THE EFFECT OF LITTER CULLING—OR FAMILY PLANNING—ON THE RATE OF NATURAL SELECTION[1]

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IN his classic paper "A Mathematical Theory of Natural and Artificial Selection," HALDANE (1924) devotes some space to the consideration of "those cases where the struggle occurs between members of the same family." HALDANE termed this *familial selection*, citing as an example the matings of yellow by yellow mice from which litters are no smaller than normal, although one quarter of the embryos die in the blastula stage. The criteria for familial selection are that the number of survivors in each family is unchanged, although differential genetic deaths occur within families.

HALDANE (1924) stated that "... familial selection occasionally occurs through natural causes, but never through human agency." However, the criteria are met whenever any arbitrary limitation of family size is regularly imposed. Genetic deaths which occur prior to such arbitrary limitation constitute familial selection. Compensation, the replacement of genetic losses with viable full subs, is implicit in all such cases.

Four general instances suggest the need for review and further consideration of the effects of familial selection on the rate of change in gene frequencies: (1) The practice by commercial and laboratory animal breeders of culling litters to uniform sizes; (2) The use of certain breeding methods which reduce genetic drift through equal representation of each sibship (GOWE, ROBERTSON and LATTER 1959; LÜNING 1960; KING 1964); (3) Certain plant genetics studies in which thinning is regularly employed; (4) The arbitrary limitation of human family size through contraception (i.e., family planning).

HALDANE (1924) demonstrated that in the case of recessives with small unfavorable effects on fitness, the rate of elimination with familial selection is half that expected in ordinary selection, and that sex linked recessives are selected against at from one third to one half the ordinary rate. His approach will be used in the present paper to extend consideration to some other classes of alleles. For the reader's benefit, HALDANE's solutions for genotypic frequencies for recessives with small effects are included. The nomenclature has been changed in accordance with modern usage, using LI (1955) as a model.

If matings in generation n are random, the adult genotypes of generation $n + 1$ are as shown in Table 1.

It should be noted that the Hardy-Weinberg distribution does not hold where

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TABLE 1

Genotypes surviving with familial selection

Mating	Mating frequency	Surviving genotypic frequencies		
		AA	*Aa*	*aa*
$AA \times AA$	D^2	D^2	....	....
$AA \times aa$	$2DR$	....	$2DR$	....
$aa \times aa$	R^2	....	....	R^2
$Aa \times AA$	$4DH$	$4DH\left(\frac{a}{a+b}\right)$	$4DH\left(\frac{b}{a+b}\right)$	....
$Aa \times Aa$	$4H^2$	$4H^2\left(\frac{a}{a+2b+c}\right)$	$8H^2\left(\frac{b}{a+2b+c}\right)$	$4H^2\left(\frac{c}{a+2b+c}\right)$
$Aa \times aa$	$4HR$	....	$4HR\left(\frac{b}{b+c}\right)$	$4HR\left(\frac{c}{b+c}\right)$
Total:	1	D_{n+1}	$2H_{n+1}$	R_{n+1}

$$[AA]\ D_{n+1} = D^2 + 4Ha\left[\frac{D}{a+b} + \frac{H}{a+2b+c}\right]$$

$$[Aa]\ H_{n+1} = DR + 2Hb\left[\frac{D}{a+b} + \frac{2H}{a+2b+c} + \frac{R}{b+c}\right]$$

$$[aa]\ R_{n+1} = R^2 + 4Hc\left[\frac{H}{a+2b+c} + \frac{R}{b+c}\right]$$

there is familial selection. For this reason it is necessary to work with genotypic frequencies as well as gene frequencies. The frequencies of genotypes AA, Aa, and aa are represented by D, $2H$, and R; their respective viabilities by a, b, and c. The frequency of allele a is $q = H + R$; of A is $1 - q = D + H$. The coefficient of selection s is such that for every unaffected zygote surviving to the age at which family size limitation is imposed, $1 - s$ affected zygotes survive.

Changes in Gene Frequency

1. *Recessive alleles with small deleterious effects on fitness:* Let $a = b = 1$; $c = 1 - s$. Then

$$H_{n+1} = DR + DH + \frac{4H^2}{4-s} + \frac{2HR}{2-s} = (D+H)(H+R) + sH\left[\frac{H}{4-s} + \frac{R}{2-s}\right] =$$

$$q(1-q) + sH\left[\frac{H}{4-s} + \frac{R}{2-s}\right];$$

$$R_{n+1} = R^2 + \frac{4H^2}{4-s} + \frac{4HR}{2-s} - 4sH\left[\frac{H}{4-s} + \frac{R}{2-s}\right] =$$

$$(H+R)^2 - sH\left[\frac{3H}{4-s} + \frac{2R}{2-s}\right] = q^2 - sH\left[\frac{3H}{4-s} + \frac{2R}{2-s}\right];$$

$$q_{n+1} = H_{n+1} + R_{n+1} = q - sH\left[\frac{2H}{4-s} + \frac{R}{2-s}\right];$$

$$\Delta q = -sH\left[\frac{2H}{4-s} + \frac{R}{2-s}\right].$$

Since H differs from $q(1-q)$ and R differs from q^2 by amounts less than sH, for small values of s

$$\Delta q \cong -sq^2(1-q)\left[\frac{2-2q}{4-s} + \frac{q}{2-s}\right] \cong -\tfrac{1}{2}sq^2(1-q) - \frac{s^2q^2(1-q)^2}{8} \cong -\tfrac{1}{2}sq^2(1-q).$$

This is one half the rate of selection without compensation (HALDANE 1924).

