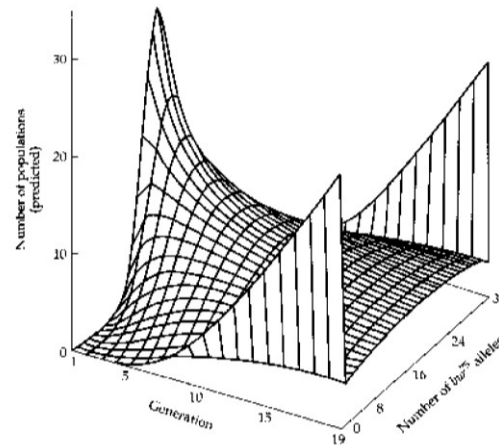
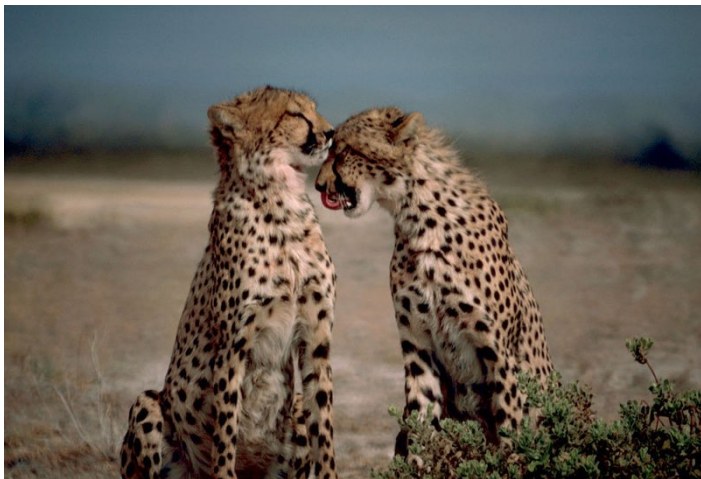
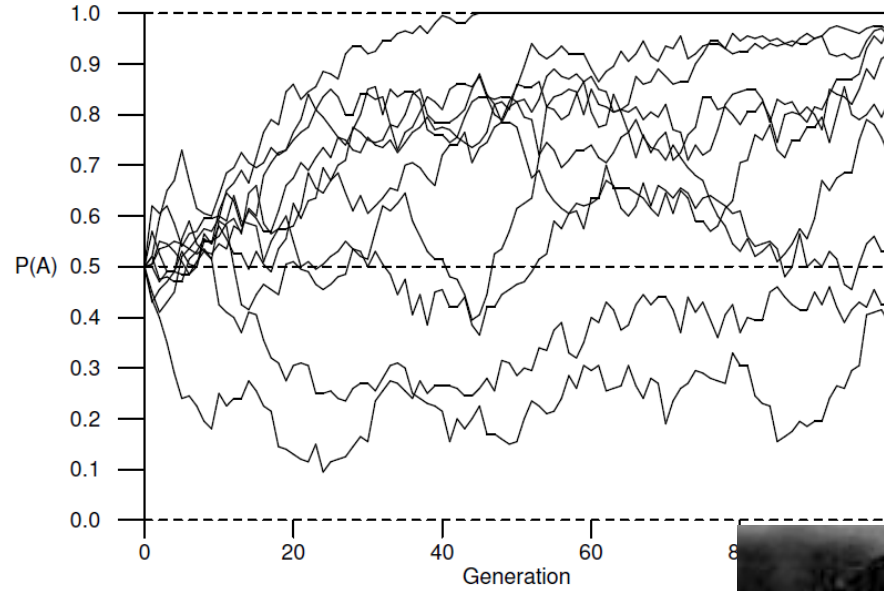


# RANDOM GENETIC DRIFT



HW: infinite population but in real world population sizes finite  
⇒ random processes, nonadaptive evolution

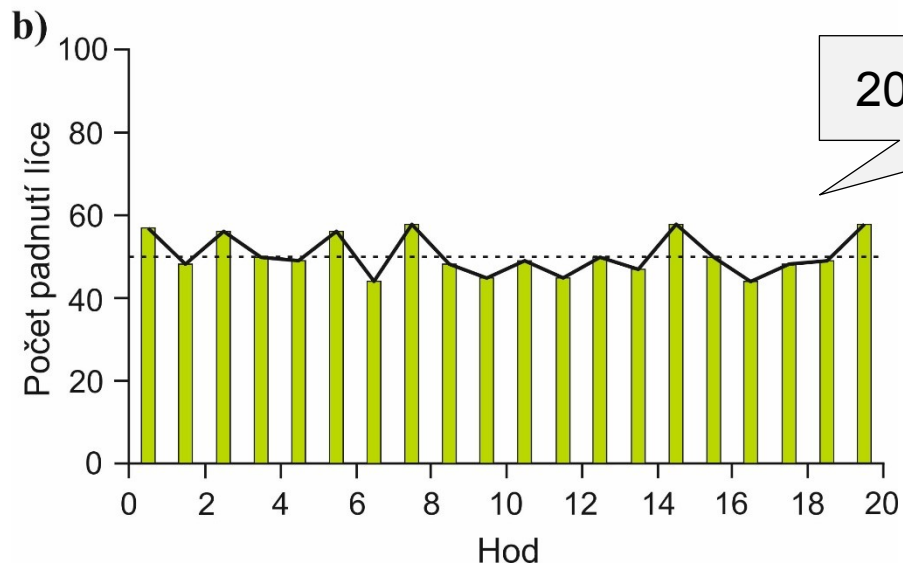
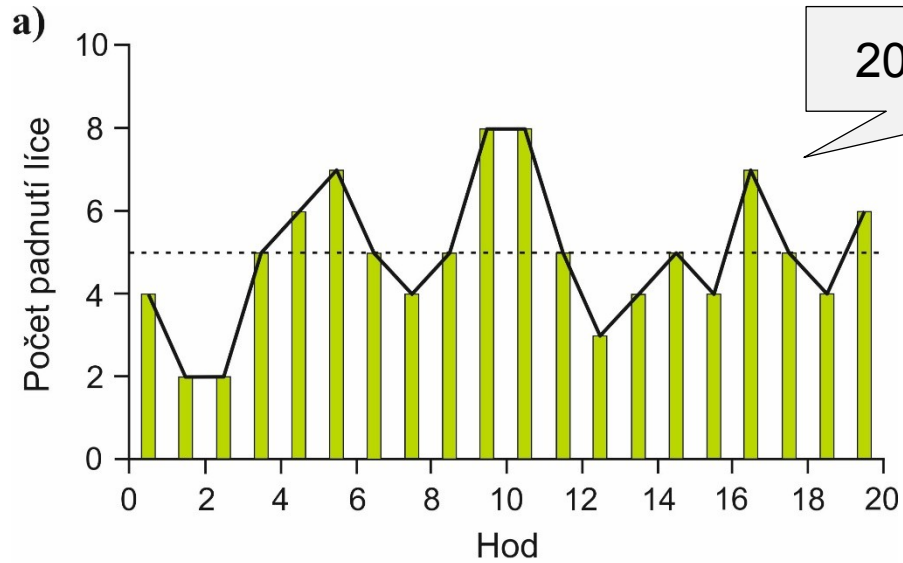
Why randomness?

when number of repetitions finite probability of an event  $\neq$  its frequency  
(cf. H-W principle)



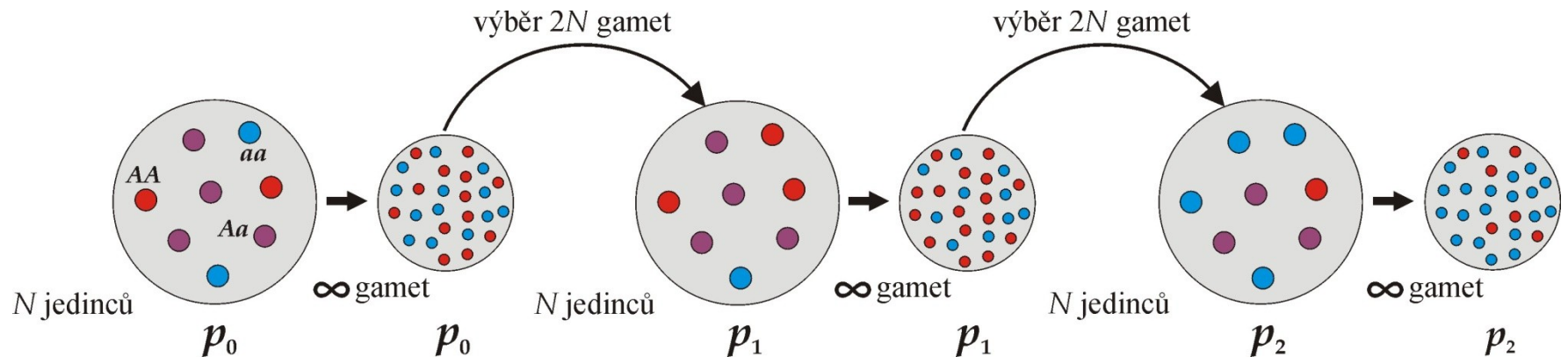
10 coins → in more than 75 % cases the ratio differs from 1 : 1





S větším počtem mincí menší rozptyl kolem očekávané hodnoty

# Náhodný výběr gamet z genofondu (*sampling error*):

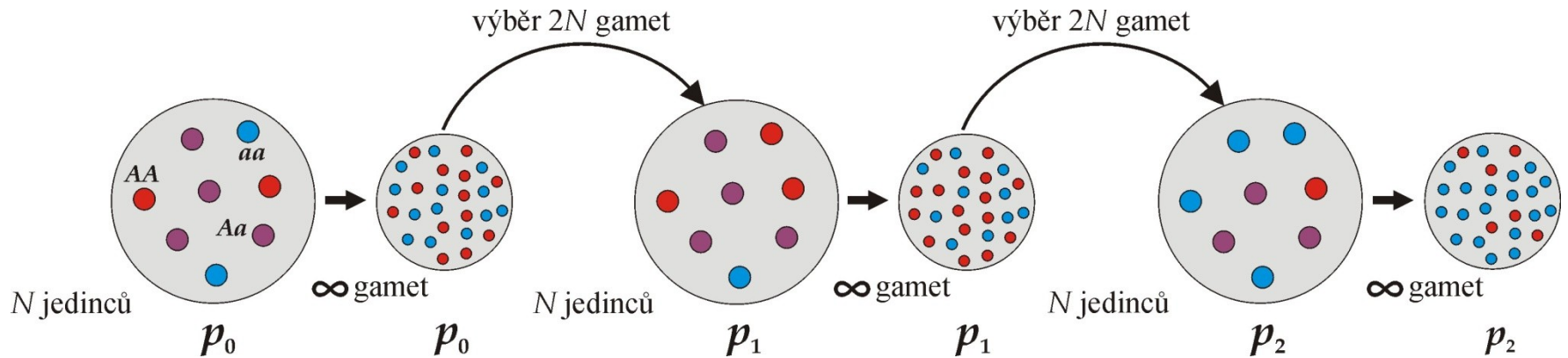


Výsledkem náhodného výběru je kolísání frekvencí mezi generacemi = „**random walk**“

## Wrightův-Fisherův model

$\approx$  Hardyho-Weinbergův model pro malé populace

# Random sampling from gene pool (sampling error):

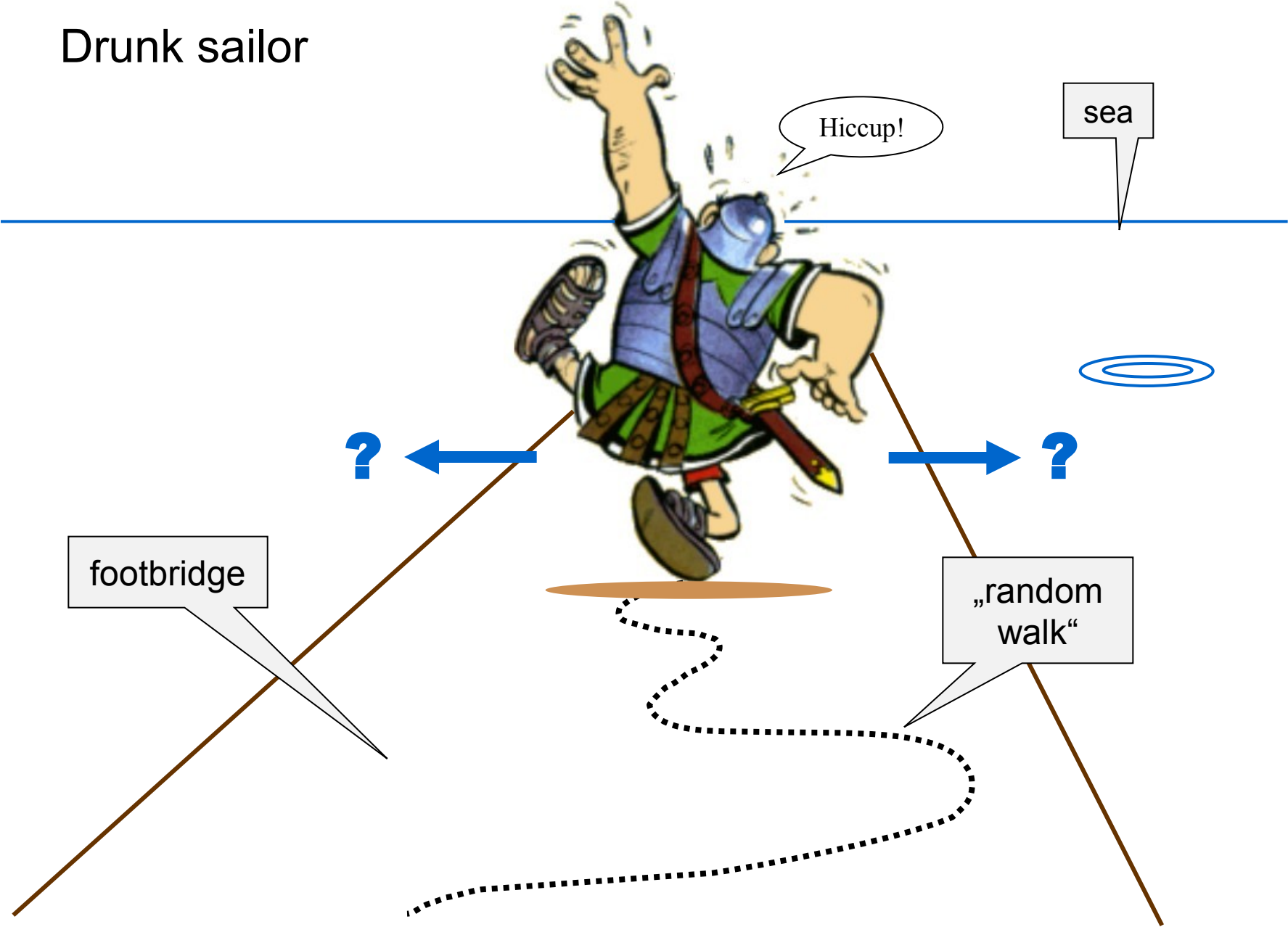


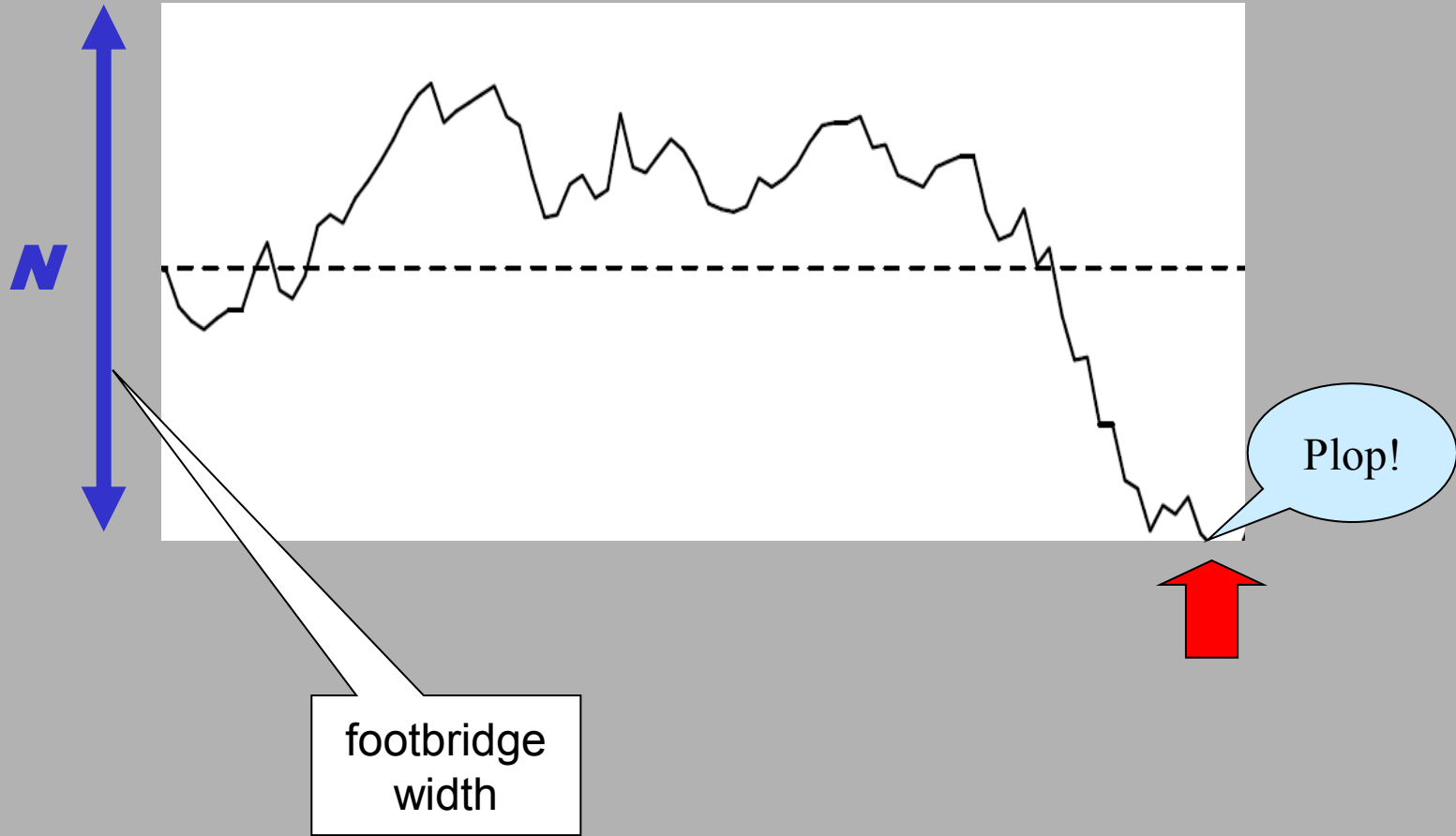
Random sampling results in fluctuations of allele frequencies across generations = „random walk“

