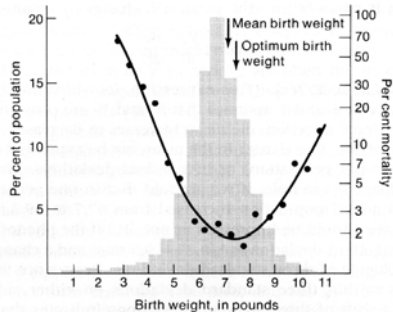


**STABILIZING SELECTION ON HUMAN BIRTH WEIGHT**



See Box 8.2 "Mapping the Fitness Landscape" in Z&E

FROM: Cavalli-Sforza & Bodmer 1971

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**STABILIZING SELECTION ON THE GALL FLY, *Eurosta solidaginis***




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**GALL DIAMETER IS VARIABLE AND HERITABLE**

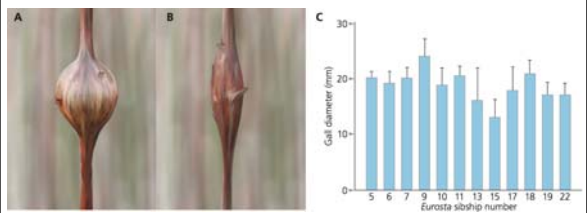


Fig. 8.10 Z&E

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STABILIZING SELECTION ON THE FLY, *Eurosta solidaginis*



Parasitoid Wasp –  
*Eurytoma gigantea*

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STABILIZING SELECTION ON THE FLY, *Eurosta solidaginis*



Downy woodpecker

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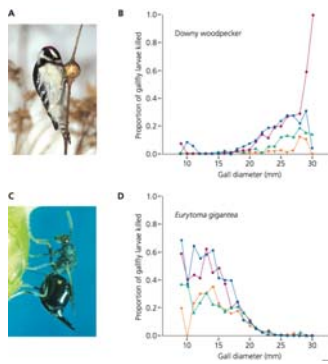
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STABILIZING SELECTION ON GALL SIZE



Intermediate size favored

Fig. 8.11 Z&E

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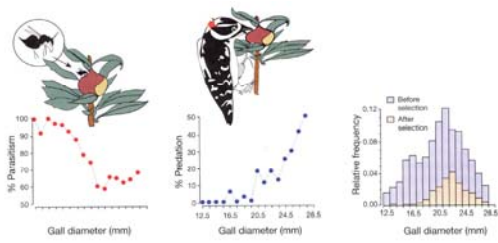
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**STABILIZING SELECTION ON THE FLY, *Eurosta solidaginis***



Two sources of mortality from predators:

- Parasitoid wasps
- Hungry Birds

FROM: Weis & Abrahamson (1996) IN: F & H 2001

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**DISRUPTIVE SELECTION**



*Pyrenestes o. ostrinus*

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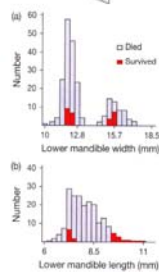
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**DISRUPTIVE SELECTION**

- Disruptive selection on bill size in the black-bellied seedcracker (*Pyrenestes o. ostrinus*)
- Juvenile birds that survive are those with *either* relatively small or relatively large beaks



FROM: Smith (1993) IN: F & H 2001

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Quantitative trait locus (QTL) analysis:

