

The effect of non-random mating within inbred lines on the rate of inbreeding

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In his classical work on inbreeding, Wright (1921) has discussed the effect of a restriction in population size on the rate of approach to homozygosis. In his ideal population, he assumes that individuals mate at random within populations and that they all have the same probability of contributing genes to the next generation. In a bisexual outbreeding population of constant size, the mean number of progeny per parent (counted at the same stage of the generation cycle as were their parents) will be two and the distribution of progeny number will be Poisson. The mean heterozygosity then decreases by a fraction $1/2N$ each generation, being given by the expression $2\bar{q}(1-\bar{q})e^{-t/2N}$ (where \bar{q} is the mean gene frequency in the population from which the lines were derived and N the population size) and the variance in the gene frequency between lines (the genetic drift) is given by $\bar{q}(1-\bar{q})(1-e^{-t/2N})$.

The consequences of the removal of the condition of a Poisson distribution of family size have been dealt with by Wright and also in greater detail by Crow and Morton. The most important conclusion of relevance here is that if the variance of family size is zero and all individuals have two offspring, the effective population size (as measured by the effect on heterozygosity and genetic drift) is doubled. This has been of some practical value in the design of control populations of domestic animals.

In a recent paper on circular mating systems, Kimura & Crow (1963) show that here the heterozygosity declines in the limit by a factor proportional to $1/N^2$, a very surprising conclusion. They discuss this result in terms of mating systems for the minimization of the two separate effects of inbreeding. I shall show in this note that this result is a consequence of non-random mating within inbred lines and that a comparison of the effect of the mating system within lines on heterozygosity and genetic drift, considered separately, can greatly illuminate Kimura and Crow's results. Following them, I shall assume zero variance of family size.

We must first define some quantities. I assume a large series of lines, derived from the same base population using a mating plan identical in all generations. Falconer (1960) used the symbol C , the coefficient of co-ancestry, to denote the probability that gametes taken at random from two individuals contain genes identical by descent. This is, of course, also the coefficient of inbreeding of the progeny of these two, when mated together. I shall use it with the subscript t to denote the mean co-ancestry of pairs of individuals chosen at random within lines at generation t . I shall use the symbol C_t^* for the mean co-ancestry of individuals actually mated together, and this will of course be equal to F_{t+1} . In the classical case, both C and C^* , defined in relation to the base population, will equal $1 - e^{-t/2N}$ but in the cases discussed here they will not necessarily be equal.

It can be shown as follows that C_t is a measure of the drift; in fact that the variance in gene frequency between lines is $C_t\bar{q}(1-\bar{q})$. After one generation of random mating, the proportion of a given homozygote in a line is the square of the gene frequency in that

line so that the average proportion over all lines will be \bar{q}^2 or $\bar{q}^2 + \sigma_q^2$. But, from the definition of C_t as the chance that two genes drawn at random from two individuals themselves drawn at random are identical by descent, we have for the proportion of homozygotes

$$C_t \bar{q} + (1 - C_t) \bar{q}^2 = \bar{q}^2 + C_t \bar{q}(1 - \bar{q})$$

We must further define the terms ‘permanent’ and ‘partial’ separation of a line into sublines. By ‘permanent’, we mean the division into separate groups with completely distinct pedigrees. In such lines, F and C^* tend to unity but C will tend to some value less than unity. Minimization of drift is thus achieved by such permanent sublining. By ‘partial’ sublining is meant the division into groups whose immediate ancestors may be different but in which all sublines become identical by descent at some distance back in the pedigree. With this type of sublining, C , C^* and F tend to unity at the same relative rate at the limit so that $1 - C$, $1 - C^*$, and $1 - F$ remain in the same relative proportion to one another.

We can now discuss various different mating systems when this limiting state has been reached. Kimura and Crow show that the increase in the drift, V , from any generation to the next is proportional to the heterozygosity, H , in the earlier generation, in fact

$$V_{t+1} - V_t = \frac{H_t}{8N}$$

But H_t is equal to $2\bar{q}(1 - \bar{q})(1 - C_{t-1}^*)$ and V_t is equal to $C_t \bar{q}(1 - \bar{q})$, so that

$$V_\infty - V_t = (1 - C_t) \bar{q}(1 - \bar{q})$$

Then

$$\begin{aligned} \frac{V_{t+1} - V_t}{V_\infty - V_t} &= \frac{1}{4N} \frac{1 - C_{t-1}^*}{1 - C_t} \\ &= 1 - \lambda \end{aligned} \tag{1}$$

where λ is the factor by which $1 - C$, $1 - C^*$ and $1 - F$ are reduced each generation.