## Wright-Fisher model

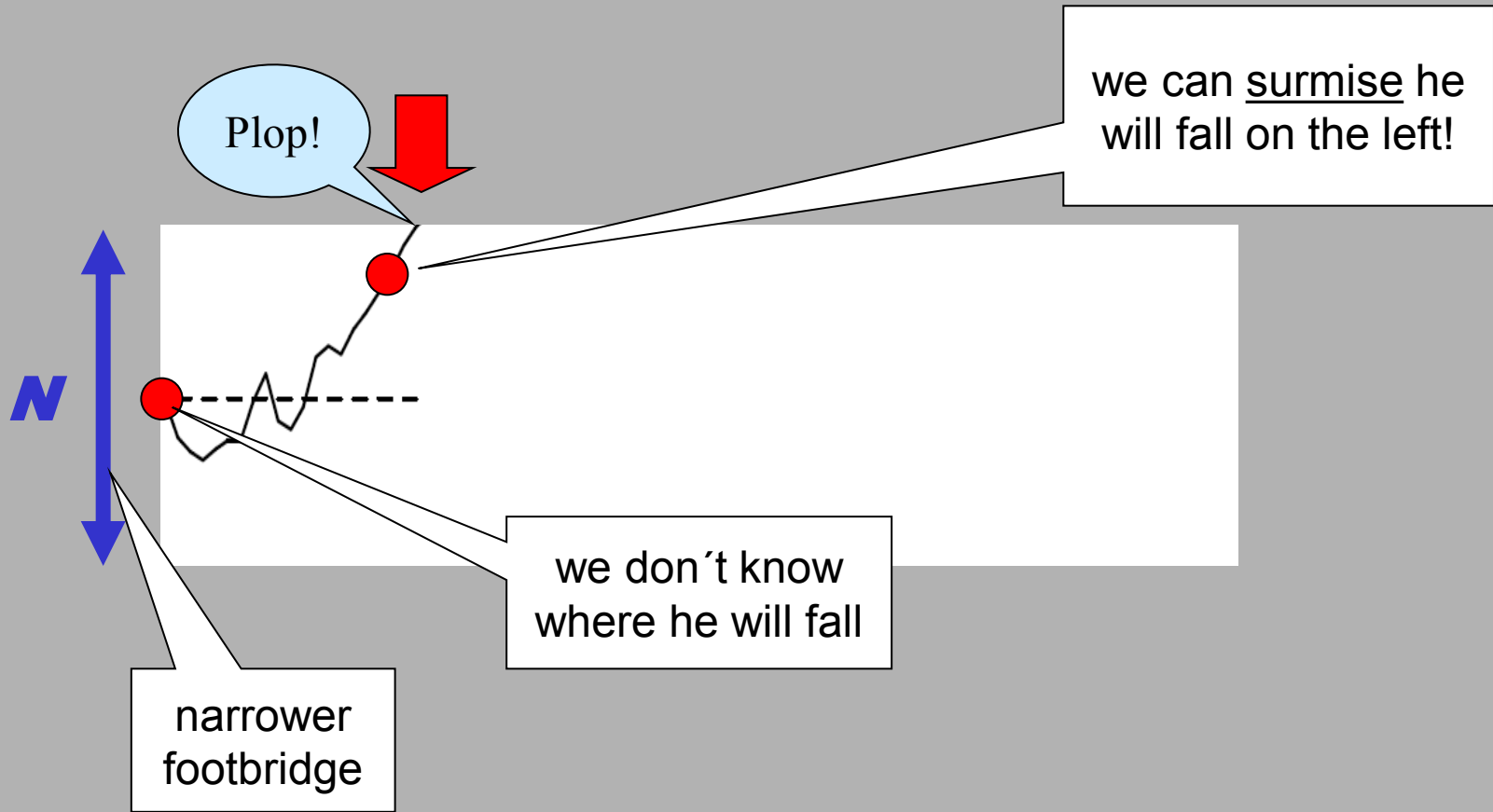
$\approx$  Hardy-Weinberg model for finite populations

# Drunk sailor

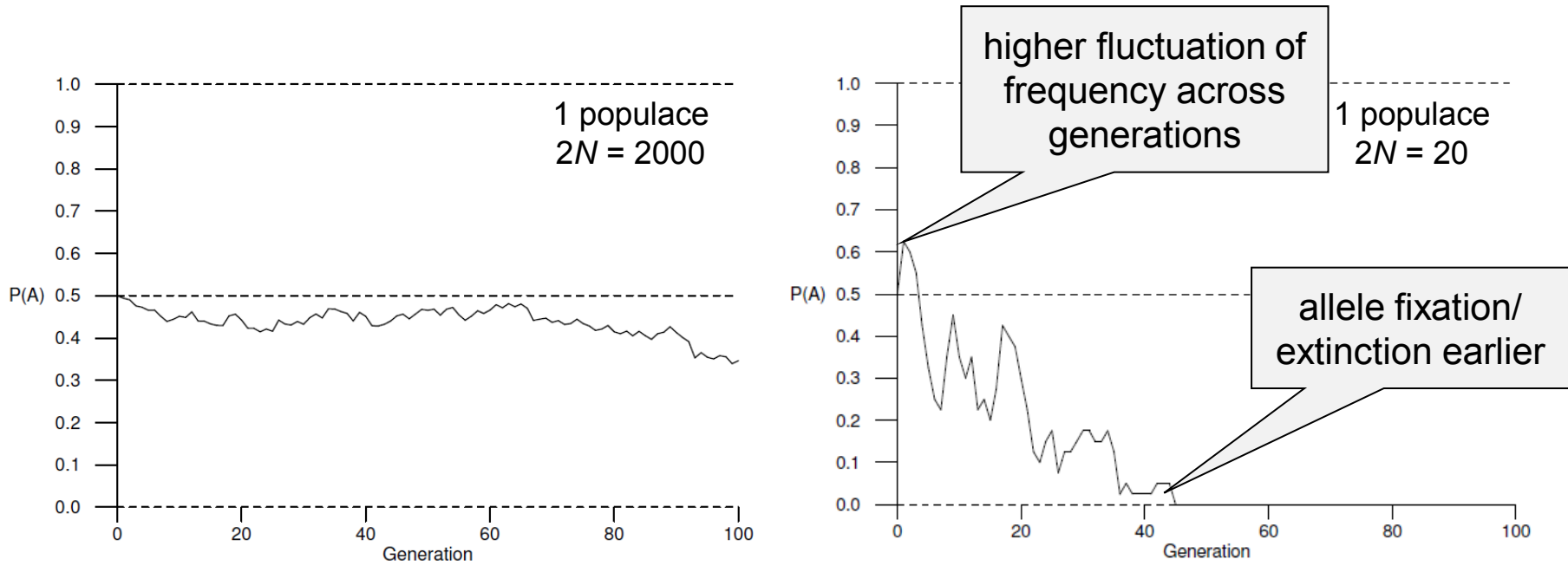






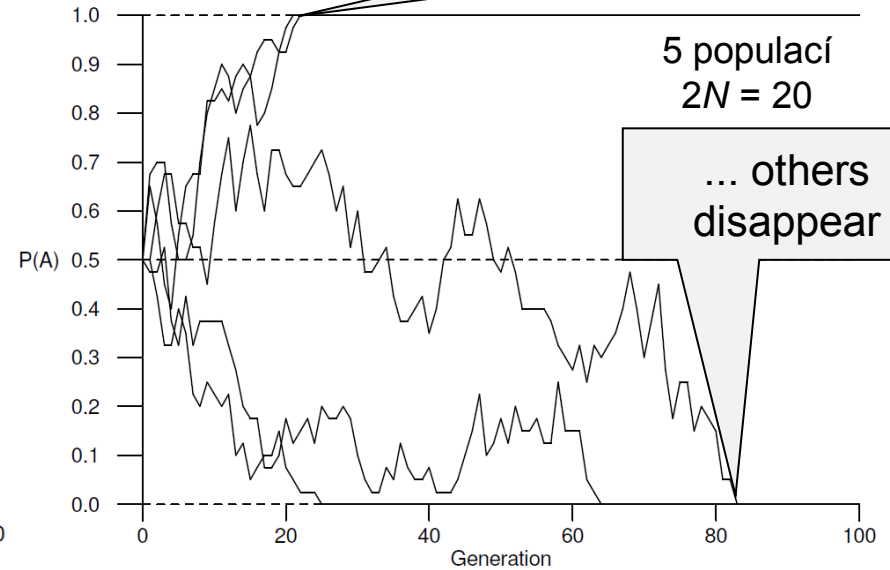
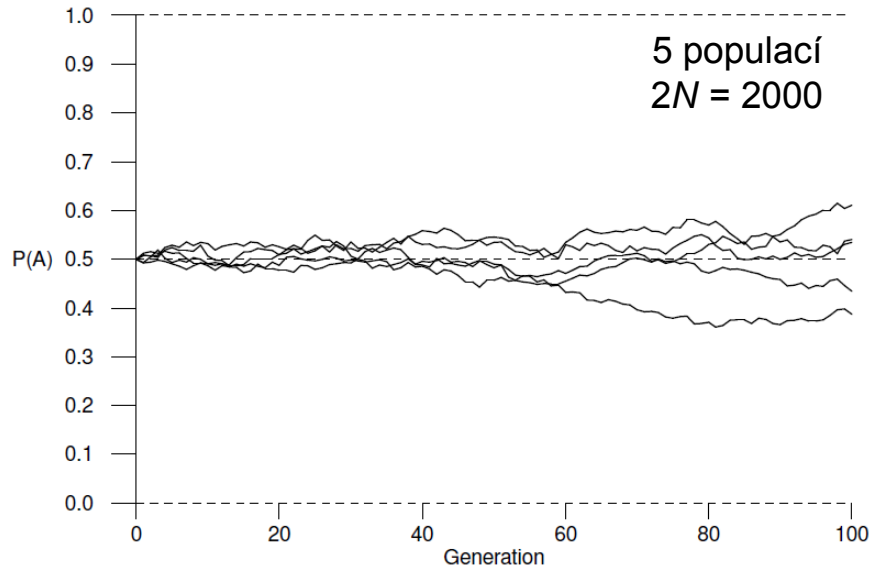


## Modelling drift:



Fluctuation of frequencies across generations stronger in small populations (~drunker sailor).

## Modelling drift:



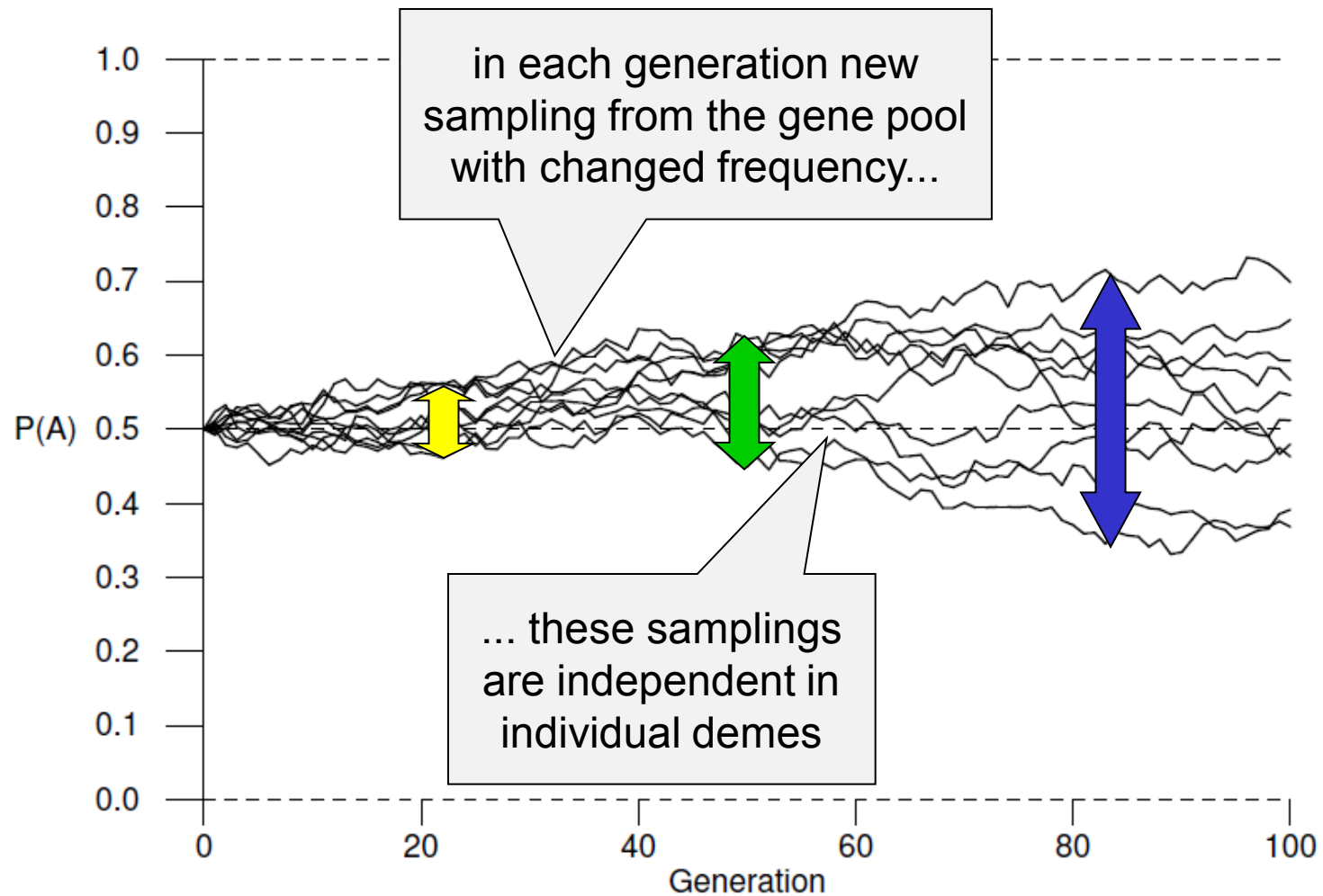
Conclusion 1: Drift results either in allele fixation or allele extinction.

Conclusion 2: Drift results in loss of variation in demes.

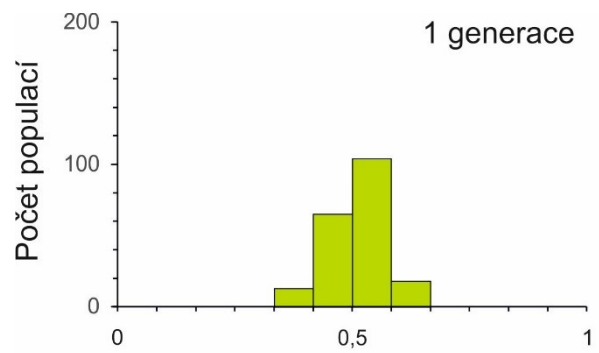
Conclusion 3: Probability of allele fixation equals its frequency.

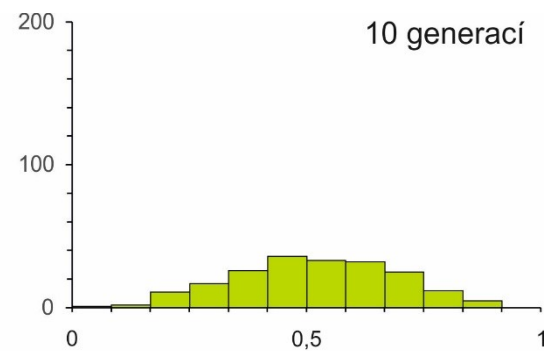
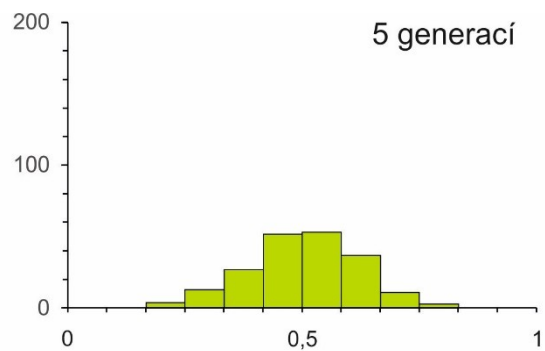
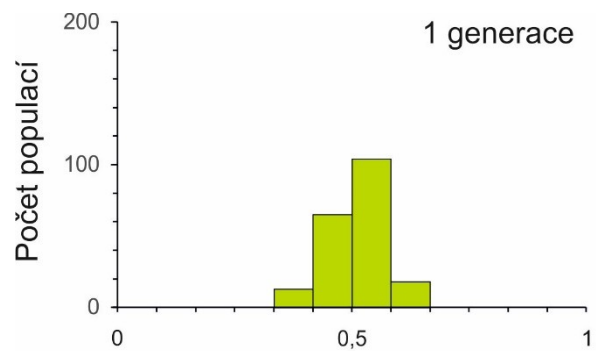
Probability of fixation of a new allele in diploids =  $1/(2N)$

