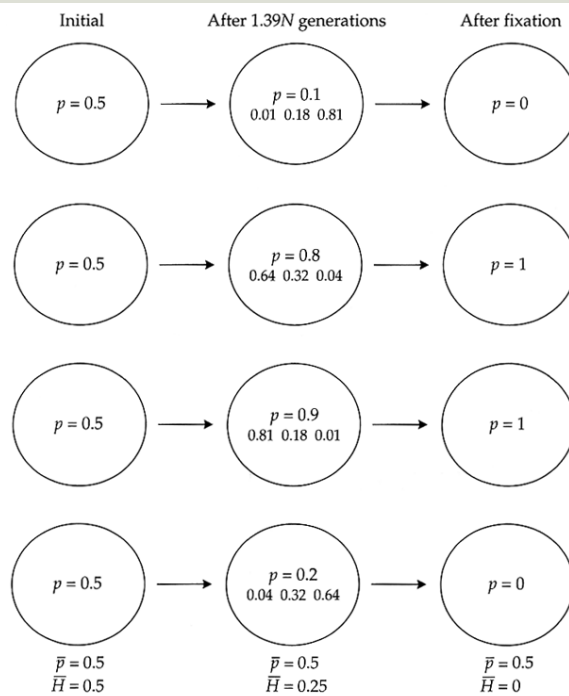


## $F_{ST}$ as variance in allele frequencies

❖ Suppose multiple subpopulations:

Overall average allele frequency stays the same but heterozygosity declines



## $F_{ST}$ as variance in allele frequencies

$$F_{ST} = \frac{\text{var}(p)}{\bar{p}\bar{q}} = \frac{\frac{1}{n} \sum_{i=1}^n (p_i - p)^2}{\bar{p}\bar{q}}$$

- ❖ where  $n$  is the number of populations (and assuming a large number of populations)

## $F_{ST}$ - relationship to genetic variance

- ❖ assuming two alleles, the total reduction in homozygosity is  $2\sigma^2$

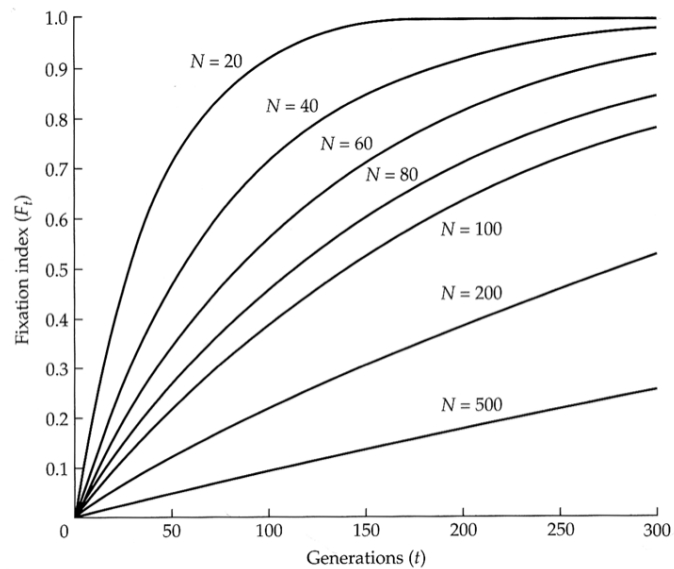
$$F_{ST} = \frac{H_T - H_S}{H_T} = \frac{2\sigma^2}{H_T} = \frac{2\sigma^2}{2\bar{p}\bar{q}} = \frac{\sigma^2}{\bar{p}\bar{q}}$$

- ❖ AMOVA - Analysis of Molecular Variance
  - ❖ partitions the total genetic variation into within and between group components

$F_{ST}$  over time w/ no migration

$$F_t = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right) F_{t-1}$$

$F_{ST}$   
increases with  
time due to  
genetic drift in  
exactly the  
same way as  
 $F_t$