Establishing the linkage between traits and genes

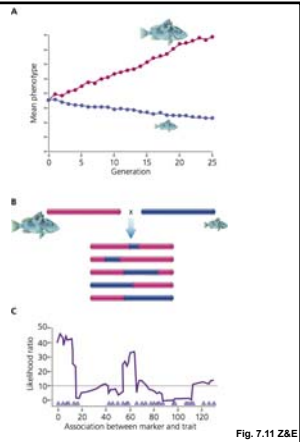


Fig. 7.11 Z&E

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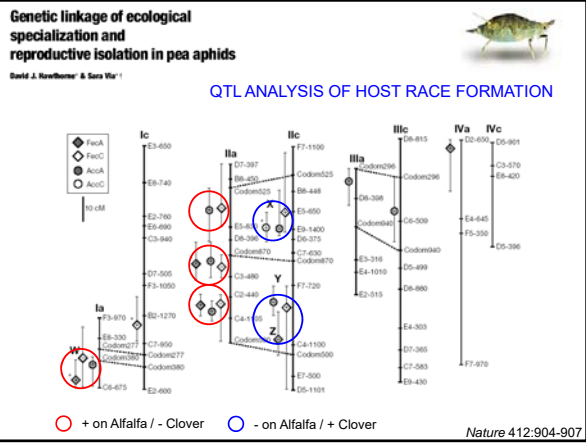
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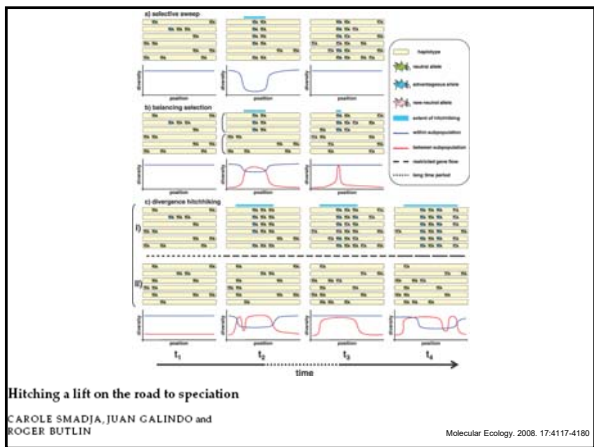
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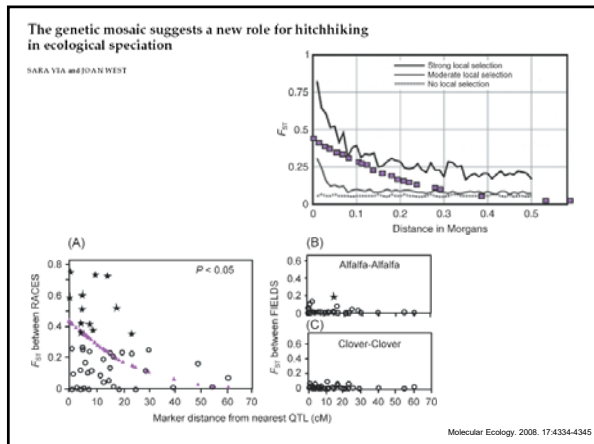
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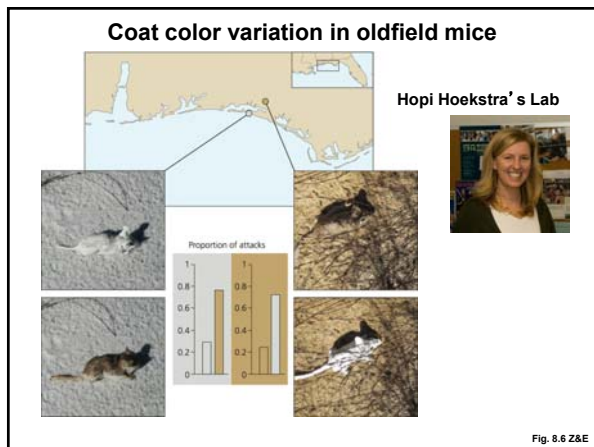
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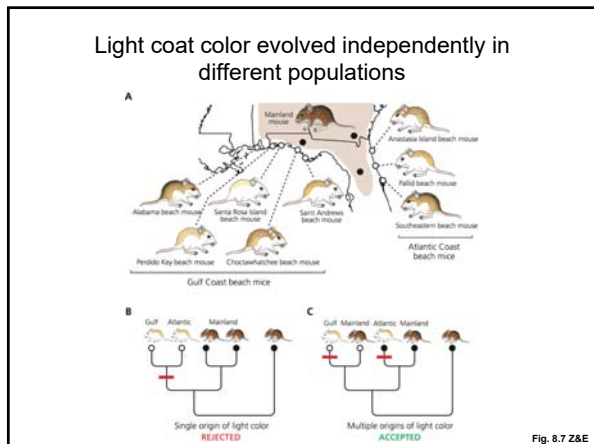
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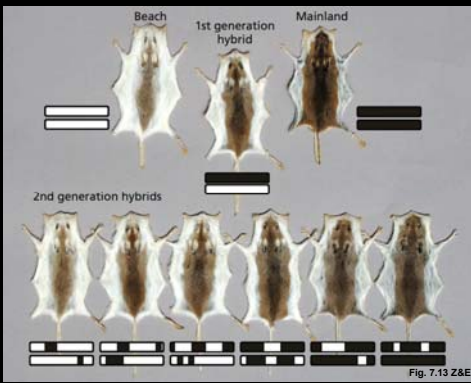
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### QTL analysis of coat color in mice




