ER, GR QTLs, Hence, appears to be different pathways for genetics vs environmental robustness

# Evidence for genetic variation in ER

- Inbred lines differ in  $\text{Var}(E)$
- Sire differences (in cattle) for variation in their offspring
  - Could also simply be due to major genes segregating in that sire
- Specific QTL mapping
  - Early QTL experiments showed marker effects on variance
  - Direct mapping of such vQTLs in more recent studies



# Selection on the environmental variance

- Genotypes can differ in their **environmental variances**
  - Example: Different inbred lines show different variances
  - Different QTL genotypes can show different trait variances
- Can get response to selection on the environmental variance
  - Response for increased canalization (greater left-right symmetry in traits like bristle number in flies)
- Hence, selection on a trait can also potentially change its environmental variance

# Modeling breeding values of $\text{Var}(E)$

- Assuming that the environmental variation is like any other complex trait, it has a breeding value (passed from parent of offspring) and residual values that are not
- Several different ways to model the genetic structure of the environmental variance

# Models of heritable environmental variation

- Base model is  $P = G + E$ , where  $E$  now varies over genotypes and hence we can speak of a breeding value for  $E$
- Gavrilets-Hastings multiplicative model
  - $E = \gamma_i * e$ , where  $e \sim (0, \sigma_e^2)$
  - A genotype-specific effect  $\gamma$  (sensitivity) + noise ( $e$ )
  - Hence,  $\text{Var}(E | G, \gamma) = \gamma^2 * \sigma_e^2$
  - Simplest approach  $\gamma = A_v$ , the BV for variance
    - Hence,  $\text{Var}(E | G, A_v) = A_v^2 * \sigma_e^2$

# Multiplicative Model (cont)

- Total environmental variance (for population)
  - $\sigma_E^2 = (\mu_\gamma^2 + \sigma_\gamma^2) * \sigma_e^2$
- Selecting  $\mu_\gamma$  to zero minimizes pop environmental variance
- When  $\gamma = A_v + D_v$ , (dominance in environmental sensitivity), then
  - $\sigma_E^2 = (\mu_{A_v}^2 + \sigma_{A_v}^2) * \sigma_e^2 + \sigma_{D_v}^2 * \sigma_e^2$
  - selection can decrease mean of  $A_v$  and also its variance (by generating negative LD), but can't impact the **dominance** term

# The exponential model

- $E = \exp(A_v/2) * e$ 
  - Where  $e \sim N(0, \sigma_e^2)$ ,  $A_v \sim N(\mu_{A_v}, \sigma_{A_v}^2)$ ,
- Also called the log-additive model, as
  - $\ln(\sigma^2(E | A_v)) = \ln(\sigma_e^2) + A_v$
- Environmental variation for the population
  - $\sigma_E^2 = \sigma_e^2 \exp(\mu_{A_v} + \sigma_{A_v}^2/2)$
  - Under this model, decreasing the mean (to negative values) continues to decrease the variance

# The additive model

- While the multiplicative and exponential models ensure a non-zero variance, they can be hard to work with
- The **additive model** is easier to use but does not ensure a positive environmental variance
  - Here,  $\sigma_E^2 = \sigma_e^2 + \mu_{A_v}$

$$E = U \cdot \sqrt{\sigma_e^2 + A_v}, \quad \text{where } U \sim N(0, 1) \quad \text{and} \quad A_v \sim N(\mu_{A_v}, \sigma_{A_v}^2)$$

**Table 13.3.** Models for heritable variation in the environmental value  $E$ . The basic model is  $z = \mu + A_m + E$ , where  $z$  is the trait value and  $A_m \sim N(\mu_{A_m}, \sigma_{A_m}^2)$  the breeding value for trait value. The table gives the assumed form of  $E$  for different models as a function of the breeding value in variance  $A_v \sim N(\mu_{A_v}, \sigma_{A_v}^2)$ , some intrinsic environmental value  $e \sim N(0, \sigma_e^2)$ , and the unit normal  $U \sim N(0, 1)$ .