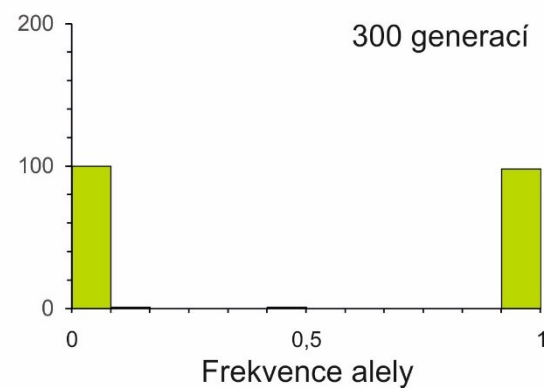
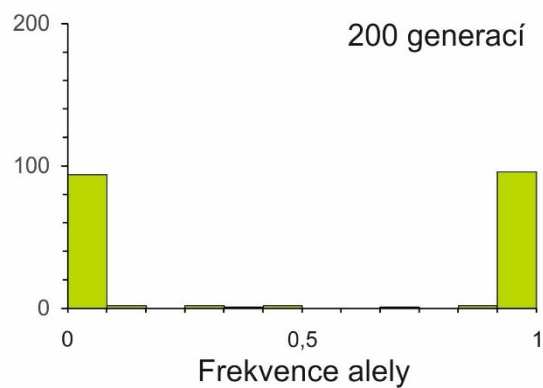
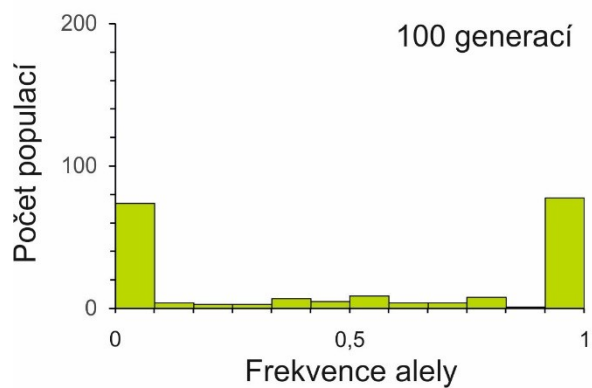
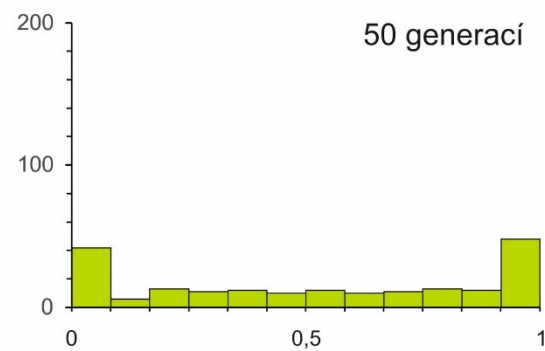
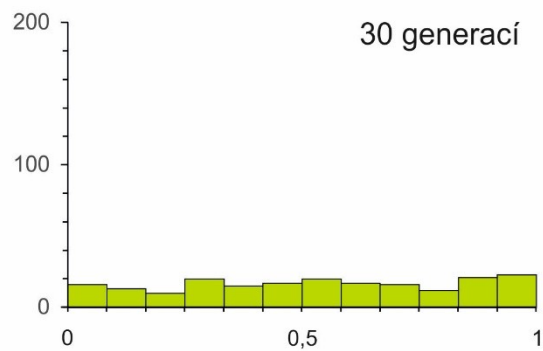
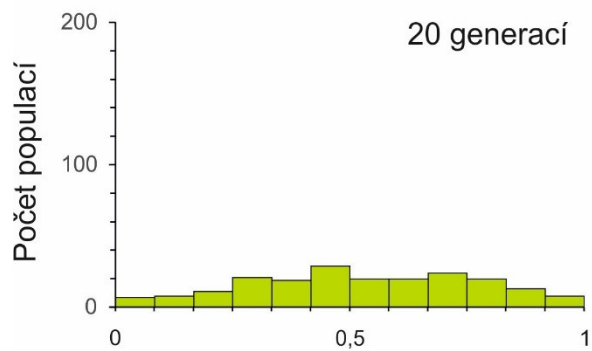
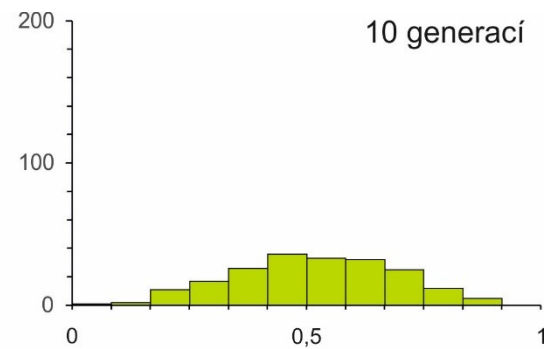
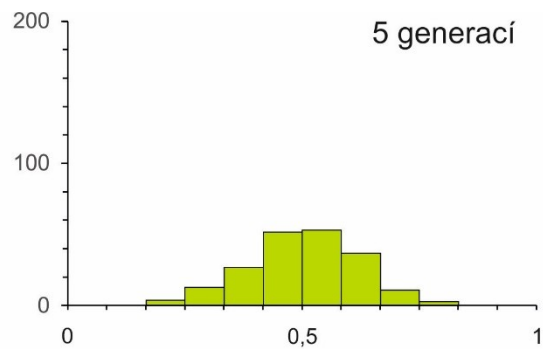
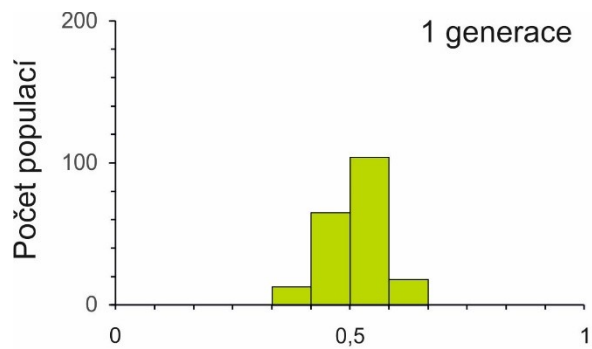
Conclusion 4: Mean time to fixation of a new allele  $\approx 4N$ .



**Conclusion 5: Drift results in divergence among demes.**







Peter Buri (1956):

107 populations of *D. melanogaster*

zeroth generation: 16 heterozygous  $bw^{75}/bw$  individuals in each population

in each generation random sampling of 8 males and 8 females

19 generations

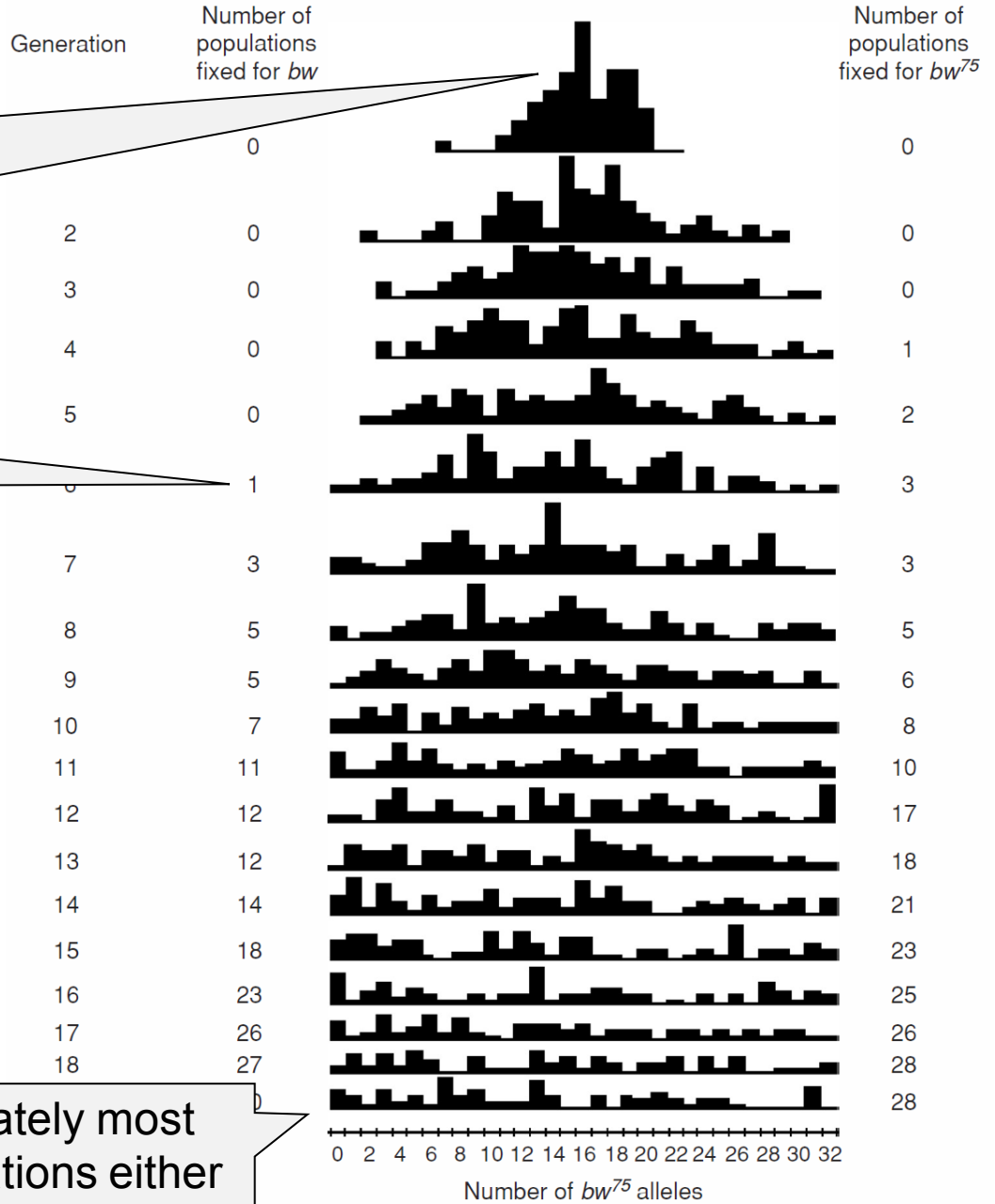
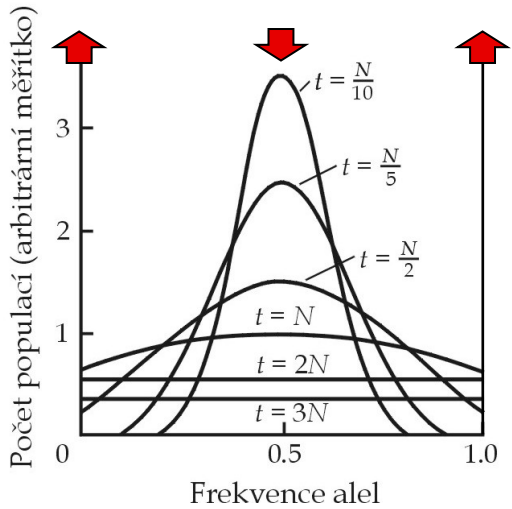




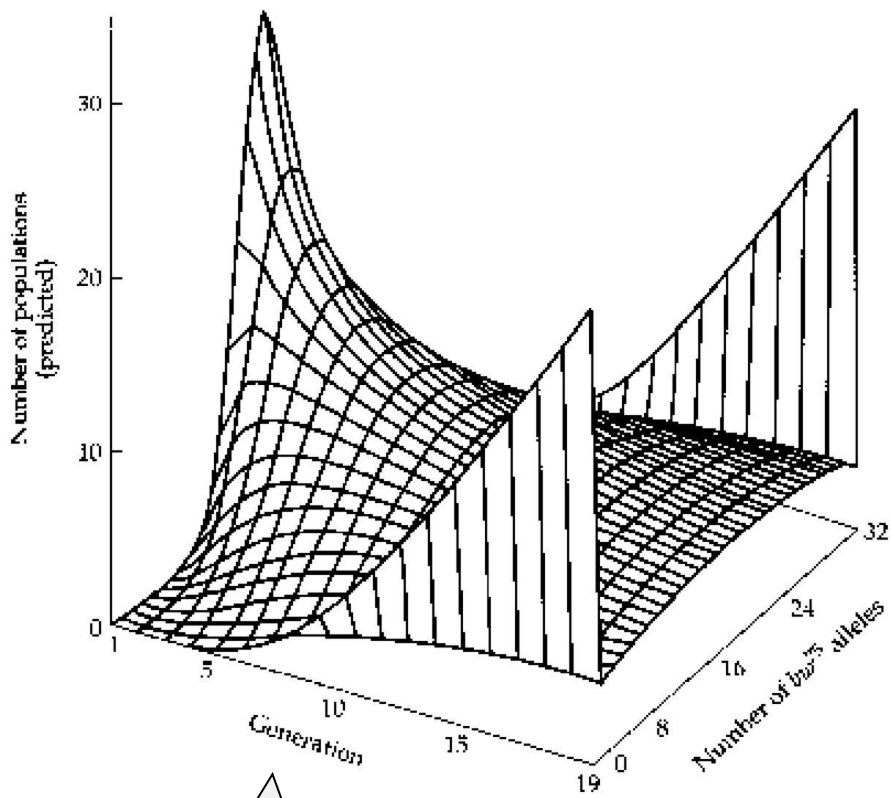
# Buri (1956):

in the first generation most populations around  $p = 0,5$

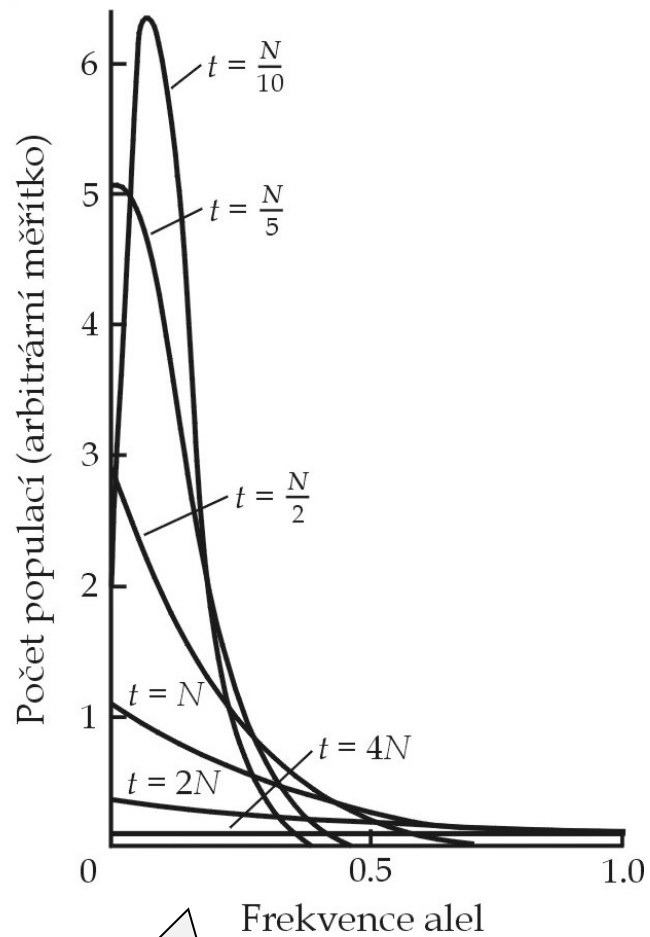
population divergence



ultimately most populations either  $p = 0$  or  $p = 1$



mathematical simulation (diffusion approximation)



simulation with initial frequency  $p = 0,1$

Eg.: Galapagos lava lizard (*Microlophus albemarlensis*)

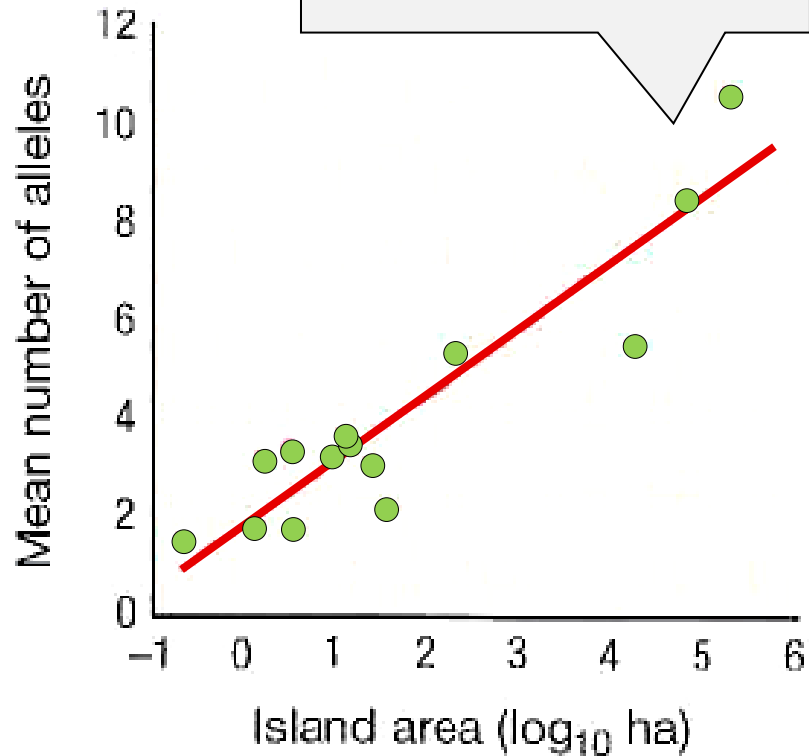


M. Jordan, H. Snell (2002):

17 populations

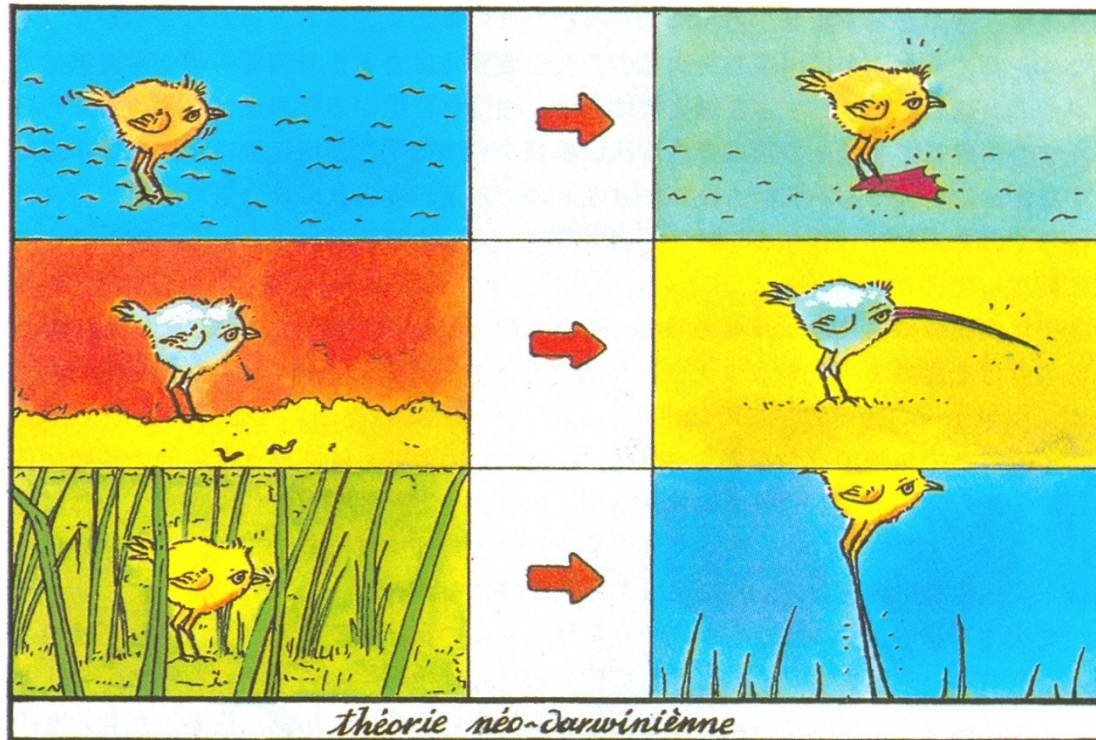
11 microsatellite loci

lizards on larger islands have higher variation

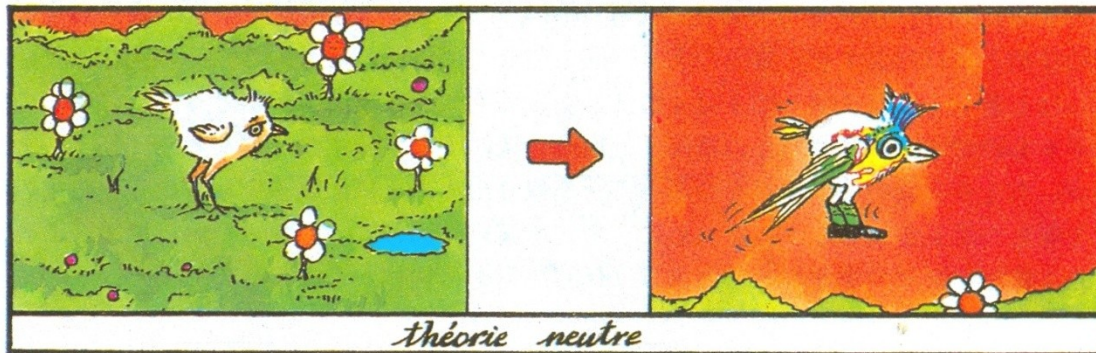


sea level 17 and 12 thousand years ago and nowadays

# Evolution of selectively neutral traits is **random**



Darwinian evolution:  
„survival of fittest“



neutral evolution:  
„survival of luckiest“

## Effective population size

Real populations differ from the WF model (fluctuations of  $N$ , different reproductive success and mortality, unequal sex ratio, ....)