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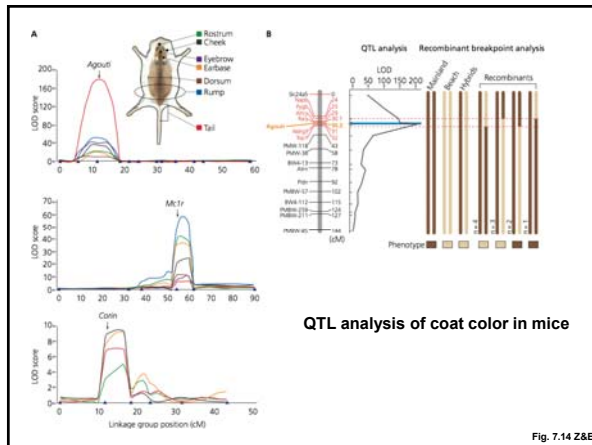
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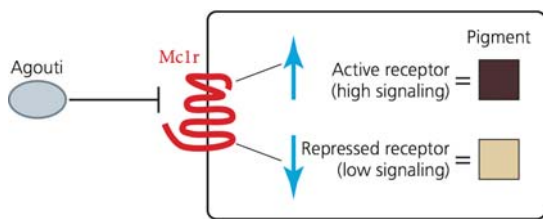
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Much of the variation in coat color is explained by differences in two genes



*Corin* also explains a small amount of variation

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▪ Expression of *Agouti* during development influences coat color

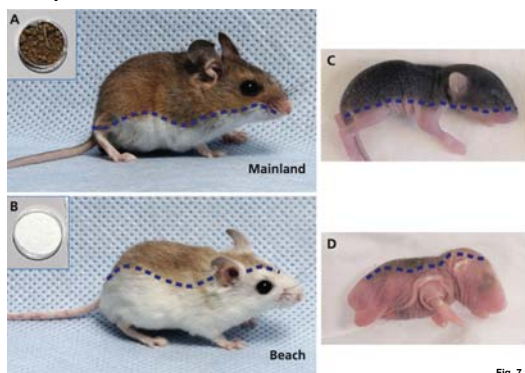


Fig. 7.16 Z&E

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**FUTURE STUDIES OF SPECIATION:**

- Quantitative Trait Loci (QTL) mapping in monkey flowers.
- QTL analysis is a powerful approach to dissecting the genetic basis of traits directly associated with pre- and post-zygotic isolation.



Characteristic	<i>M. cardinalis</i>	<i>M. lewisii</i>
Purple pigment (anthocyanins) in petals	high	low
Yellow pigment (carotenoids) in petals	low	high
Corolla width	low	high
Petal width	low	high
Nectar volume	high	low
Nectar concentration	low	high
Stamen (male structure) length	high	low
Pistil (female structure) length	high	low

Notes:

- The yellow pigment in *M. lewisii* petals is arranged in stripes called nectar guides, which are interpreted as a "smile" for bees as they land on the wide petals.
- Nectar volume and concentration are thought to contrast in bird- and bee-flowers simply because of the enormous difference in body size (hummingbirds can drink a lot more).
- The difference in stamen and pistil length is important: in *M. cardinalis* these structures extend beyond the flower and make contact with the hummingbird's forehead as it feeds.