Model	$E$	$\sigma^2(E   A_v)$	$\sigma^2(E)$
Multiplicative	$A_v e$	$A_v^2 \sigma_e^2$	$(\mu_{A_v}^2 + \sigma_{A_v}^2) \sigma_e^2$
Exponential (or log-additive)	$\exp(A_v/2) e$	$\sigma_e^2 \exp(A_v)$	$\sigma_e^2 \exp[\mu_{A_v} + \sigma_{A_v}^2/2]$
Additive	$\sqrt{A_v + \sigma_e^2} \cdot U$	$A_v + \sigma_e^2$	$\mu_{A_v} + \sigma_e^2$

Under the additive model, we can define a heritability in  $\text{Var}(E)$  as

$$h_v^2 = \frac{\sigma(A_v, z^2)}{\sigma^2(z^2)}$$

Under normality assumptions,

$$h_v^2 = \frac{\sigma^2(A_v)}{2\sigma_z^4 + 3\sigma_{A_v}^2}$$

Average heritability is small (0.038), but potential for response is significant, its evolvability  $CV(A) = 0.41$ . Thus, while the actual response can be small, the percentage increase in the trait is not

here,  $CV(A)^2 = 0.16$  is the expected change in the trait mean given a standard unit of selection

Breeding values for trait mean, trait  $\text{Var}(E)$  tends to be negatively correlated ( $r \sim -0.24$ )