→ effective population size  $N_e$  allows us to measure drift in non-ideal populations

**Effective population size** = the number of individuals of ideal Wright-Fisher population displaying the same rate of drift as the studied non-ideal population

Like in the inbreeding coefficient there is no single effective population size!!

## Some factors decrease $N_e$ relative to $N$ :

overlapping generations

fluctuating population size across generations

different number of breeding males and females

high variation of the number of offspring within populations

**Caution! Under some circumstances  
the effective population size can be higher than  $N$ !!**

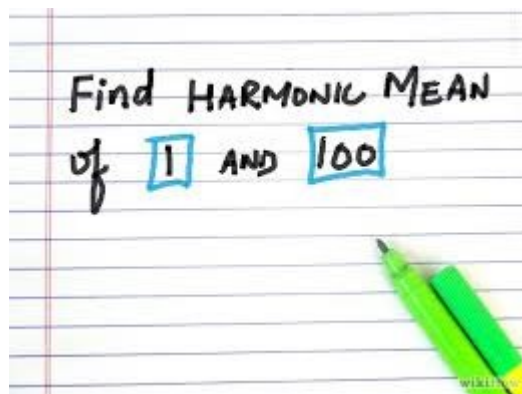
## Effect of fluctuating population size:

effective size can be approximated as harmonic mean  $\Rightarrow$  strong influence of small  $N$ !!

$$N_e = \frac{t}{\frac{1}{N_1} + \frac{1}{N_2} + \dots + \frac{1}{N_t}}$$

harmonic mean

mean much closer to the lower value



$$H = \frac{2}{\frac{1}{a_1} + \frac{1}{a_2}}$$
$$= \frac{2}{\frac{1}{1} + \frac{1}{100}}$$

A handwritten calculation on lined paper with a green highlighter. The numbers 1 and 100 in the denominator are boxed in blue.

$$= \frac{2}{1.01}$$
$$= 1.9802$$

Harmonic Mean of 1 and 100

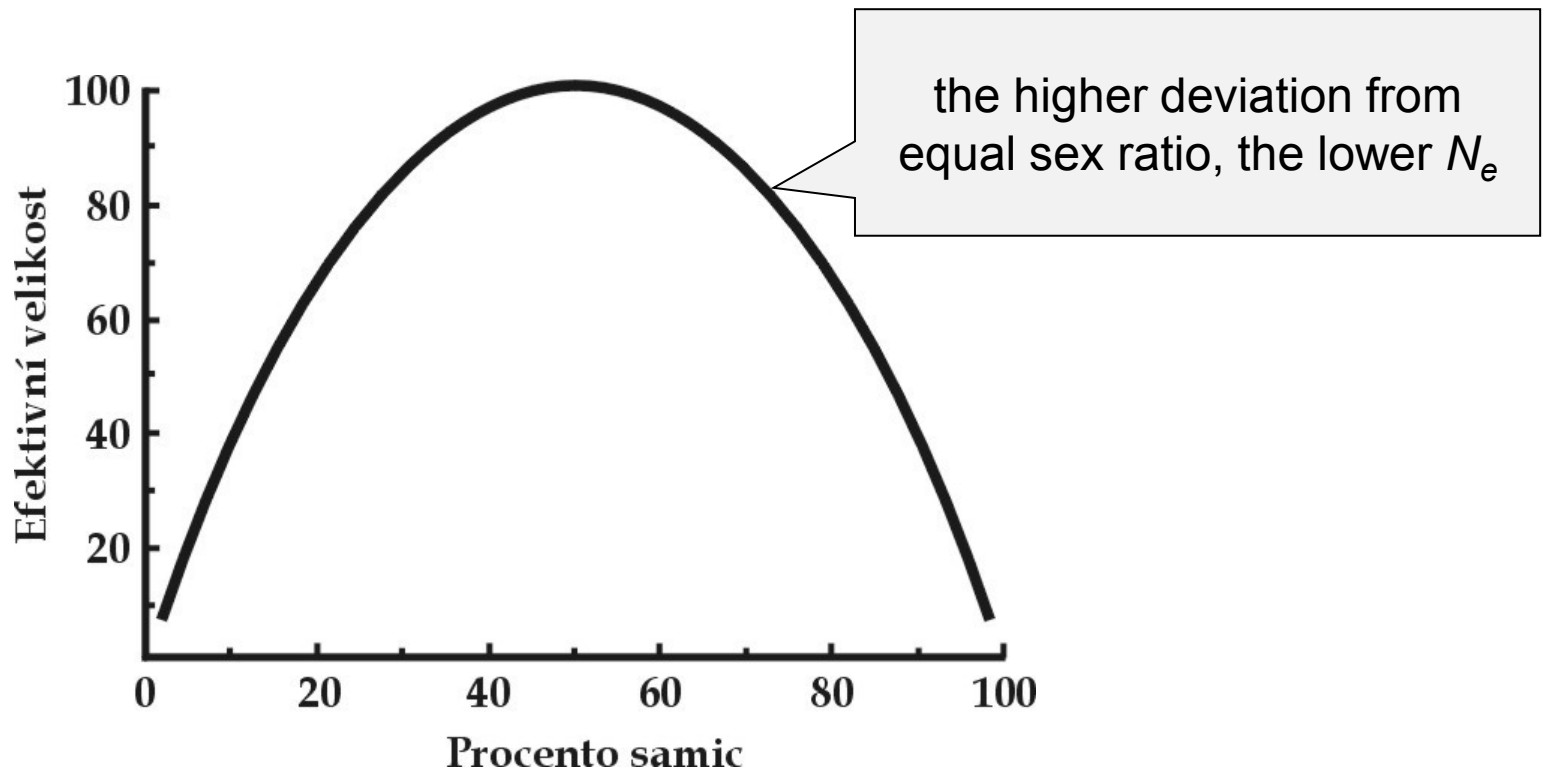
A handwritten calculation on lined paper with a green highlighter. The result 1.9802 is boxed in blue. A blue arrow points from the box to the text below. A speech bubble from the top right points to the result.



## Effect of biased sex ratio:

Till now we assumed the same number of breeding males and females

$N_m$  = number of breeding males,  $N_f$  = number of breeding females



# Effect of biased sex ratio:

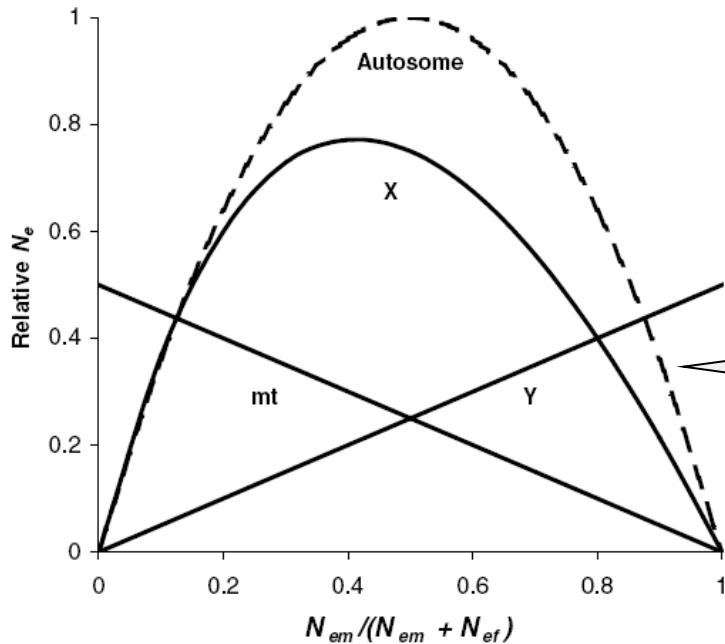
$$N_m = 1:$$

$$N_e = \frac{4N_m N_f}{n_m + n_f}$$



$$N_e = \frac{4N_f}{1} \approx 4$$

it follows from this formula that if there is only a single breeding male in the population  $N_e \approx 4$  regardless of the total number of individuals



effect of sex ratio on  $N_e$  different for various genetic traits!

## Effect of unequal reproductive success:

southern elephant seal:

sex ratio within a harem 1:40<sup>\*)</sup>

<sup>\*)</sup> effective ratio 1:4-5 due to cuckoldry and short period of male's dominance (1-2 years)



## Reproductive success on the gene level:

If a gene is affected by selection variance of the number of offspring among members of a population is high (individuals with a positive allele have more offspring)

⇒  $N_e$  for this gene is lower than for a neutral gene

## Each genetic trait requires its own $N_e$ :

For genes on autosomes, sex chromosomes, and mtDNA there are different effective population sizes:

|              |                   |         |
|--------------|-------------------|---------|
| autosomes:   | $N_e$             | $4 N_e$ |
| X, Z:        | $\frac{3}{4} N_e$ | $3 N_e$ |
| Y, W, mtDNA: | $\frac{1}{4} N_e$ | $1 N_e$ |

# COALESCENT

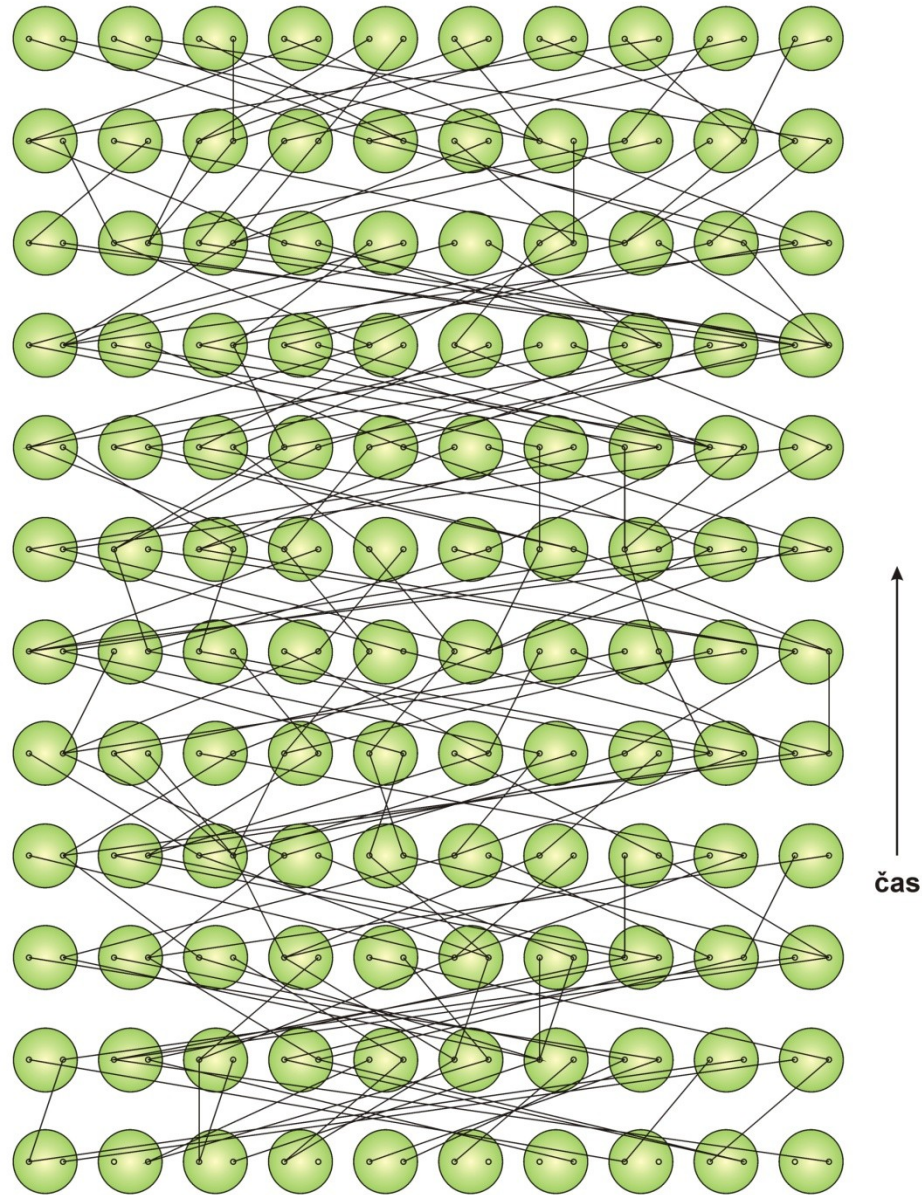
under drift some alleles disappear from a population  $\Rightarrow$  when there are no mutations ultimately all gene copies have a common ancestor

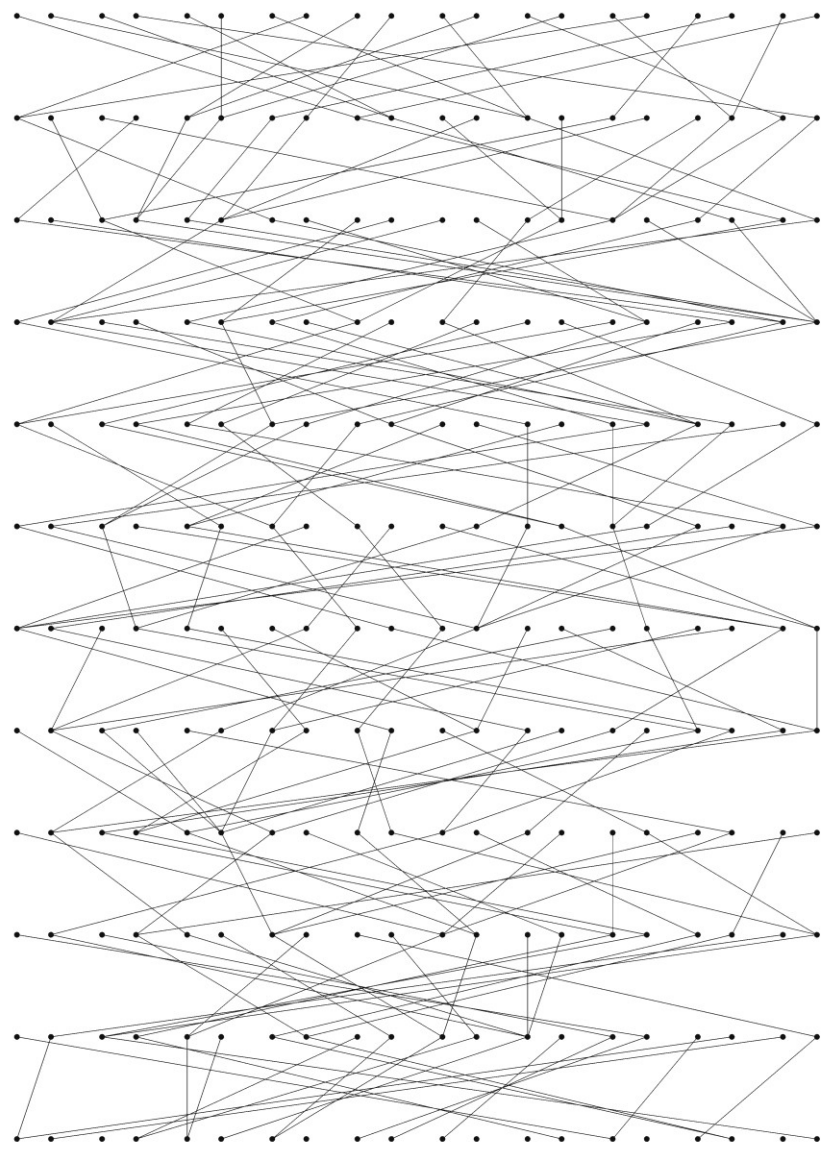
„forward“ approach

we can proceed also back in time – „backward“ approach  $\rightarrow$   
moving back in time till two or more gene copies „fuse“  
= **coalescent event**