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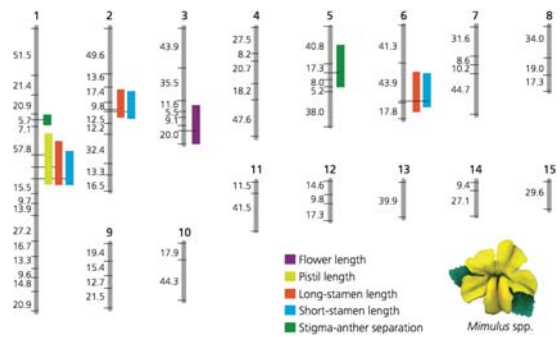
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QTL analysis of floral traits in *Mimulus*



See Fig. 7.12 Z&E

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### PRICE'S RULE

- The directional selection differential for a character is equal to (and can be measured by) the covariance of individual phenotypes with relative fitness.

$$S = \text{Cov}(\text{relative fitness, phenotype})$$

$$S = \frac{1}{N} \sum [(w_i - \bar{w})(P_i - \bar{P})]$$

- Where  $w_i$  = relative fitness of individual i  
= absolute fitness of i / mean absolute fitness  
 $\bar{w}$  = population mean relative fitness = 1  
 $P_i$  = phenotypic measurement of individual i  
 $\bar{P}$  = population mean phenotype

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### FISHER'S FUNDAMENTAL THEOREM OF NATURAL SELECTION

- The rate of evolution of mean population fitness is equal to the additive genetic variance in relative fitness.



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### FISHER'S FUNDAMENTAL THEOREM OF NATURAL SELECTION

- From Price's Rule, if the character of interest is fitness itself, then the directional selection differential on fitness itself is,

$$S = \text{average value of } [(w_i - \bar{w})(P_i - \bar{P})]$$

$$= \text{average value of } [(w_i - \bar{w})(w_i - \bar{w})]$$

$$= \text{Var}(w_i) = \text{phenotypic variance in relative fitness}$$

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**FISHER'S FUNDAMENTAL THEOREM OF NATURAL SELECTION**

From the Breeder's equation,  $R = h^2S$ ,  
Response of relative fitness to selection,  $R$   
= heritability of relative fitness x  $S$   
=  $\frac{\text{additive genetic variance of } w}{\text{Var}(w_i)} \times \text{Var}(w_i)$   
= **additive genetic variation in fitness**

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**FISHER'S FUNDAMENTAL THEOREM OF NATURAL SELECTION**

- If there is any genetic variance in fitness in a population, then natural selection will act on it.
- Strong directional selection on fitness is expected to erode genetic variance in fitness.
- However, in natural populations there still seems to be genetic variance for fitness related traits.

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**THE INPUT OF VARIATION BY MUTATION**

How much variation for quantitative characters is introduced by mutation each generation?

$V_m$  = mutational variance = genomic mutation rate (per gen.) x average squared mutation effect

$V_e$  = environmental variance for the trait

$V_m / V_e$  = **MUTATIONAL HERITABILITY**

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**THE RATE OF POLYGENIC MUTATION**

Species	Characters	$V_m/V_e$
Drosophila	Bristle numbers	0.0017
Daphnia	Life-history traits	0.0017
Tribolium	Pupal weight	0.0091
Mouse	Skull measures	0.0111
	Limb bones	0.0234
	Growth rate	0.0160
Corn	Vegetative and reproductive traits	0.0051
Rice	Vegetative and reproductive traits	0.0031

FROM: Lynch, M. 1988. Genetical Res. 51:137-148

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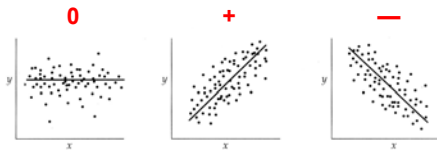
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**CORRELATIONS AMONG CHARACTERS OR RELATIVES**



**Covariance:**

$$Cov(x, y) = \frac{1}{N} \sum (x_i - \bar{x})(y_i - \bar{y})$$

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**CONSTRAINTS DUE TO TRADE-OFFS**

- Negative correlations among life-history traits may constrain evolution and maintain genetic variation.
- This is called the **Antagonistic – Pleiotropy** hypothesis.