**FIGURE 3.11** Increase of  $F_t$  in ideal populations as a function of time and effective population size  $N$ .

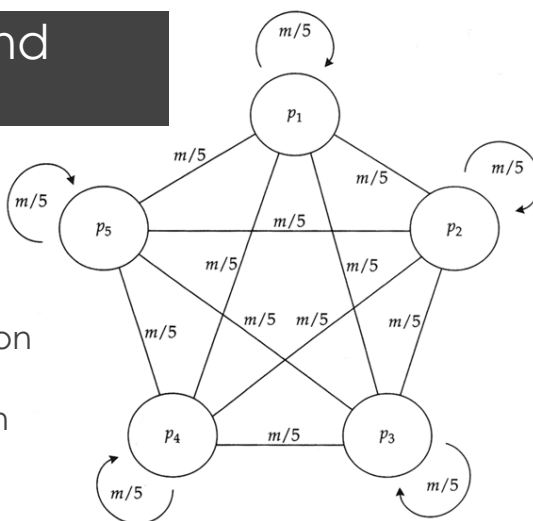
## Migration

- ❖ migration between populations results in *gene flow*, which counters the effects of genetic drift (and selection) and tends to homogenize allele frequencies
- ❖ what level of migration is sufficient to counter the effects of genetic drift?
  - ❖  $Nm \sim 1$  (error on pg. 137?)
- ❖ what level of migration is sufficient to counter the effects of selection?
  - ❖  $m > s$

## The Island Model

assumptions:

- ❖ equal population sizes
- ❖ equal migration rates in all directions



**FIGURE 6.18** The island model of migration with five subpopulations. Migration is completely symmetrical. Each subpopulation contributes individuals or gametes to a pool of migrants, which then distribute themselves randomly among the subpopulations. In this model, a migrant can re-enter the same subpopulation it came from, indicated by the loops.

## Equilibrium value of $F_{ST}$

❖ change in  $F_t$  with migration

$$F_t = \left(\frac{1}{2N}\right)(1-m)^2 + \left(1 - \frac{1}{2N}\right)(1-m)^2 F_{t-1}$$

setting  $\hat{F} = F_t = F_{t-1}$

some algebra + ignoring terms in  $m^2$  and  $m/N$ ...

$$\hat{F} \approx \frac{1}{1+4Nm}$$

## Migration versus mutation

❖ migration

$$F_t = \left(\frac{1}{2N}\right)(1-m)^2 + \left(1 - \frac{1}{2N}\right)(1-m)^2 F_{t-1} \quad \hat{F} \approx \frac{1}{1+4Nm}$$

❖ mutation

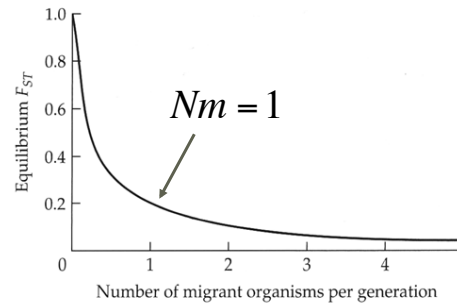
$$F_t = \left(\frac{1}{2N}\right)(1-\mu)^2 + \left(1 - \frac{1}{2N}\right)(1-\mu)^2 F_{t-1} \quad \hat{F} \approx \frac{1}{1+4N\mu}$$

$$m \gg \mu$$

## Equilibrium value of $F_{ST}$

$$\hat{F} \approx \frac{1}{1 + 4Nm}$$

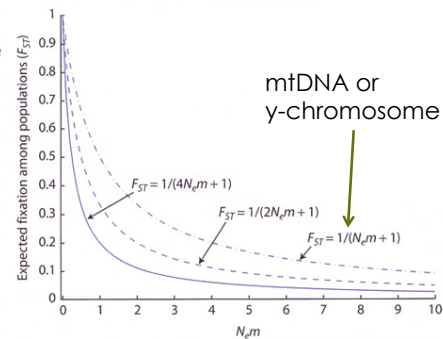
**FIGURE 6.20** Decrease in the fixation index  $F_{ST}$  among subpopulations at equilibrium in the island model of migration. The curve is that in Equation 6.23, giving  $\hat{F}$  as a function of  $Nm$ . In the island model,  $Nm$  is the number of migrant organisms that come into each subpopulation in each generation.