Thus, because the increase in drift is proportional to the heterozygosity ($1 - C^*$), whereas the distance the system still has to go is dependent on $1 - C$, any mating plan which will make C^* greater than C , i.e. in which the mates are more closely related than the average of the line, will reduce the final rate of approach to homozygosity.

Two special cases

Let us now examine the two extreme cases of circular mating on the one hand and a maximum avoidance system on the other. Kimura and Crow show that with circular mating between N individuals, the final rate of approach to homozygosity is given by

$$\lambda = 1 - \frac{\pi^2}{4(N+2)^2}$$

To derive this, they make use of the symbol $K_t(n)$, which is equivalent to our $1 - C(n)$, the integer inside the bracket referring to the distance apart of the individuals in the circle. Matings are then made between individuals with $n = 1$. They then develop a matrix of equations expressing the K values for one generation in terms of those in the previous generation and derive the characteristic roots of the matrix, the largest of which tends to $1 - \pi^2/4(N+2)^2$ when N is large. Unfortunately, they did not derive the general expression for $K(n)$ which is crucial to this argument. This proves to be

$$K(n) \simeq k \sin \frac{\pi(n+1)}{N+2}$$

where k is a constant, decaying by a proportion λ each generation. $C(n)$, equal to $1 - K(n)$ is then an inverted sine curve, with a value of $1 - (2\pi k)/(N + 2)$ between the individuals adjacent to each other in the circle, which are mated together, and a value of $1 - k$ between the individuals diametrically opposite to each other in the circle. As the average value of a sine curve between 0 and π is $2/\pi$, the value of $1 - C_t$ is $(2k)/(\pi)$ and that of $1 - C_t^*$ is $(2\pi k)/(N + 2)$. We have then from (1)

$$1 - \lambda = \frac{1}{4N} \frac{\pi^2}{(N + 2)}$$

in good agreement with Kimura and Crow's result. We see then that a circular mating system is a special case of sublining in which the relationship between individuals falls off the further apart they are in the circle.

Let us turn now to the maximum avoidance system, most simply considered for a population size which is an integral power of 2. By adequate control of the mating system in a population of size 2^m it is possible to avoid mating together individuals which have a common ancestor in the last m generations. C^* thus lags m generations behind C so that we may write

$$\frac{1 - C_{t-1}^*}{1 - C_t} = \lambda^{-(m+1)}$$

which then gives from (1)

$$1 - \lambda = \lambda^{-(m+1)}/2^{m+2} \tag{2}$$

as an equation for λ which has an approximate solution

$$1/(1 - \lambda) = 2^{m+2} - (m + 1)$$

Examination of the mating system using classical methods shows that the characteristic equation is

$$1 + 2\lambda + \dots + 2^m \lambda^m - 2^{m+1} \lambda^{m+1} = 0$$

which simplifies to

$$2^{m+2} \lambda^{m+1} (1 - \lambda) = 1$$

which is identical to equation (2). The effective population size is thus not 2^{m+1} but $2^{m+1} - (m + 1)/2$. The 'maximum avoidance' system thus avoids inbreeding in the initial generations at the expense of slightly greater rate of loss of heterozygosity at the limit.

We may therefore summarize our conclusions as follows:

1. Reduction of genetic drift to a minimum requires the formation of permanent sublimes.
2. If sublining is only partial, then the proportional rate of decline in heterozygosity is equal to the rate of approach of genetic variance between lines to its final value.
3. If mating is at random, the decline in heterozygosity lags one generation behind the genetic drift.
4. If mating is not at random within a line, then the decline in heterozygosity may be ahead of the drift (implying the mating together of close relatives and the formation of partially separate sublimes) or it may be behind it if matings between relatives are avoided as much as possible.
5. The mating together of close relatives within the line leads to greater initial inbreeding but a lower final rate of approach to the limit. The converse will be true for maximum avoidance systems.
6. Any degree of sublining will reduce the final rate of decline in heterozygosity and the more the sublining the lower the rate of decline. The extreme case of this is a set of selfed lines which are intermated every thousand or so generations. As a corollary to this, we

have the paradox that the occasional insertion of a generation of selfing in an otherwise random breeding population actually reduces the rate of inbreeding. Circular mating systems are thus a special type of sublining in which the mating system follows the same plan in each generation.

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