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**WHAT ARE THE LIMITS TO PHENOTYPIC EVOLUTION?**

“A slow sort of country!” said the Queen. “Now, *here*, you see, it takes all the running *you* can do, to keep in the same place. If you want to get somewhere else you must run at least twice as fast as that”



From *Alice in Wonderland*  
Lewis Carroll

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The **Red Queen** may permanently prevent populations from evolving to maximum fitness



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**WHAT ARE THE EVOLUTIONARY CONSEQUENCES OF SMALL POPULATION SIZE?**



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### THE PRIMARY **GENETIC** CONSEQUENCES OF SMALL POPULATION SIZE

- Loss of additive genetic variance and heterozygosity within populations.
- Divergence of mean phenotypes among isolated subpopulations (random genetic drift)
- Reduction in mean fitness due to consanguineous matings (inbreeding resulting from exposure of deleterious recessive alleles).
- Long-term accumulation of deleterious mutations and eventual extinction due to “mutational meltdown”.

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TABLE 7.1 Recorded extinctions, 1600 to the present

Taxon	Recorded extinctions <sup>a</sup>			Total	Approximate number of species	Percentage of taxon extinct
	Mainland <sup>b</sup>	Island <sup>b</sup>	Ocean			
Mammals	30	51	4	85	4,000	2.1
Birds	21	92	0	113	9,000	1.3
Reptiles	1	20	0	21	6,300	0.3
Amphibians <sup>c</sup>	2	0	0	2	4,200	0.05
Fishes <sup>d</sup>	22	1	0	23	19,100	0.1
Invertebrates <sup>e</sup>	49	48	1	98	1,000,000+	0.01
Flowering plants <sup>f</sup>	245	139	0	384	250,000	0.2

Source: After Reid and Miller 1989; data from various sources.

<sup>a</sup> Numerous additional species have presumably gone extinct without ever being recorded by scientists.

<sup>b</sup> Mainland areas are those with landmasses of 1 million km<sup>2</sup> or greater (the size of Greenland or larger); smaller landmasses are considered islands.

<sup>c</sup> There has been an alarming decrease in amphibian populations in the last 20 years; some scientists believe that many amphibian species are on the verge of becoming extinct.

<sup>d</sup> The figures given are primarily representative of North America and Hawaii.

<sup>e</sup> The numbers for flowering plants include extinctions of subspecies and varieties as well as species.

In: R. B. Primack. 1998. *Essentials of Conservation Biology*. Sinauer

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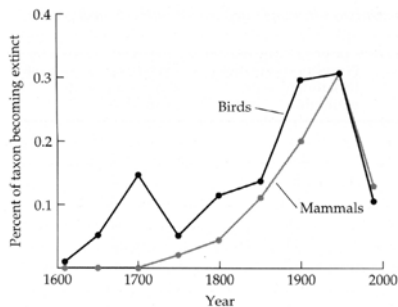
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### EXTINCTION RATES OF BIRDS AND MAMMALS SINCE 1600



In: R. B. Primack. 1998. *Essentials of Conservation Biology*. Sinauer

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TABLE 7.2 Numbers of species threatened with extinction in major groups of animals and plants, and some key families and orders

Group	Approximate number of species	Number of species threatened with extinction	Percentage of species threatened with extinction
<b>VERTEBRATE ANIMALS</b>			
Fishes	24,000	452	2
Amphibians	3,000	59	2
Reptiles	6,000	167	3
Boidae (constrictor snakes)	17 <sup>a</sup>	9	53
Varanidae (monitor lizards)	29 <sup>a</sup>	11	38
Iguanidae (iguanas)	25 <sup>a</sup>	17	68
Birds	9,500	1,029	11
Anseriformes (waterfowl)	109 <sup>a</sup>	36	33
Psittaciformes (parrots)	302 <sup>a</sup>	118	39
Mammals	4,500	505	11
Marsupialia (marsupials)	179 <sup>a</sup>	86	48
Canidae (wolves)	34 <sup>a</sup>	13	38
Cervidae (deer)	14 <sup>a</sup>	11	79
<b>PLANTS</b>			
Gymnosperms	758	242	32
Angiosperms (flowering plants)	240,000	21,895	9
Palmae (palms)	2,820	925	33

Source: Data from Smith et al. 1993 and Mace 1994.  
<sup>a</sup>Number of species for which information is available.