2. *Recessive lethal alleles:* Let $a = b = 1$; $c = 0$. Then $R = 0$; $H = q$; $D = 1-2q$. $R_{n+1} = R^2 = 0$;

$$q_{n+1} = H_{n+1} = q(1-2q) + \frac{4q^2}{3} = q - \frac{2q^2}{3}$$

$$\Delta q = -\frac{2q^2}{3}.$$

The rate of selection without compensation (ibid.) is:

$$\Delta q = -\frac{q^2}{1+q}.$$

With familial selection recessive lethals are eliminated about two thirds as rapidly as under ordinary selection, or more precisely $\frac{2}{3}(1+q)$ as rapidly.

3. *Dominant deleterious alleles with recessive lethality:* Let $a = 1$; $b = 1-s$; $c = 0$. Then $D = 1-2q$; $H = q$; $R = 0$; and

$$q_{n+1} = H_{n+1} = 2q(1-s)\left[\frac{1-2q}{2-s} + \frac{2q}{3-2s}\right] = q - q\left[\frac{4q+s-4qs}{2-s} + \frac{4q-4qs}{3-2s}\right];$$

$$\Delta q = -\frac{sq}{2-s} - \frac{2q^2}{3} + sq^2\left[\frac{2}{3} + \frac{2}{9-6s} + \frac{1}{4-2s}\right].$$

The corresponding rate of change in a population without compensation is:

$$\Delta q = -\frac{sq}{1+q} - \frac{q^2}{1+q} + \frac{2sq^2}{1+q-2sq}.$$

Thus, in both types of selection Δq can be expressed as the sum of three terms of the order of sq, q^2, and sq^2. If q is small relative to s, the first terms are operative, and the allele is selected against as a heterozygote; the relative efficiency of familial selection is $\frac{1+q}{2-s}$. If s is small relative to q, the allele is selected against primarily as a recessive lethal homozygote, the second terms are operative, and the relative efficiency of familial selection is $\frac{2}{3}(1+q)$.

4. *Additive alleles affecting fitness:* In noncompensating panmictic populations the within-sibship component of additive genetic variance is half the total additive genetic variance; one might expect then that limiting selection to within

sibships should reduce the rate of selection by half. (The author is indebted to PROF. JAMES F. CROW for this observation.) The HALDANE method confirms this. Let $a = 1+s$; $b = 1$; $c = 1-s$. Then, with familial selection,

$$H_{n+1} = DR + 2H\left[\frac{D}{2+s} + \frac{H}{2} + \frac{R}{2-s}\right] = (D+H)(H+R) - sH\left[\frac{D}{2+s} - \frac{R}{2-s}\right];$$

$$R_{n+1} = R^2 + 4H(1-s)\left[\frac{H}{4} + \frac{R}{2-s}\right] = (R+H)^2 - sH\left[H + \frac{2R}{2-s}\right];$$

$$q_{n+1} = H_{n+1} + R_{n+1} = q(1-q) + q^2 - sH\left[\frac{D}{2+s} + \frac{2H}{2} + \frac{R}{2-s}\right];$$

$$\Delta q = -\frac{sH}{2} + s^2H\left[\frac{D}{2+s} - \frac{R}{2-s}\right].$$

For small values of s, $H \cong q(1-q)$ and

$$\Delta q \cong -\tfrac{1}{2}\, sq(1-q),$$

or half the corresponding rate with ordinary selection.

DISCUSSION

Familial selection on a population level, as calculated above, requires complete and rigorous compensation for every genetic loss. Obviously, this is rarely possible. There will always be some matings which will never produce the predetermined number of living offspring, resulting in the possibility of direct genetic losses without compensation. Furthermore, not all genetic effects on fitness are subject to compensation. Those causing deaths prior to the arbitrary culling of litters (animals), or deaths prior to the termination of the parental reproduction period (humans) are subject to compensation; those affecting adult longevity, or causing complete sterility, are not.

Aside from complete sterility, however, genotypes which affect fertility are even more drastically affected by compensation. This applies also to genetically based maternal effects on early survival—and, surprisingly, includes the semisterility of translocation heterozygosis. Familial selection acts only on the genetic differences between sibs; deleterious parental genotypes are not selected against at all so long as the predesignated number of viable progeny is attainable. For these genetic effects, so long as full compensation occurs, $\Delta q = 0$.

Some measure of compensation is present in all mammalian populations. In animals with large litters, the embryonic and perinatal deaths of a few individuals increase the survival chances of their sibs, and the number of reproducing adults from that sibship may be unchanged. In human populations, even in the absence of deliberate progeny-limiting practices, there is probably a high degree of compensation for preimplantation losses, since the female then becomes able to conceive again sooner than would have been the case had implantation been successful.

Intermediate degrees of compensation should presumably result in intermediate rates of selection. With overcompensation (more than one viable additional zygote for every zygote lost) the rates of selection are further reduced and

even, in some cases, reversed; LEWONTIN (1953) has shown that a high degree of overcompensation can result in a stable genetic equilibrium. If mutation is taken into account, a more modest degree of compensation or overcompensation could result in a fairly high equilibrium frequency. Complete compensation (familial selection), over a long period, will result in equilibria at which genetic losses are between 1½ and 2 times as frequent as new mutations.

Family planning frequently has other objectives than the limitation of progeny number to an arbitrary size. It is often employed in consideration of the physical or mental health of the parents or other members of the family, or even in consideration of known familial genetic defects. In such cases, contraception should often have the effect of increasing the rate of selection against deleterious alleles.

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SUMMARY

Familial selection, or the arbitrary limitation of the number of progeny of each mating pair in a population (as by litter culling or family planning), reduces the rate of natural selection by eliminating between-family selection. Selection against recessive lethals is reduced to about two thirds of the normal rate; the rates of selection against recessive, dominant and additive alleles with small deleterious effects on fitness are halved. Selection rates against many alleles affecting fecundity are likely to be still more sharply reduced.

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