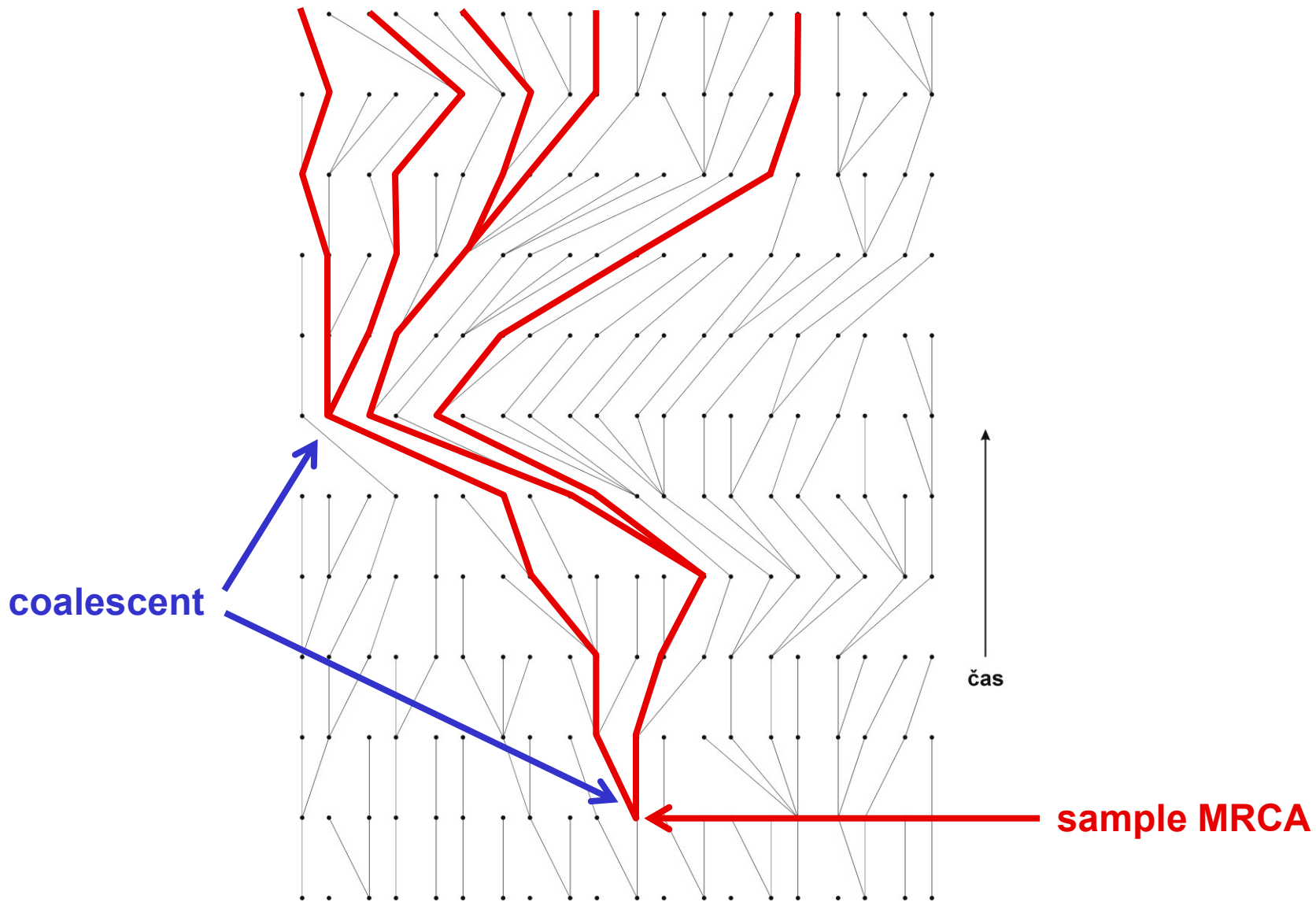
**the most recent common ancestor (MRCA)**

# Wright-Fisher model:





↑  
čas





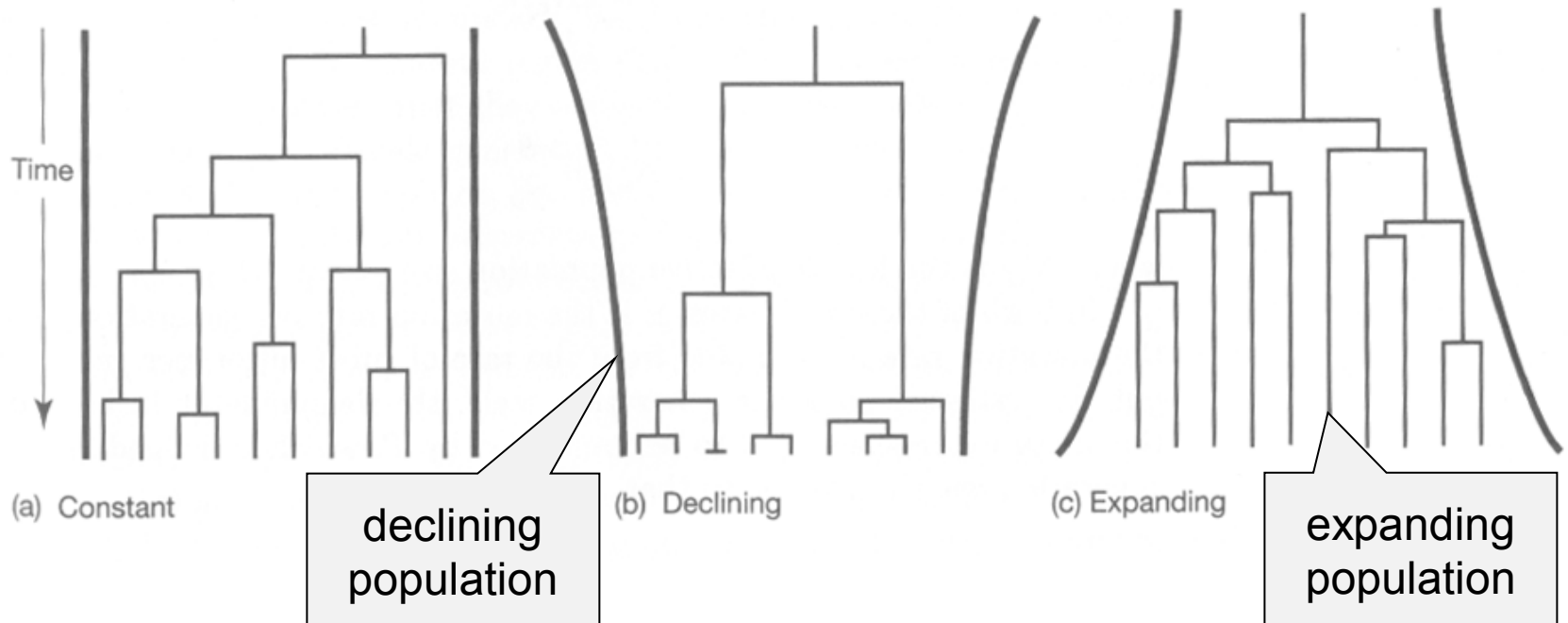
# Coalescence and effective population size

from the coalescent theory several interesting consequences follow:

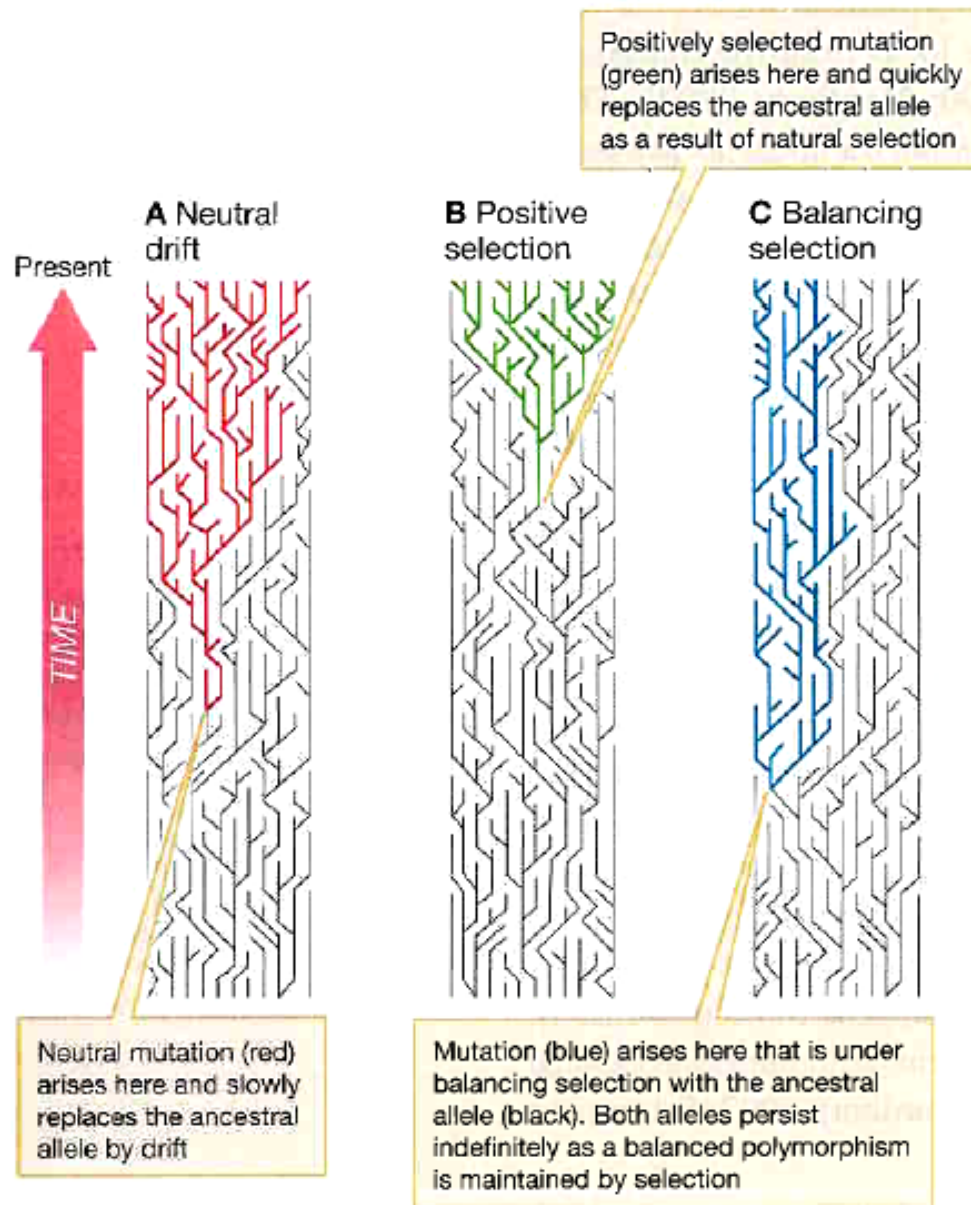
in small populations coalescent rate higher than in large populations

⇒ we can estimate  $N_e$

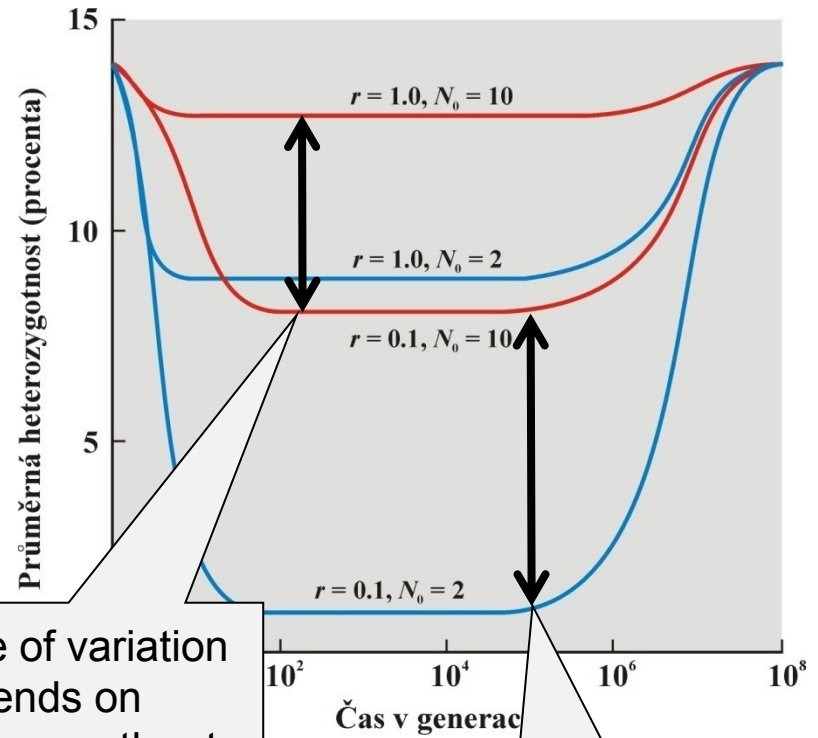
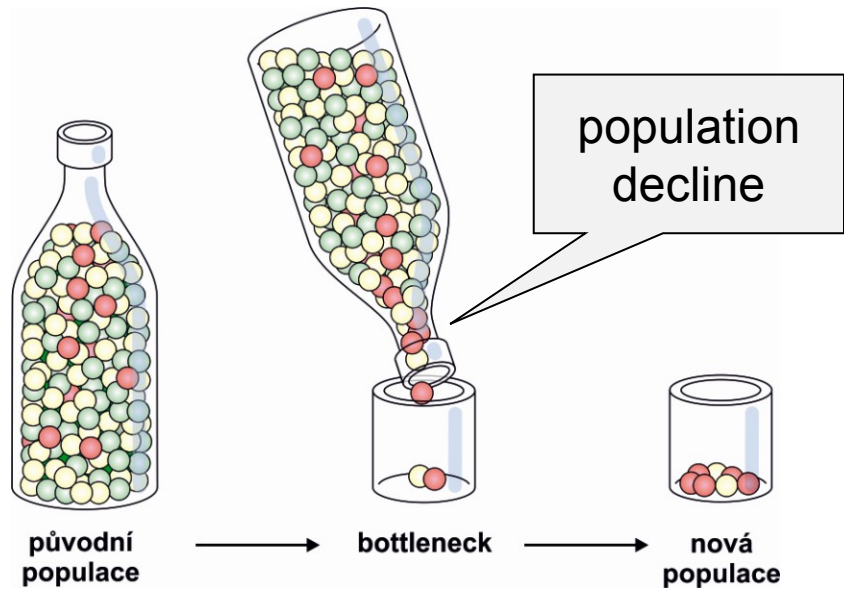
but we can estimate also changes of  $N_e$  in time



# The same effect of selection on the coalescent tree shape:



# BOTTLENECK and FOUNDER EFFECT



bottleneck reduces variation

magnitude of this reduction

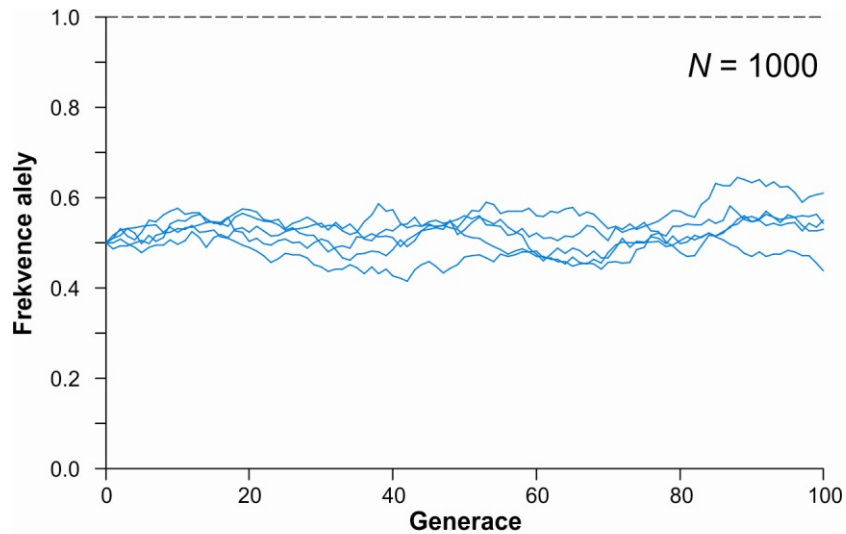
depends on reduction of  $N_e$  and duration of bottleneck

rate of decrease of variation different for various genetic traits (autosomes, mtDNA, Y...) – different  $N_e$ !