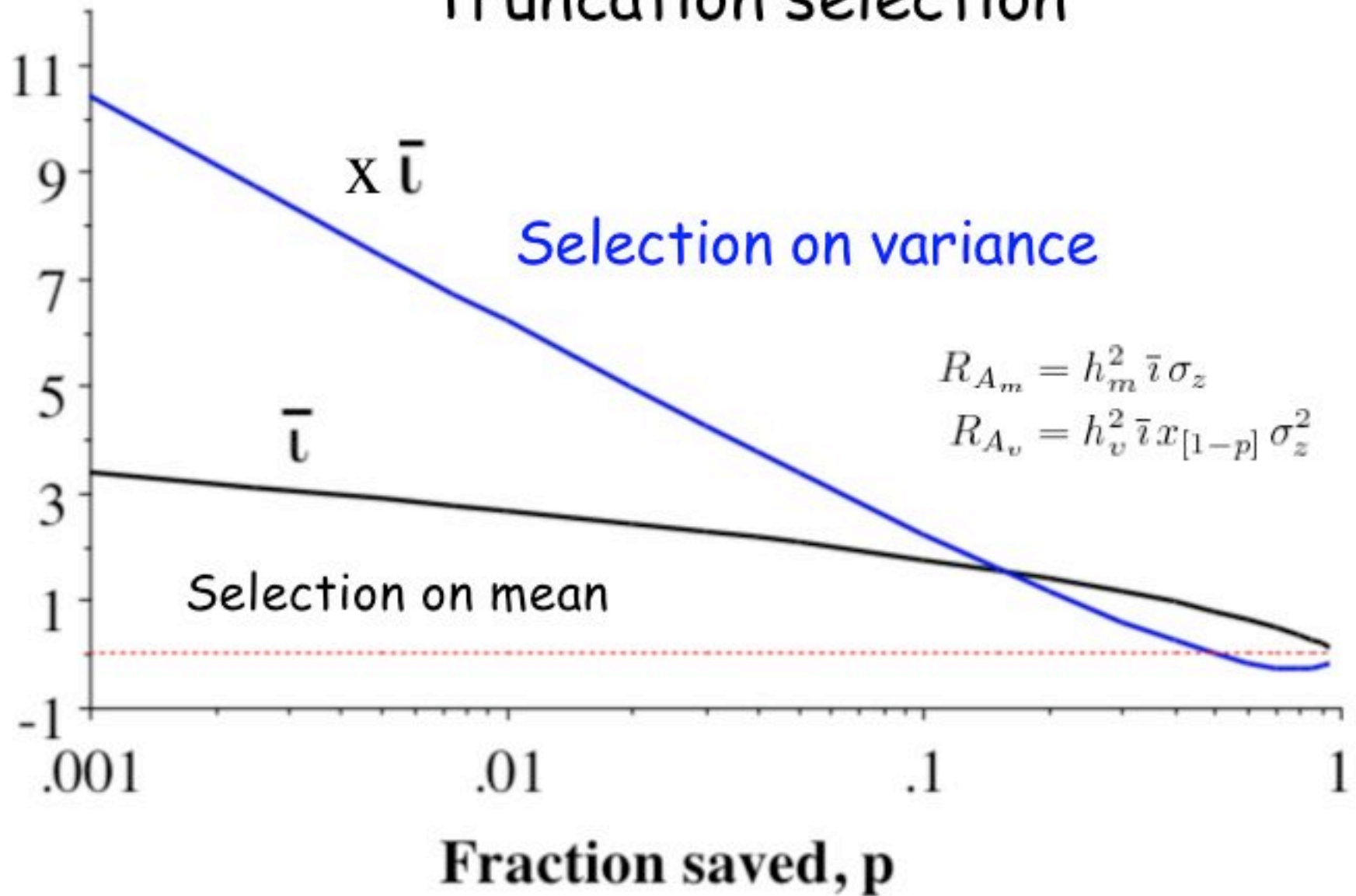


Species	Trait	$h_v^2$	$CV_{A_v}$	$\rho$	Reference
Pig ( <i>Sus</i> )	Meat pH	0.039	0.40	0.79	SanCristobal-Gaudy et al. (1998)
	Litter size	0.026	0.31	-0.62	Sorensen & Waagepetersen (2003)
		0.021	0.27	-0.64	Yang et al. (2011)
		0.012	0.19	0.70	Yang et al. (2011), BC
	Weight	0.011	0.34	-0.07	Ibáñez-Escriche et al. (2008c)
Sheep ( <i>Ovis</i> )	Litter size	0.048	0.51	0.19	SanCristobal-Gaudy et al. (2001)
Snail ( <i>Helix</i> )	Body weight	0.017	0.58	-0.81	Ros et al. (2004)
Chicken ( <i>Gallus</i> )	Body weight (male)	0.029	0.30	-0.17	Rowe et al. (2006)
		0.046	0.49	-0.45	Mulder et al. (2009)
		0.030	0.32	-0.23	Wolc et al. (2009)
	Body weight (female)	0.031	0.32	-0.11	Rowe et al. (2006)
		0.047	0.57	-0.41	Mulder et al. (2009)
		0.038	0.37	-0.27	Wolc et al. (2009)
Rabbit ( <i>Lepus</i> )	Litter Size	0.045	0.42	-0.74	Ibáñez-Escriche et al. (2008b)
		0.041	0.37	-0.73	Yang et al. (2011)
		0.017	0.24	0.28	Yang et al. (2011), BC
	Birth weight	0.013	0.25	—	Garreau et al. (2008)
Mouse ( <i>Mus</i> )	Litter size	0.048	0.44	-0.93	Gutierrez et al. (2006)
	Litter weight	0.039	0.37	-0.81	Gutierrez et al. (2006)
	Birth weight	0.208	1.21	0.97	Gutierrez et al. (2006)
	Body weight	0.006	0.36	-0.31	Ibáñez-Escriche et al. (2008a)
	Weight gain	0.018	0.47	-0.19	Ibáñez-Escriche et al. (2008a)
Average		0.038	0.41	-0.24	

# Selection response

- Assume the additive model for  $\text{Var}(E)$  and consider truncation selection with the upper  $p$  saved. Hill & Zhang (2004) showed that the probability  $P(a,b)$  that a genotype with mean value  $\mu + a$  and variance effect  $\sigma^2 + b$  is selected is
- $P(a,b)/p \sim 1 + a (i/\sigma_z) + (b/2) i x_{[1-p]} / \sigma_z^2$
- Where  $i$  is the selection intensity and  $x_{[1-p]}$  is defined by  $P(\text{unit normal} > x_{[1-p]}) = p$ .
- Hence, direction selection favors higher  $\text{Var}(E)$

# Truncation selection



# Selection response (additive model)

Assume the additive model for  $\sigma_E^2$  (Equation 13.26b) and truncation selection on a normally-distributed trait. Recall (Equation 10.26) that for a given fraction  $p$  saved under truncation selection on a normally-distributed trait, the selection intensity is  $\bar{i} = \varphi(x_{[1-p]})/p$ , where  $\varphi(x)$  is the unit normal distribution function evaluated at  $x$ , while for a unit normal  $U$   $x_{[1-p]}$  satisfies  $\Pr(U \geq x_{[1-p]}) = p$ . For the special case where  $A_m$  and  $A_v$  are uncorrelated, the expected responses become simply

$$R_{A_m} = h_m^2 \bar{i} \sigma_z \quad (13.31a)$$

$$R_{A_v} = h_v^2 \bar{i} x_{[1-p]} \sigma_z^2 \quad (13.31b)$$

where  $h_m^2$  is the heritability for trait mean and  $h_v^2$  is the heritability for the additive component of trait variance (Equation 13.27b). Equation 13.31a is simply our standard result for the change in mean under truncation selection, while 13.31b is the analog for the change in the breeding value of the variance (under the additive model).

Hence strong directional selection (by selecting outliers) can result in a significant increase in  $\text{Var}(E)$ , reducing  $h^2$ .