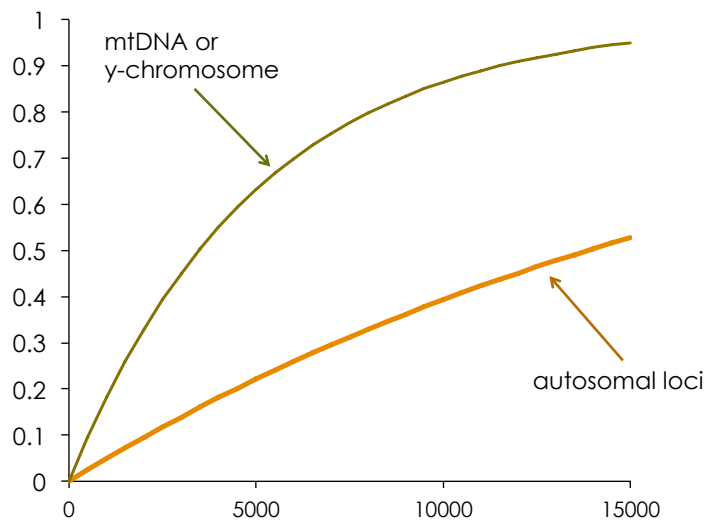
## Equilibrium value of $F_{ST}$

**Figure 4.15** Expected levels of fixation among subpopulations depend on the product of the effective population size ( $N_e$ ) and the amount of gene flow ( $m$ ) in the infinite island model of population structure. Each line represents expected  $F_{ST}$  for loci with different probabilities of autozygosity (from bottom to top  $\frac{1}{2N_e}$ ,  $\frac{1}{N_e}$ , and  $\frac{2}{N_e}$ ).

Marked divergence of allele frequencies among subpopulations ( $F_{ST} \geq 0.2$ ) are expected when  $N_e m$  is below 1 for biparentally inherited nuclear loci with an autozygosity of  $\frac{1}{2N_e}$ . Y-chromosome or mitochondrial loci (autozygosity =  $\frac{2}{N_e}$ ) are examples where marked divergence among populations is expected at higher levels of  $N_e m$ .



## $F_{ST}$ over time w/ no migration

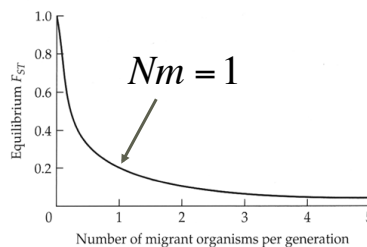


## $Nm = 1$ corresponds to $F_{ST} = 0.2$

### ❖ Wright (1978)

- ❖  $F_{ST} = 0.05$  to  $0.15$  - “moderate differentiation”
- ❖  $F_{ST} = 0.15$  to  $0.25$  - “great genetic differentiation”
- ❖  $F_{ST} > 0.25$  - “very great genetic differentiation”

**FIGURE 6.20** Decrease in the fixation index  $F_{ST}$  among subpopulations at equilibrium in the island model of migration. The curve is that in Equation 6.23, giving  $\bar{F}$  as a function of  $Nm$ . In the island model,  $Nm$  is the number of migrant organisms that come into each subpopulation in each generation.



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## Migration rate vs. Number of migrants

❖ migration rates yielding  $Nm = 1$

❖  $N_e = 100, m = 0.01$

❖  $N_e = 1000, m = 0.001$

❖  $N_e = 10000, m = 0.0001$

❖  $N_e = 100000, m = 0.00001$

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