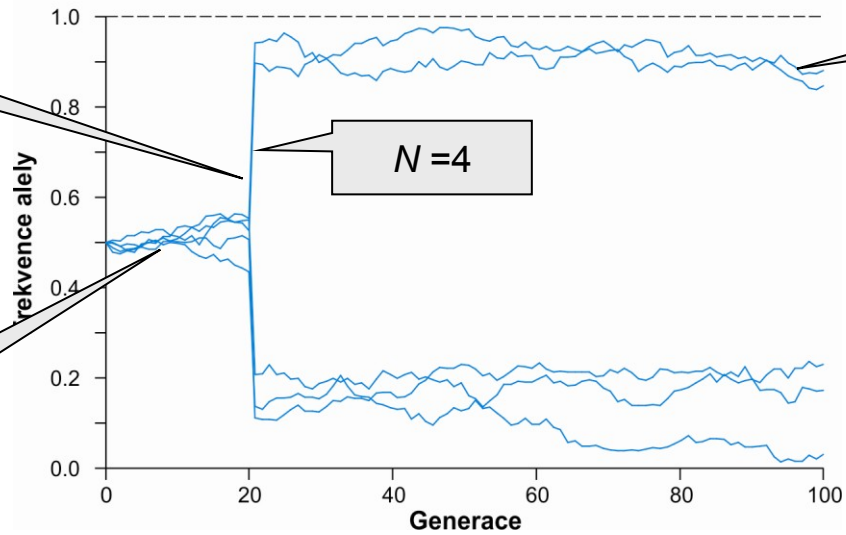
decrease of variation depends on population growth rate

variation more reduced under stronger bottleneck

# Bottleneck:



bottleneck

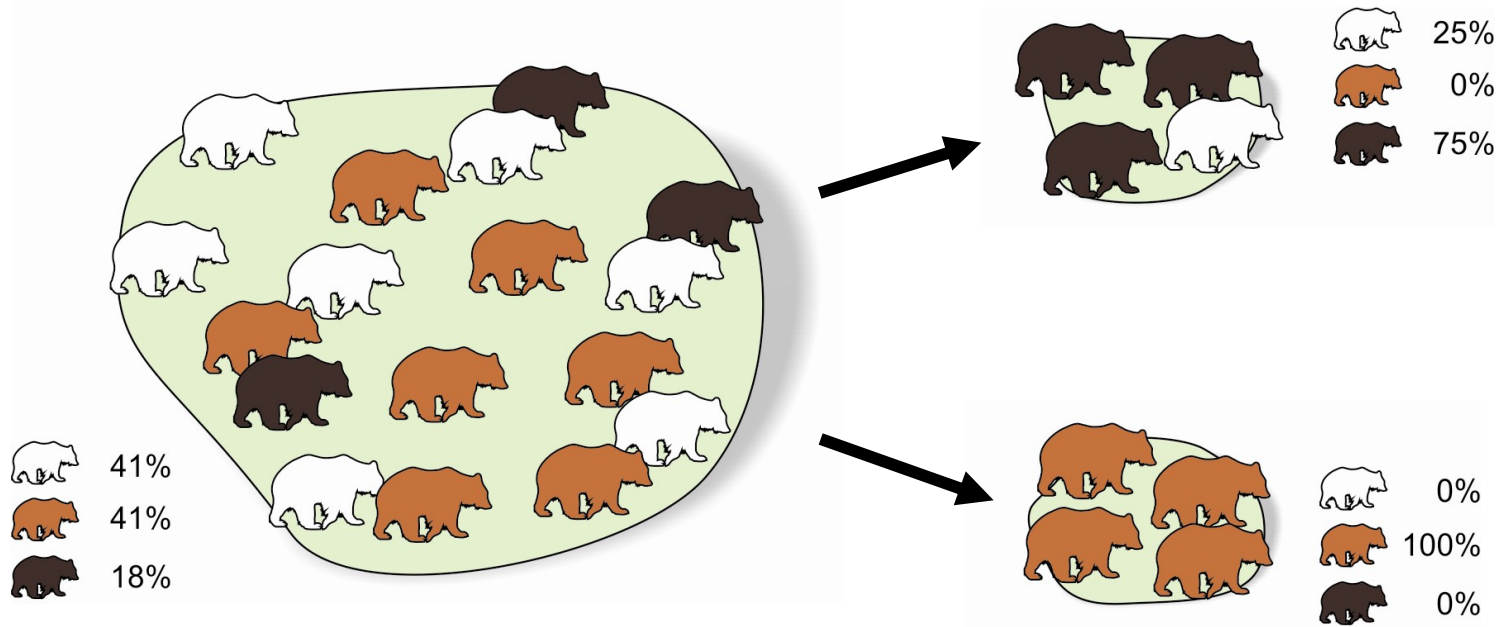


$N = 1000$

$N = 4$

$N = 1000$

## Founder effect:



colonization of a novel territory (eg. island)

because of a small number of founders (even a single pregnant female)

→ random change of allele frequencies

→ reduction of variation

different environmental conditions → speciation

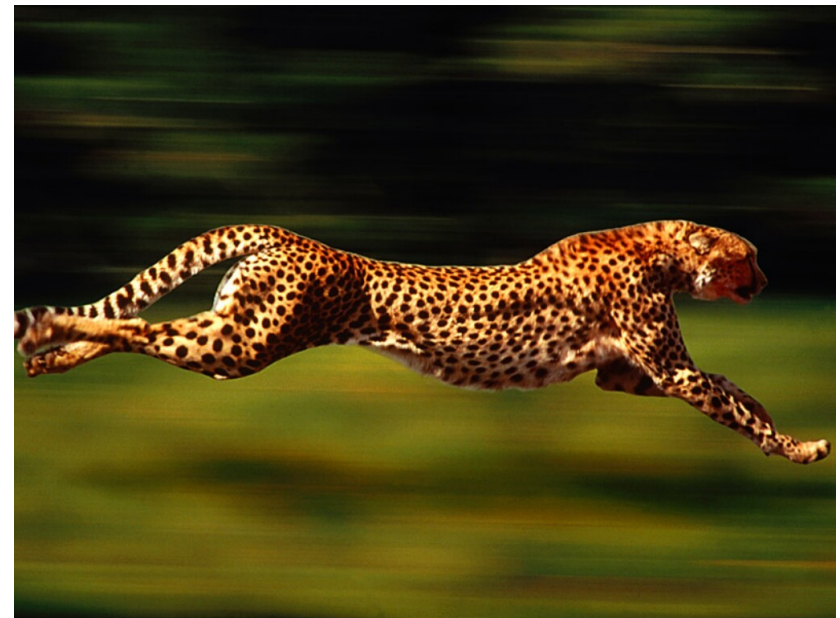
## Examples of founder effect and bottleneck cheetah

30 individuals of *Acinonyx jubatus reineyi* from E Africa, 49 protein loci:  
only 2 loci polymorphic ( $P = 0,04$ ), mean heterozygosity  $H_o = 0,01$

98 individuals of *A. j. jubatus* from S Africa:  $P = 0,02$ ,  $H_o = 0,0004$ !

south-African individuals accept skin grafts of the east-African subspecies  
without problems  $\Rightarrow$  monomorphism of MHC genes

assumed strong bottleneck  
in the past



## golden hamster

1930: [Israel Aharoni](#) (Hebrew Univ., Jerusalem) – female with offspring

escape of several individuals from captivity

1931: transport of several individuals to Britain 1937: private breeders

Recent genetic analyses including mtDNA → all golden hamsters currently kept in breeding colonies are descendants of a single female, probably that of 1930

mostly presented as an example of bottleneck but it is rather an example of founder effect



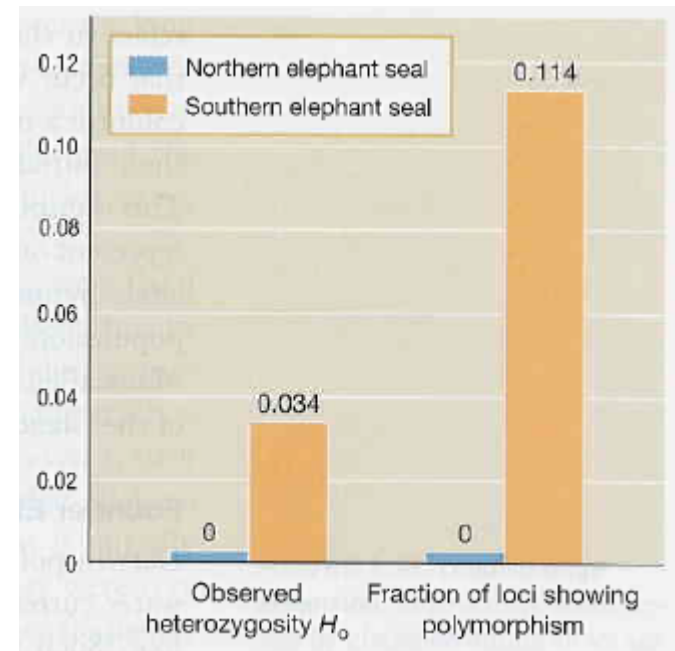
## northern elephant seal

*Mirounga angustirostris*: in 19th century almost eradicated

→ 1892 last 8 individuals on the island of Guadelupe killed for museum collections

fortunately 10-20 individuals passed unnoticed → today > 100 000 inds.

M. Bonnell a R.K. Selander (1974): blood samples of 159 individuals electrophoresis at 21 loci → no variation  
likewise Hoelzel et al. (1993), 62 loci

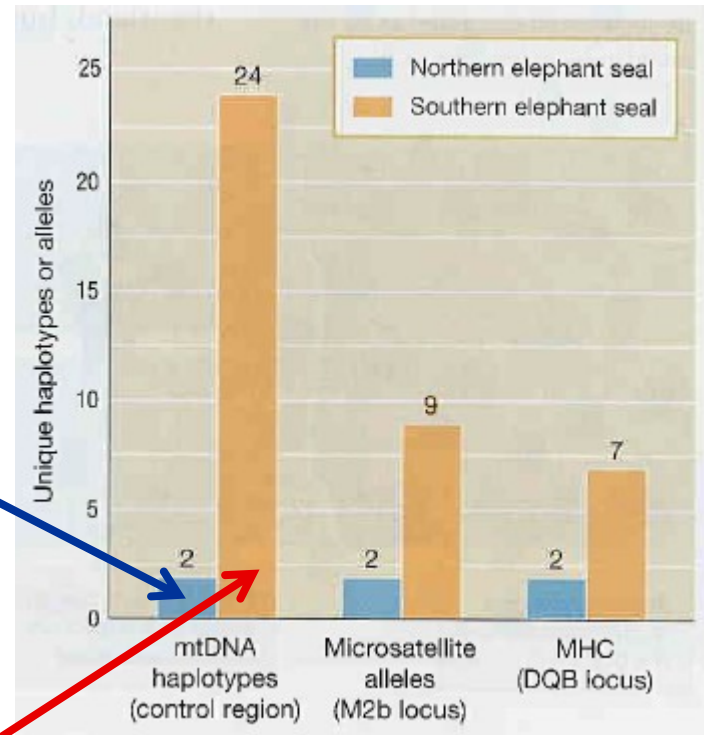




# Hoelzel et al. (1999): DNA markers

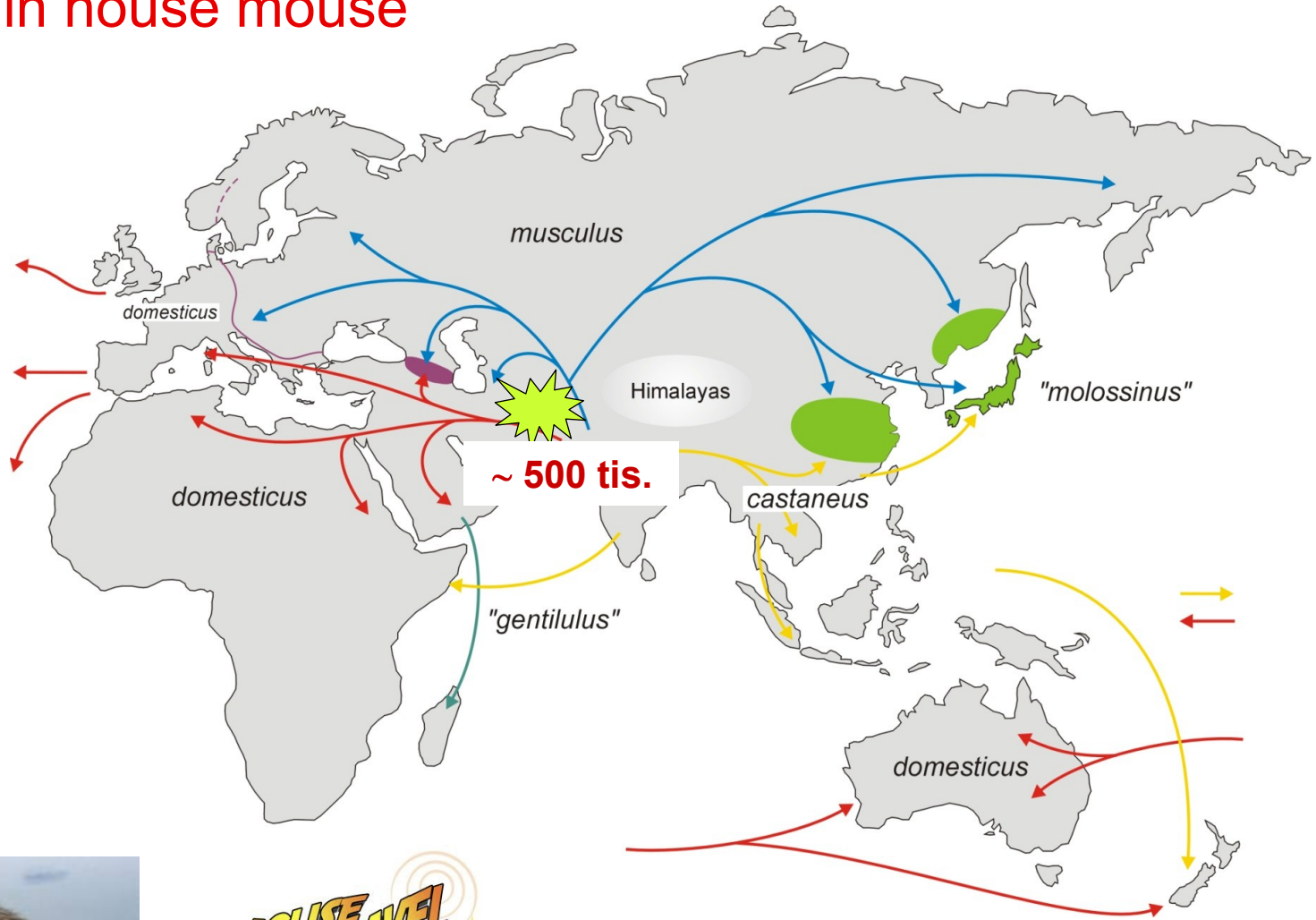


northern elephant seal  
(*Mirounga angustirostris*)

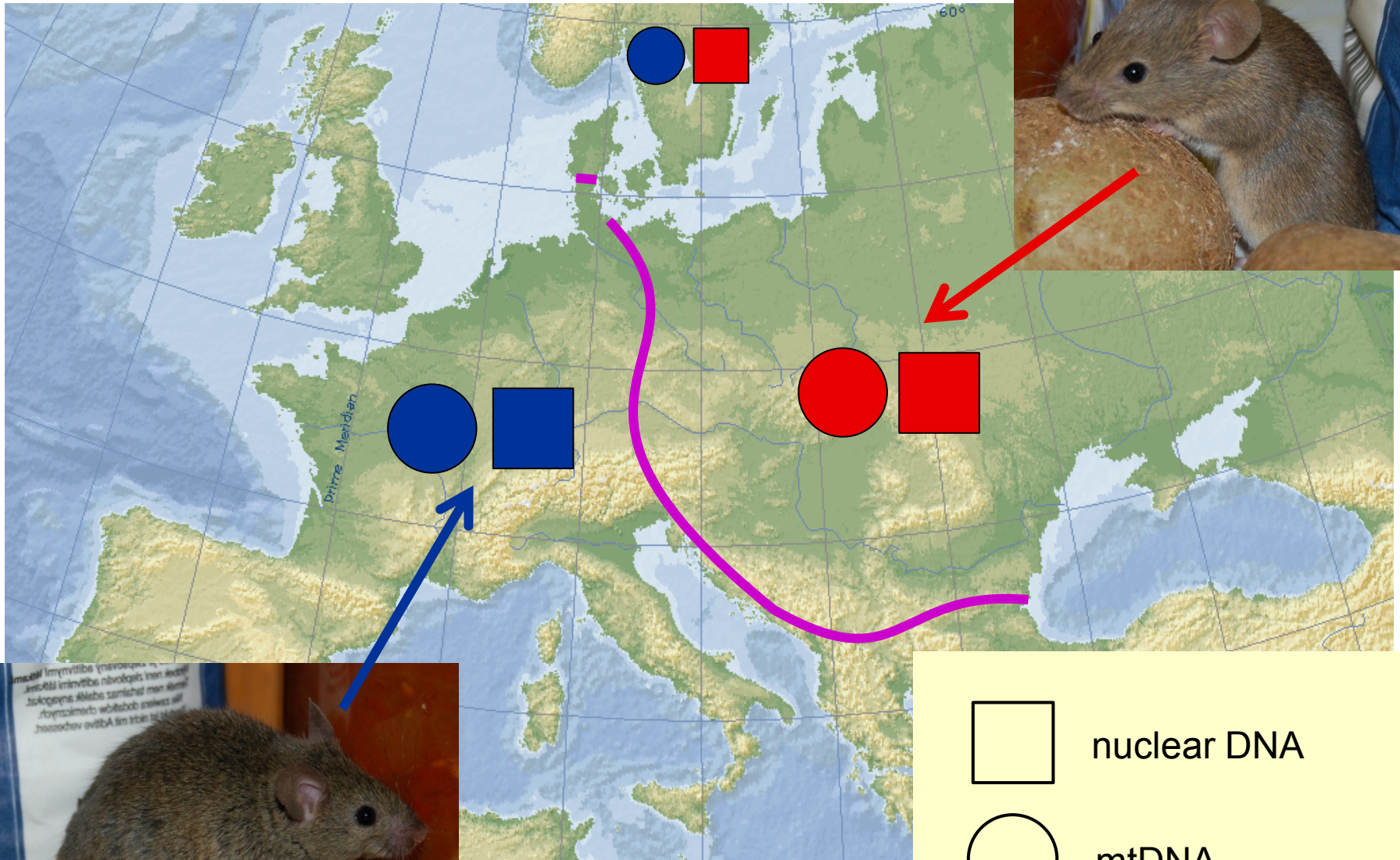


southern elephant seal  
(*Mirounga leonina*)