In: R. B. Primack. 1998. *Essentials of Conservation Biology*. Sinauer

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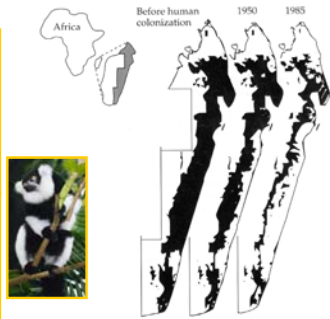
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### DEFORESTATION AND HABITAT FRAGMENTATION IN MADAGASCAR



Extent of eastern rainforest

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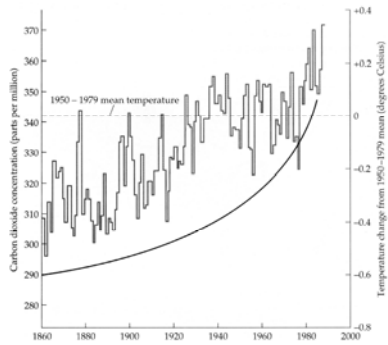
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### CHANGING ENVIRONMENTS: GLOBAL WARMING



In: R. B. Primack. 1998. *Essentials of Conservation Biology*. Sinauer

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The source of our concern over rapidly changing environments, habitat loss, and fragmentation, is the direct relationship between these environmental issues and **human population growth**.

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**CONSERVATION PRIORITIES**

- In the *short-term*, the demographic consequences of small populations are likely to be the more important than genetic consequences.

However,

- In the *long-term*, genetic factors may be more important in determining whether populations are able to persist.

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**GENETIC CONSEQUENCES OF SMALL POPULATIONS**

**I. INBREEDING DEPRESSION**

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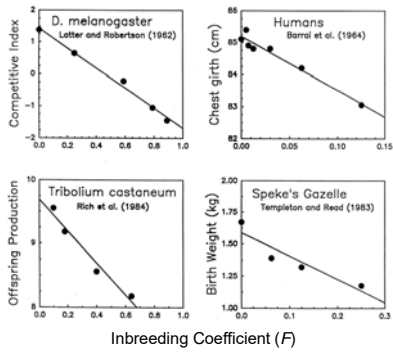
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**Plots of trait value vs. Level of Inbreeding ( $F$ )**




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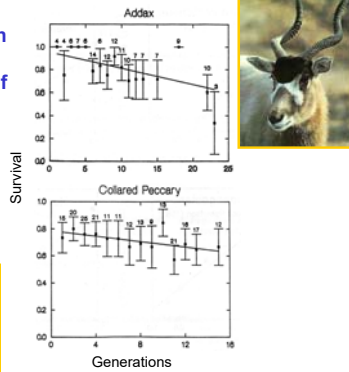
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**Relationship Between Infant Survival and Time Since Closing of the Herd**

- Captive populations of ungulates, Brookfield Zoo, Chicago



FROM: Lacy et al. 1993. In, *The Natural History of Inbreeding and Outbreeding*. Ed. N. W. Thornhill. Univ. Chicago Press

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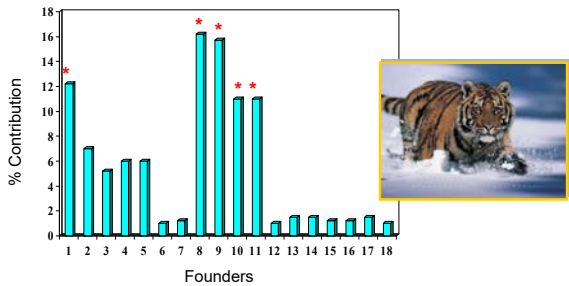
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**Contribution of the 18 founders of the North American zoo population of Siberian tigers to the gene pool in 1981.**



FROM: Foose & Seal (1981).

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**STRATEGIES TO REDUCE THE IMPACT OF SMALL CAPTIVE POPULATIONS**

- Genetic augmentation – Introduction of unrelated individuals to the breeding program. This strategy minimized the reduction in fitness due to inbreeding depression.
- Pedigree analysis – Tracking the reproductive success of individuals with molecular markers to ensure equal contribution to the gene pool. This maximizes the effective population size ( $N_E$ ) and reduces the loss of genetic variation due to drift.