**Example 13.8.** Consider a trait with  $h_m^2 = 0.3$  and  $h_v^2 = 0.03$  (which is a typical value of the known estimates, see Table 13.4). Suppose  $\sigma_z^2 = 100$ . What is the expected response in the mean and  $\sigma_E^2$  following a single generation of truncation selection with  $p = 0.1$ ? Noting that  $\Pr(U > 1.282) = 0.1$ , we have  $x_{[1-p]} = 1.282$  and  $\bar{i} = \varphi(1.282)/0.1 = 1.755$ , giving

$$R_{A_m} = 0.3 \cdot 1.755 \cdot 10 = 5.265, \quad \text{and} \quad R_{A_v} = 0.03 \cdot 1.755 \cdot 1.282 \cdot 100 = 6.750$$

Here selection increased the mean by 5.3 and the environmental variance by 6.75. Now consider stronger selection,  $p = 0.01$ . Here  $x_{[1-p]} = 2.326$  and  $\bar{i} = 2.666$ , giving

$$R_{A_m} = 0.3 \cdot 2.666 \cdot 10 = 7.998, \quad \text{and} \quad R_{A_v} = 0.03 \cdot 2.666 \cdot 2.326 \cdot 100 = 18.603$$

This is roughly a 50% increase in the mean, but a 275% increase in the variance.

# Artificial selection

- An increase in the environmental variance is often seen following several generations of directional selection
- As the models show, this is expected when there is heritable variation in  $\text{Var}(E)$  and is expected to be more dramatic the stronger the directional selection

# Stabilizing selection

- Selection to minimize deviations from some optimal value can occur through three pathways
  - Change the mean to the optimal value
  - Reduce the additive genetic variation (generation of negative LD)
  - Reduce the environmental variance



# Stabilizing selection (cont)

Assume  $W(z) = 1 - s(z - \theta)^2$ . Multiplicative model

$$\begin{aligned}W(A_m, A_v) &= 1 - s \mathbb{E} [(A_m + A_v e - \theta)^2] \\&= 1 - s [(A_m - \theta)^2 + 2(A_m - \theta)A_v \mathbb{E}[e] + A_v^2 \mathbb{E}(e^2)] \\&= 1 - s [(A_m - \theta)^2 + A_v^2 \sigma_e^2]\end{aligned}\tag{13.29b}$$

Thus, under phenotypic stabilizing selection, there is selective pressure to shift the breeding value of the trait towards  $\theta$  and to decrease  $A_v$  towards zero (and hence direct selection to decrease  $\sigma_E^2$ ). There are two important consequences of this. First, the reduction in phenotypic variance can be much greater than predicted from the simple reduction in the additive variance from the Bulmer effect. Second, there can be cases where the heritability will *increase* under stabilizing selection. Since both additive and environmental variances are decreased, if the decrease in environmental variance is sufficiently larger,  $h^2$  can actually increase.



# Direct selection on $\text{Var}(E)$ using repeated records

- While direct and stabilizing selection apply indirect selection on  $\text{Var}(E)$ , direct selection can be applied for traits with repeated records
- Construct an index  $I$  for each individual which amounts to their sample variance in the records, then selection on  $I$  directly

$$I_i = \frac{1}{n-1} \sum_{j=1}^n (z_{ij} - \bar{z}_i)^2,$$

## Assuming the exponential model for the variance

$$R_{A_a} \simeq \bar{i} \frac{\sigma^2(A_v)}{\sqrt{\exp[\sigma^2(A_v)] [(n+1)/(n-1)] - 1}},$$

A related design is to select based on variation in a trait value among the *offspring* of an individual. For example, Garreau et al. (2008) selected rabbit dams based upon Equation 17.11, but now the observations were the weights of her offspring (suitably corrected for fixed effects such as litter size and parity). As mentioned previously, offspring mortality is lower within litters with more similar weights, and such selection conceivably occurs in natural populations as well. Here the multiple records are based on individuals with potentially different genotypes, and hence a large litter variance could arise from a high breeding value for  $\sigma_{E'}^2$ , segregation of a major gene, nonadditive variance, or (most likely) some combination of these. Garreau et al. observed a significant response in the first generation in both up- and down-selected lines. In subsequent generations, the selection pressure was weaker in their experiment, but response was largely flat. While these data are consistent with a response in  $\sigma_{E'}^2$ , the majority of the initial response may simply arise from selection for, or against, females heterozygous for major genes influencing weight.