# FE in house mouse



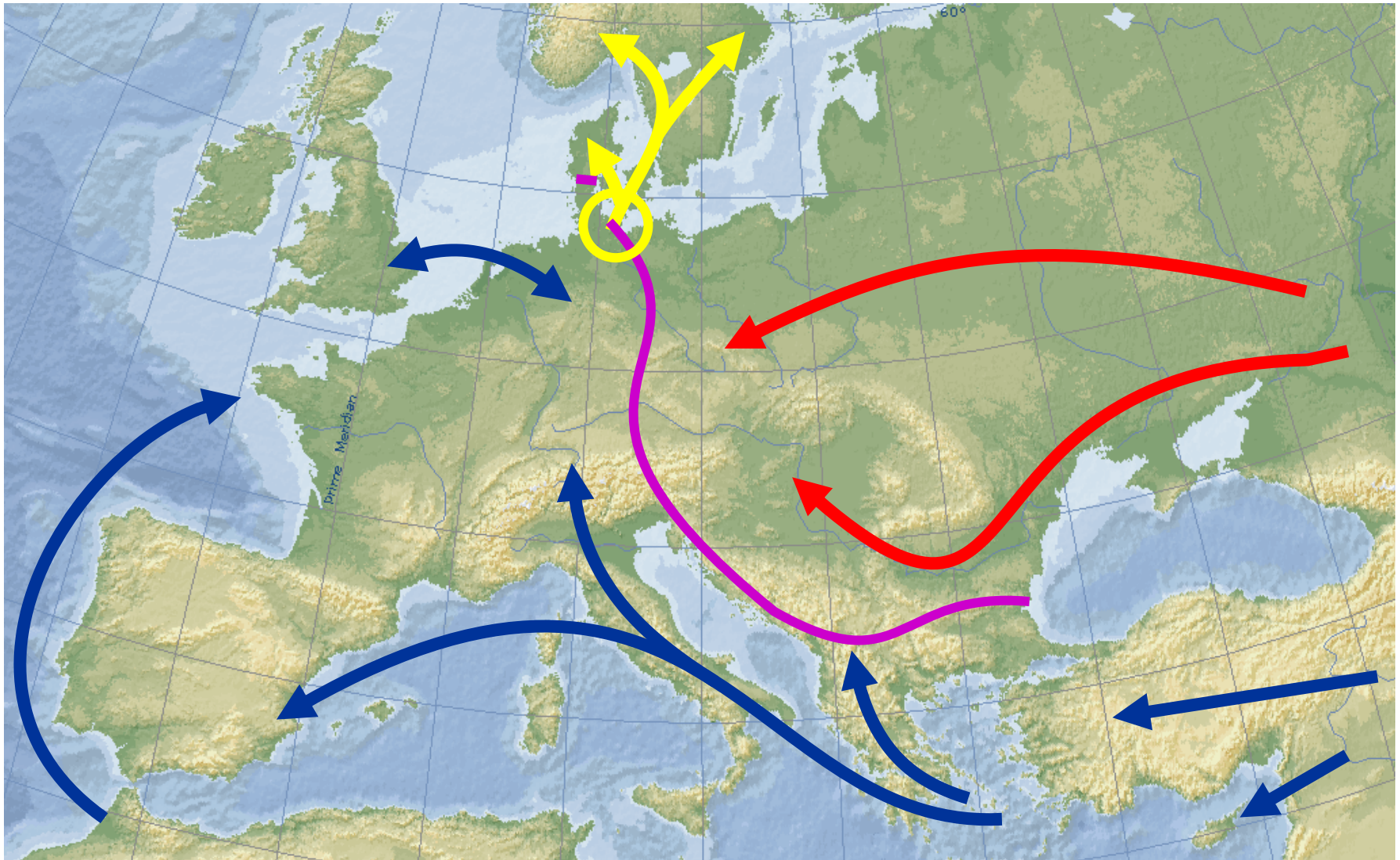
*Mus musculus musculus*



*M. m. domesticus*

□ nuclear DNA  
○ mtDNA

# mouse colonization of Europe



# humans

## a) Las Salinas (Dominican Republic):

Altagracia Carrasco:

several children with at least 4 men

Carrasco heterozygous for substitution  $T \rightarrow C$  in 5th exon of the 5- $\alpha$ -reductase 2 gene  $\Rightarrow$  TGG (Trp)  $\rightarrow$  CGG (Arg) at the 246th position of the protein

the enzyme catalyzes transformation of testosterone to DHT (dihydrotestosterone)

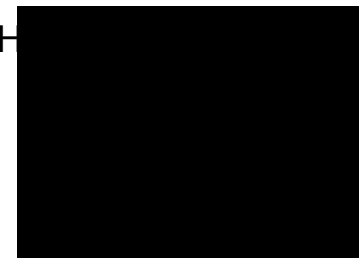
low activity of the mutant enzyme in homozygotes  $\Rightarrow$  boys have testes but other traits are female

in puberty testosterone production increases  $\Rightarrow$  transformation to men

in Salinas high frequency of the mutation  $\Rightarrow$  the word *guevedoces* (= „penis in 12“)



DH



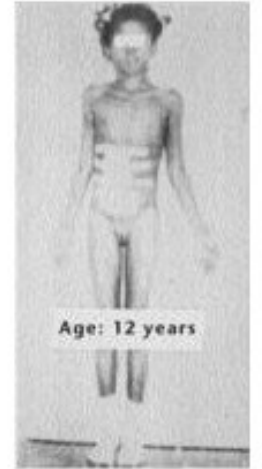




Age: 4 years



Age: 8 years



Age: 12 years



Age: 18 months



Age: 19 years

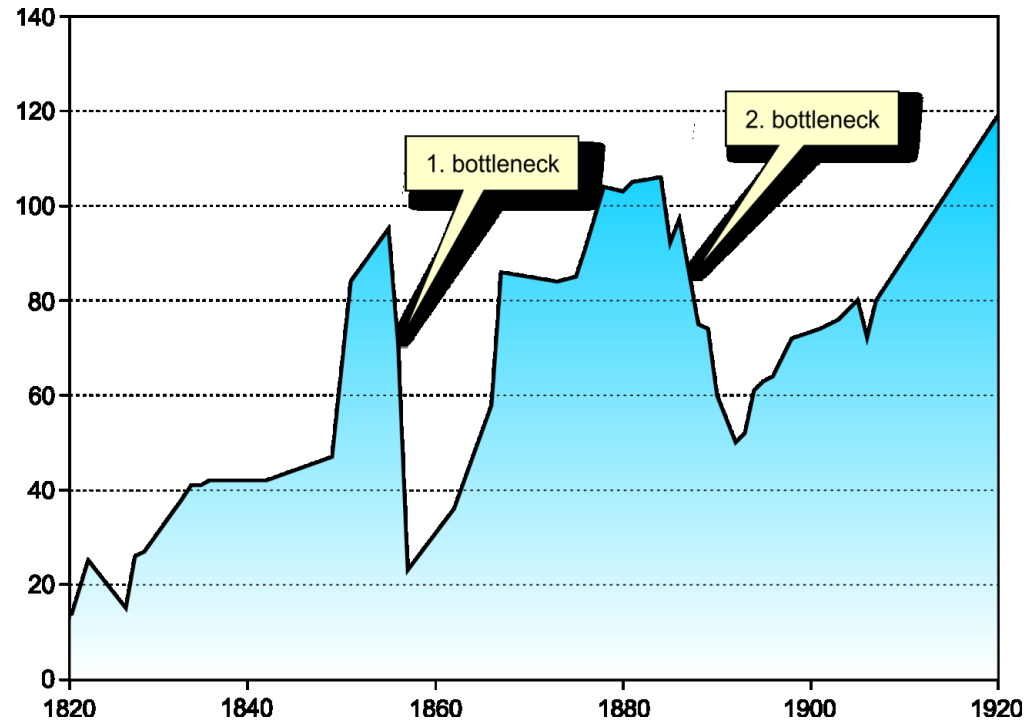
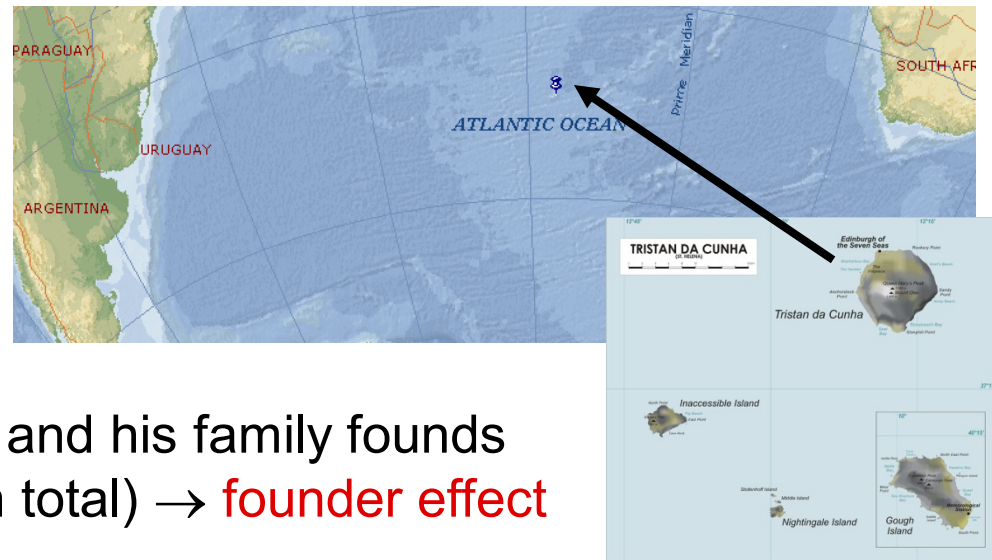
# Tristan da Cunha:

1816 military garrison

1817 garrison withdrawn;

Scottish corporal **William Glass** and his family founds a small colony (20 individuals in total) → **founder effect**

during 80 years 2 strong bottlenecks



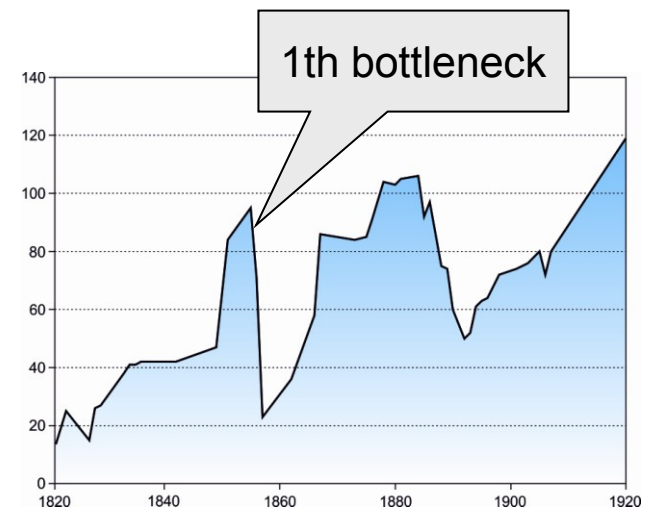
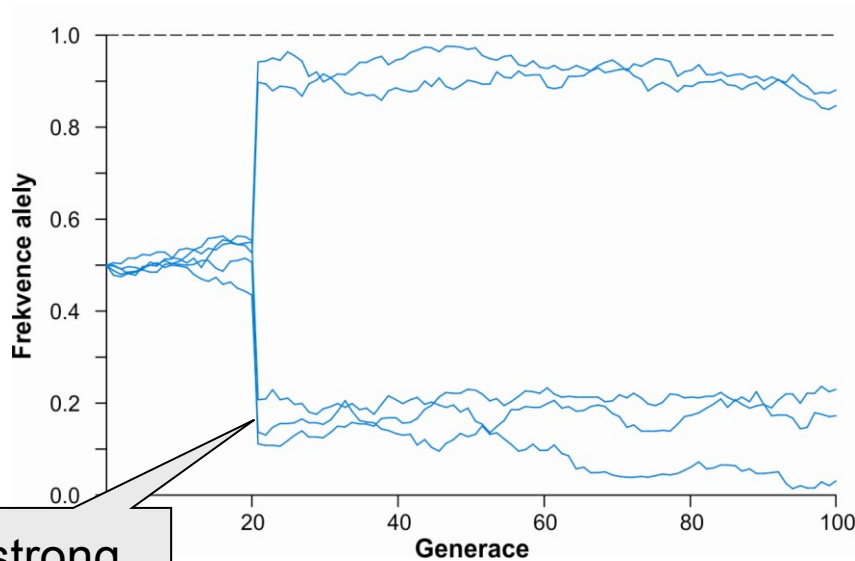


1851: a missionary arrival

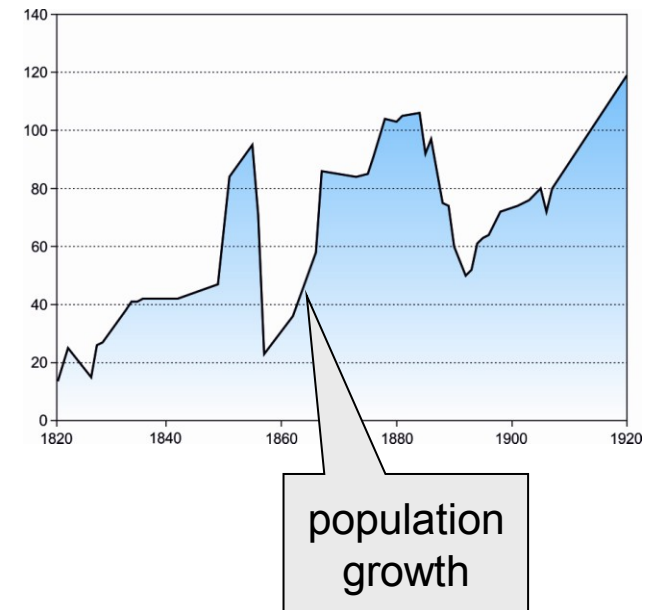
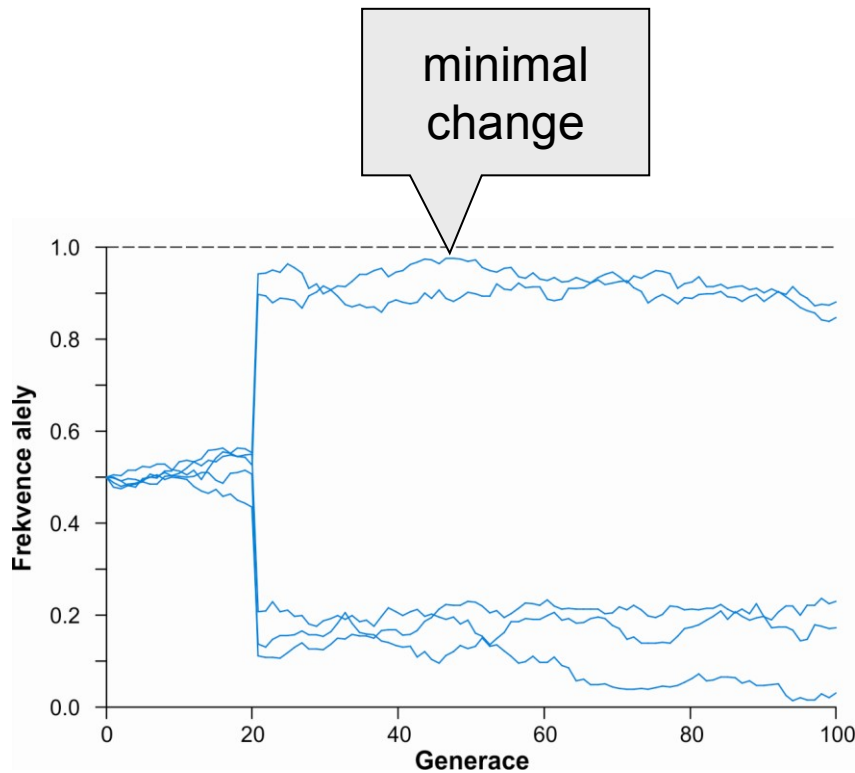
1853: death of W. Glass

1856: departure of 25 Glass's descendants to America, departure of other 45 people with the missionary

⇒ 103 inds. (1855) → 33 (1857) ... **1st bottleneck**

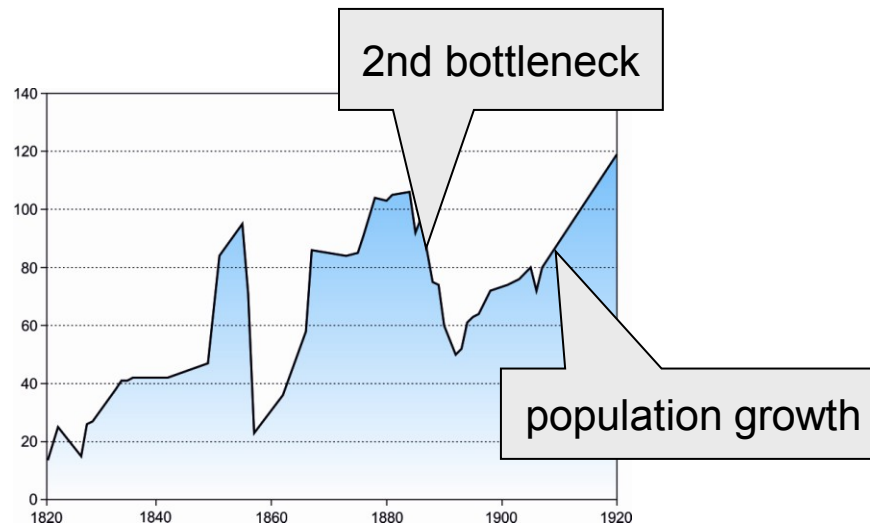


1857–1884: population growth  $\Rightarrow$  conservation of changes caused by previous bottleneck  $\rightarrow$  less changes during 27 years than during 2 years 1855–1857

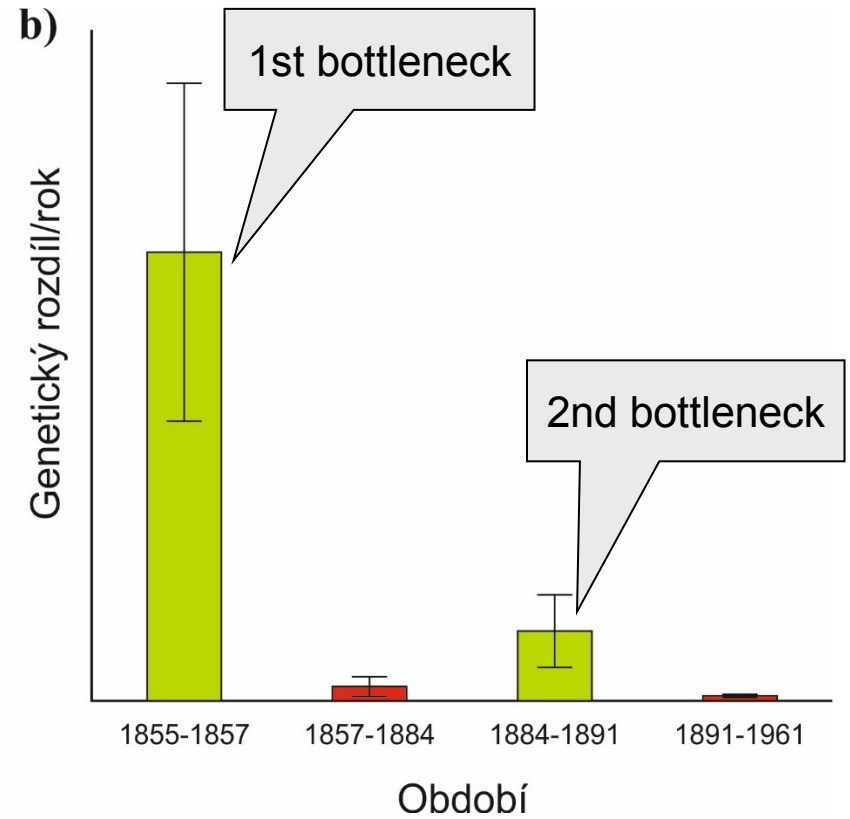
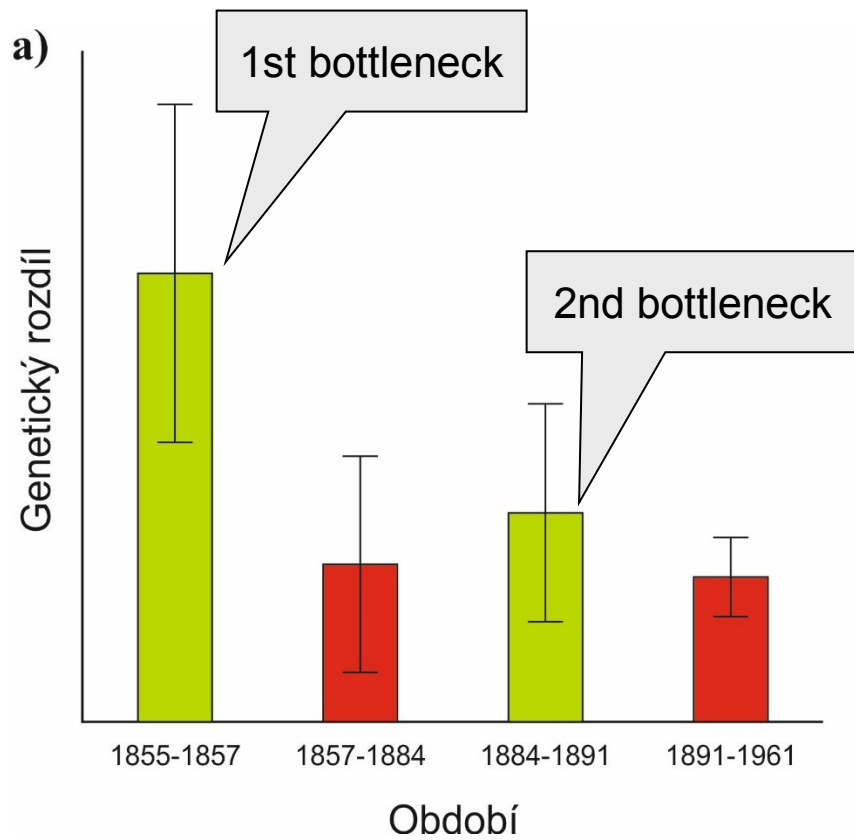