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**GENETIC CONSEQUENCES OF SMALL POPULATIONS**

**II. LOSS OF GENETIC VARIATION**

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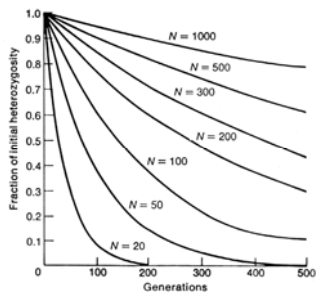
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**LOSS OF HETEROZYGOSITY VS. POPULATION SIZE**



Rate of loss of genetic variation =  $1/2N$  per generation

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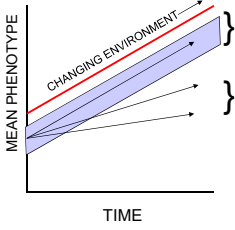
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### CRITICAL RATE OF EVOLUTION



Populations that are able to "track" a changing environment **persist**.

Populations that cannot achieve the critical rate of evolution, decline and eventually go **extinct**.

- Since the level of additive genetic variation ( $V_A$ ) determines the response to selection, populations lacking in  $V_A$  may not be able to respond to persistent environmental changes.

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### INFLUENCE OF RANDOM GENETIC DRIFT AND MUTATION ON ADDITIVE GENETIC VARIANCE ( $V_A$ )

The amount of genetic variance in generation  $t =$

Genetic variance in generation  $t-1$  – loss due to drift + input due to mutation

$$V_{A,t} = V_{A,t-1} - (V_{A,t-1} / 2N) + V_m$$

At equilibrium,  $V_{A,t} = V_{A,t-1}$

$$V_A = 2NV_m$$

- The amount of genetic variation in a population is function of **both** the **population size** and the **mutation rate**.

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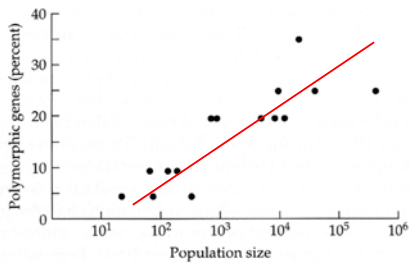
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### GENETIC DIVERSITY AND POPULATION SIZE IN A NEW ZEALAND SHRUB (*Halocarpus bidwillii*)



In: R. B. Primack. 1998. *Essentials of Conservation Biology*. Sinauer

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### THE INPUT OF VARIATION BY MUTATION

- How much variation for quantitative characters is introduced by mutation each generation?

$V_m$  = mutational variance = genomic mutation rate (per gen.) x average squared mutation effect

$V_e$  = environmental variance for the trait

$V_m / V_e$  = **MUTATIONAL HERITABILITY**

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### THE RATE OF POLYGENIC MUTATION

Species	Characters	$V_m / V_e$
Drosophila	Bristle numbers	0.0017
Daphnia	Life-history traits	0.0017
Tribolium	Pupal weight	0.0091
Mouse	Skull measures	0.0111
	Limb bones	0.0234
	Growth rate	0.0160
Corn	Vegetative and reproductive traits	0.0051
Rice	Vegetative and reproductive traits	0.0031

FROM: Lynch, M. 1988. *Genetical Res.* 51:137-148

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### IMPLICATIONS FOR GENETIC CONSERVATION:

- Short term population bottlenecks do not lead to large losses of genetic variation.
- Mutation can replenish lost variation fairly rapidly.
- For a captive population, a doubling in population size ( $N_e$ ) will double the amount of genetic variation that can be maintained.
- Equilibration of family sizes further reduces the effects of drift, resulting in an additional doubling of the level of genetic variation that can be maintained.

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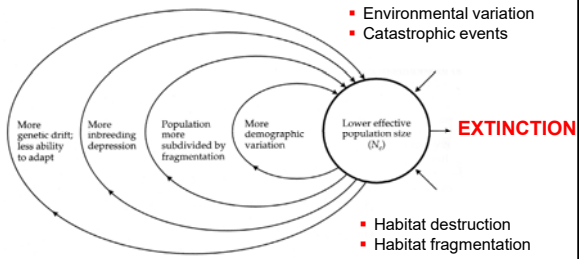
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### THE EXTINCTION VORTEX



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