1884–1891: drowning of 15 men, only 4 adult remains, of which 2 very old („Island of Widows“) → departure of many widows with their children

⇒ 106 inds. (1884) → 59 (1891) ... **2nd bottleneck**

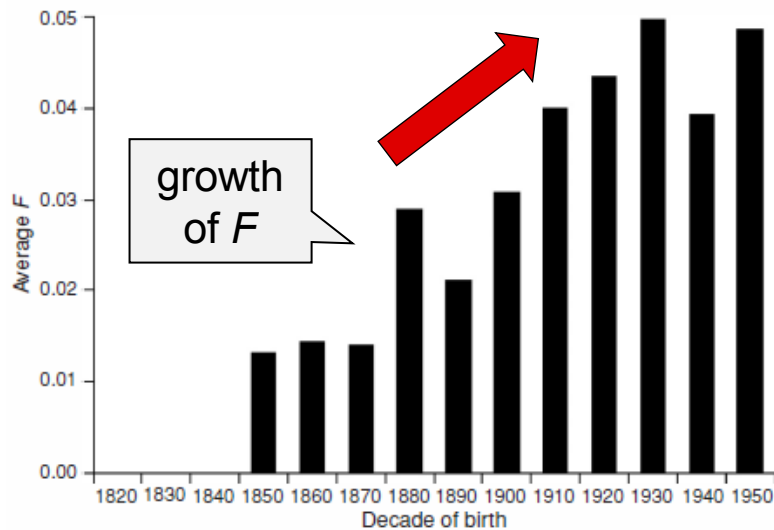


again, the following growth has „frozen“ the changes



Genetic changes during population growth lower than during bottlenecks

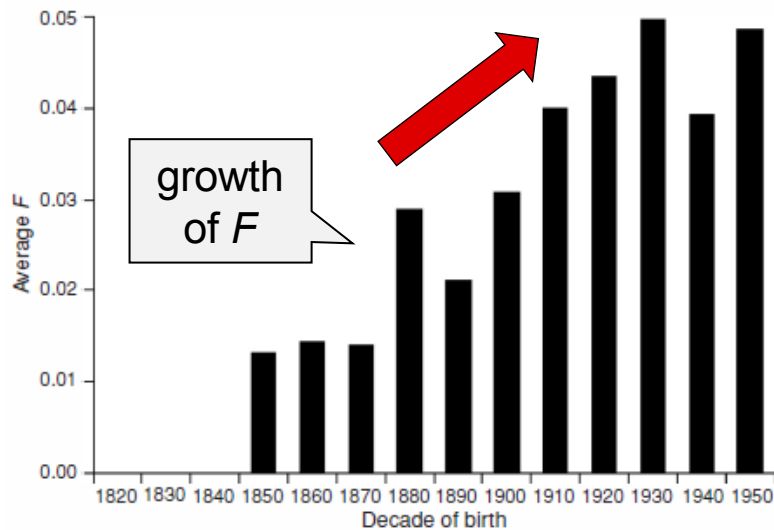
## Inbreeding on Tristan da Cunha:



Despite the outbreeding strategy (choice of the least related partner), ie.  $F_{IS} < 0$ , the level of autozygosity increased



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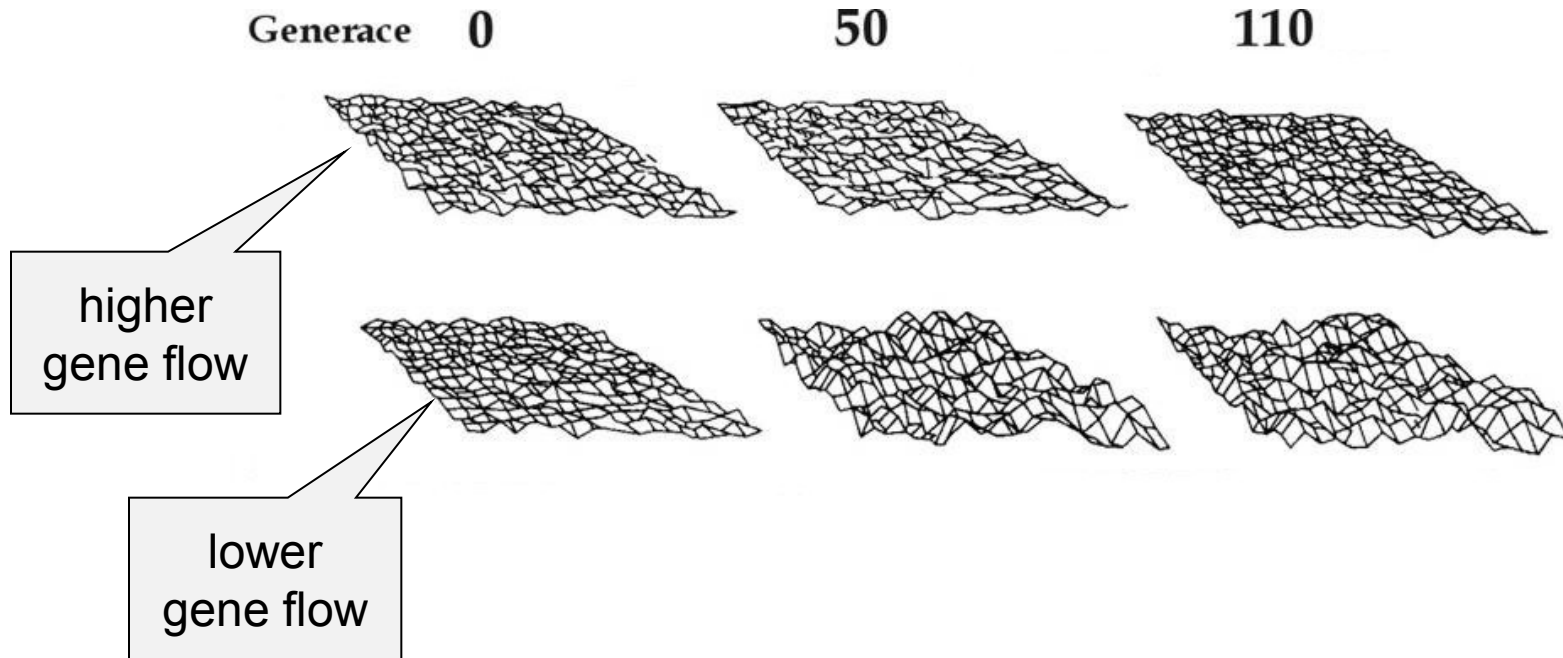
**Table 3.3. First Eight Marriages between Biological Relatives on Tristan da Cunha Showing Date of Marriage, Number of Available Women of Marriageable Age,<sup>a</sup> and Number of Available Women Not Related to Groom**

| Marriage between Relatives | Date of marriage | Number of available women | Number of non relatives |
|----------------------------|------------------|---------------------------|-------------------------|
| 1                          | 1854             | 7                         | 3                       |
| 2                          | 1856             | 9                         | 2                       |
| 3                          | 1871             | 1                         | 0                       |
| 4                          | 1876             | 1                         | 0                       |
| 5                          | 1884             | 7                         | 1                       |
| 6                          | 1888             | 8                         | 0                       |
| 7                          | 1893             | 3                         | 0                       |
| 8                          | 1898             | 1                         | 0                       |

no unrelated woman available!

<sup>a</sup> Sixteen years and over, single, and not a sister of the groom.

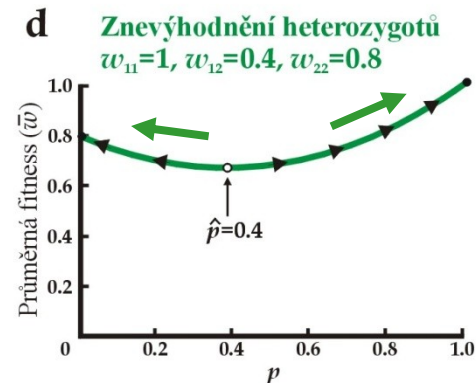
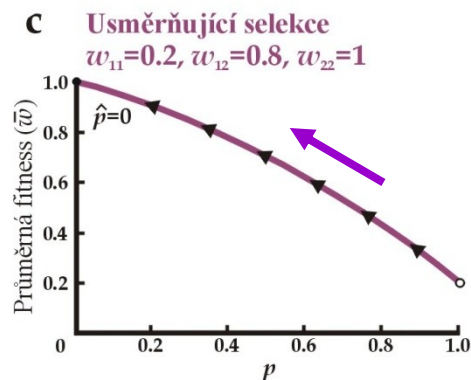
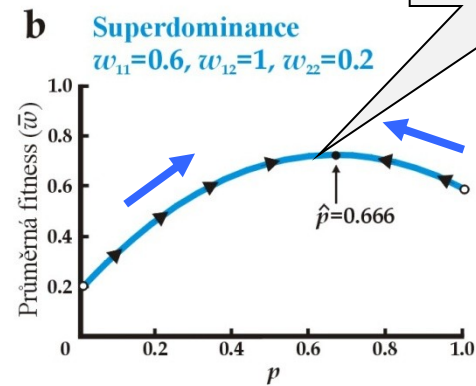
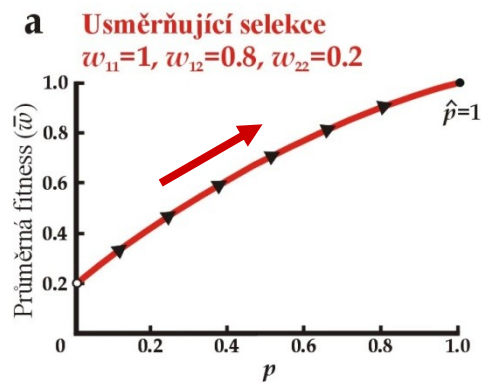
# RELATION BETWEEN DRIFT AND GENE FLOW



Gene flow and drift have opposite effects:  
drift increases divergence among demes × migration „homogenizes“ demes

# RELATION BETWEEN DRIFT AND SELECTION

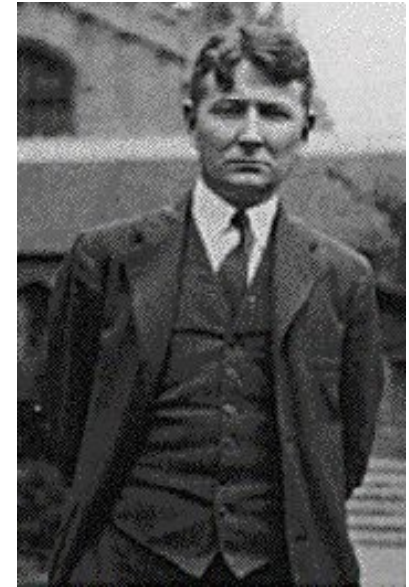
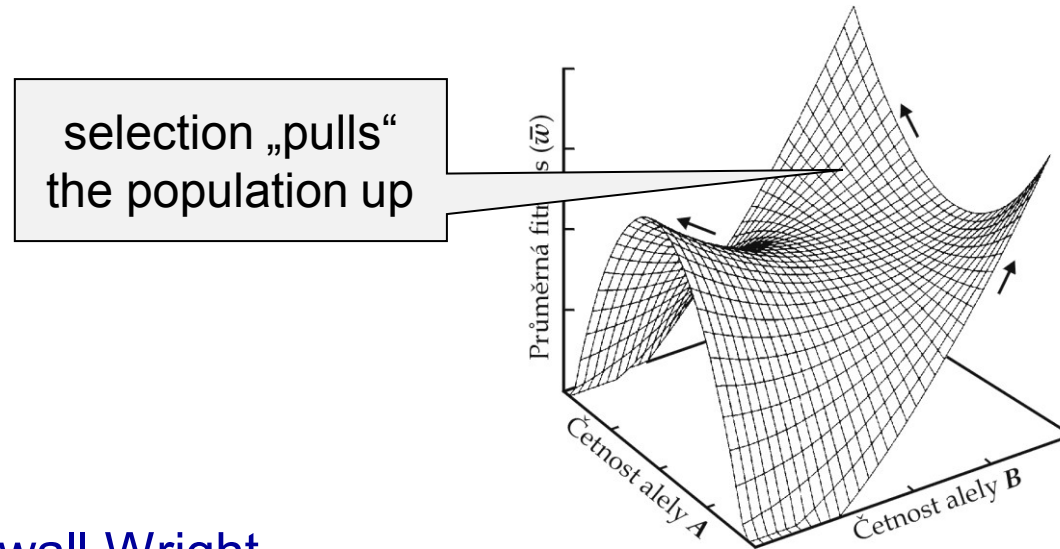
relation between fitness and allele frequency:



adaptive  
landscape



# Adaptive landscape:



## Sewall Wright

The notion of adaptive landscape has 2 mutually incompatible meanings:

1. Allele combinations: fitness values assigned to genotypes  
 $N$  genotypes  $\rightarrow N + 1$  dimensions  
discontinuous surface, population = cluster of points
2. Average allele frequencies  
number of dimensions = number of sets of allele frequencies  
continuous surface

# Shifting balance theory (SBT)

Assumptions:

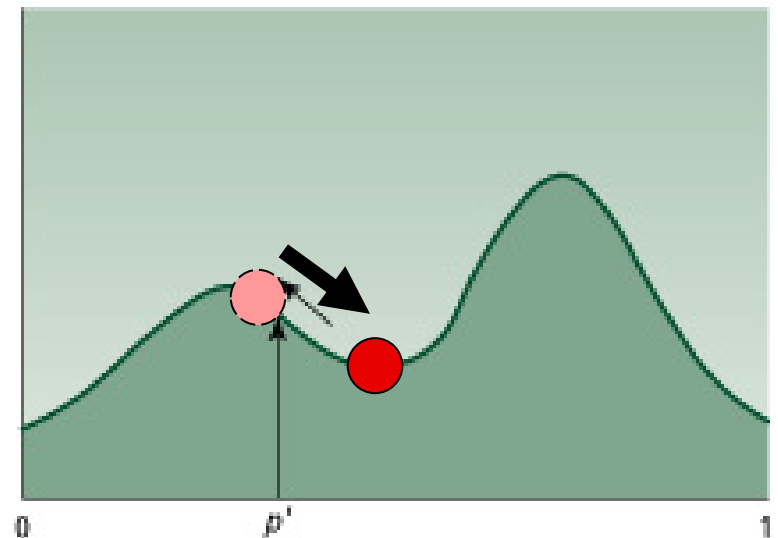
environment changes  $\Rightarrow$  populations in constant change

mutations  $\Rightarrow$  new dimensions, new ways upwards

small populations (drift)  $\Rightarrow$  possibility to move down to adaptive valleys

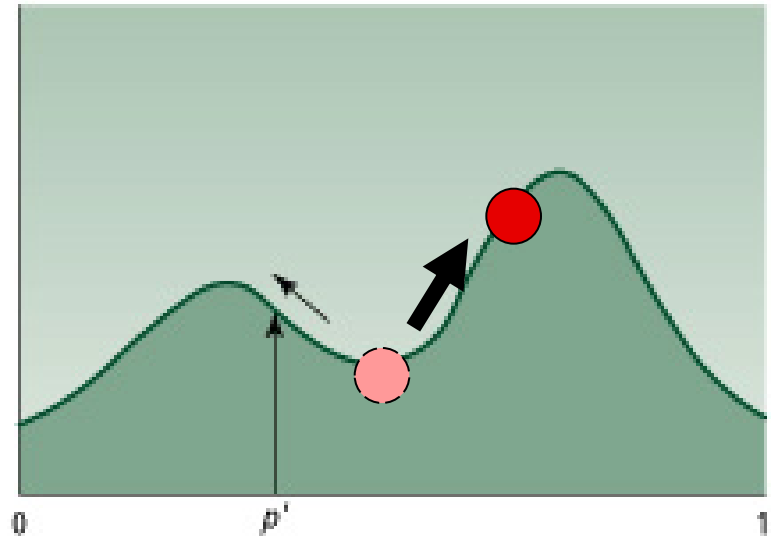
**3 phases of SBT:**

1. contemporary fitness reduction of a local population due to drift  $\rightarrow$  chance to approach the area of attraction of a higher peak



### 3 phases of SBT:

2. intrademic selection → „pulling“ of the population towards a new peak



3. interdemic selection → spread of the deme's members at the higher peak to surrounding demes

The whole process seen as shifting of the balance between drift, intrademic, and interdemic selection

## 2 views on evolution in populations:



S. Wright



R.A. Fisher

small local populations

combination of selection, drift and migration

epistasis, pleiotropy,  
dependence of allele effects on context

speciation as a byproduct of local adaptations in epistatic systems

large panmictic populations

mutation and selection

additive effects of genes,  
allele effects independent of context

disruptive or locally divergent selection