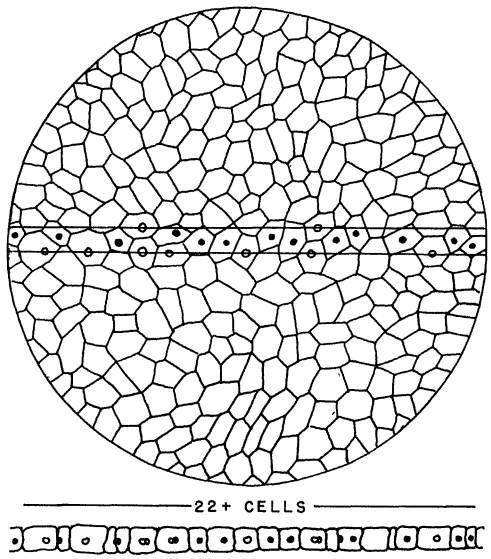

FIG. 2. Surface and hypothetical sectional views of a layer of amphibian epidermal cells.

of length stabilized within ±1% of 53.5 μ and those of width within ±1% of 12.5 μ after 100 measurements. The cumulative estimates of the length of the long (7.6 μ) and short (5.6 μ) axes of the oblately spheroidal nuclei stabilized within ±1% after 40 measurements. Equal stability of the cytoplasm/nucleus ratio (28.7) was not obtained until after 1800 hits had been registered. Palisade cell volume by the length/width formula was 5540 μ^3 and by the nuclear volume–cytoplasm/nucleus ratio method was 5025 μ^3. The two values differ by less than ±5% of their mean.

In sections tangent to the surface of an epithelium, the number of cells per unit area can be determined by direct counts per field or per unit area of an ocular counting grid. When it is necessary to make similar determinations on tissues section at right angles to the surface these can be based on measurements on the mean chord of the cell cross section measured in a plane parallel to the epithelial surface. Cross sections of epithelial cells have, in general, the six sides of the 14-hedron cross section. Since the area a of any regular polygon with n sides of length s can be expressed as $a = \frac{1}{4}ns^2 \cot 180/n$ we can substitute this for a in the mean chord formula, $c = \pi a/ns$, and obtain $c = \pi/4 (ns^2 \cot 180/n)/ns$. Simplifying we get $s = (4c \tan 180/n)\ \pi$ which, substituted in the original area formula yields $a = (4nc^2 \tan 180/n)\pi^2$ or, $0.405\ nc^2 \tan 180/n$ for any polygon, $1.405c^2$ for the hexagon and $1.460c^2$ for the pentagon.

In the stretch preparation of frog epidermis outlined in Fig. 2, an average of 23 cells is intercepted along the field diameter ($2r$) and the length of the mean chord is $0.087r$. Assuming the number of sides per cell to be 6, the area of the cross section of the average cell is $0.0106r^2$ in a field of area of $3.142r^2$. The number of cells per field is then 3.142/0.0106 or 296. If the cell outline is assumed to be pentagonal the count is 286. The actual count in the field is 287. With either assumption, the error does not exceed 3%.

The assumption that closely packed cells in parenchymatous and epithelial tissues are 14-hedra permits formulation of the cell volume and density in terms of parameters easily measured by ocular micrometry or camera lucida methods. In general these parameters are the largest linear dimensions of the cell or can be measured in terms of numbers of cells intercepting a line of optimal length (*7*). In contrast, the check method, while more applicable to cells of highly irregular shape, requires an assumption as the shape of the smaller and hence less easily measured nucleus. Other methods applicable to cells regardless of shape (*9*) are dependent upon the use of special apparatus.

References

1. DUFFY, R. M. *Am. J. Botany,* **38**, 393 (1951).
2. LEWIS, F. T. *Proc. Am. Acad. Arts Sci.,* **68**, 251 (1933).
3. ———. *Am. J. Botany,* **30**, 74 (1943).
4. MARVIN, J. W. *Ibid.,* **26**, 487 (1939).
5. MATZKE, E. B. *Bull. Torrey Botan. Club,* **54**, 341 (1927).
6. ———. *Am. J. Botany,* **36**, 799 (1949).
7. CHALKLEY, H. W., CORNFIELD, J., and PARK, H. *Science,* **110**, 295 (1949).
8. CHALKLEY, H. W. *J. Natl. Cancer Inst.,* **4**, 47 (1943).
9. ———. *Anat. Record,* **103**, 17 (1949).

Manuscript received July 27, 1953.

An Effect of Negative Assortative Mating on Gene Frequency[1]

Ray Moree

Department of Zoology,
State College of Washington, Pullman

In the theory of the genetic structure of populations it is a common consideration that a change in mating system does not result in a change in gene frequency, selective mating excepted. Although this relation holds for inbreeding and for positive assortative mating, it can be shown that under at least some conditions it does not hold for negative assortative mating. One of such conditions is that involving a single autosomal gene-pair in which one member is completely dominant over its allele. The common point of departure for discussion of the effect of assortative mating (either positive or negative) on a population so composed is that deviation from panmixia occurs on a phenotypic basis, while within the dominant phenotype mating remains at random when it occurs at all (*1–6*). The simplest example is afforded by complete negative assortative mating, wherein matings occur only between phenotypically unlike individuals.

Suppose, as have Hogben (*2*) and Li (*4*), that the initial population consists of genotypes *AA, Aa,* and *aa,* and that, as defined, the only matings occurring be $AA \times aa$ and $Aa \times aa$. Then the next generation will consist of *Aa* and *aa* and the only mating occurring will be $Aa \times aa$. Regardless of the frequencies of these

[1] Supported in part by funds provided for medical and biological research by the State of Washington Initiative Measure No. 171.

TABLE 1

CHANGE IN FREQUENCY (q) OF A RECESSIVE GENE UNDER DIFFERENT DEGREES OF NEGATIVE ASSORTATIVE MATING

Generation	c				
	0	−0.25	−0.50	−0.75	−1.00
0	0.50	0.50	0.50	0.50	0.50
1	0.50	0.54	0.58	0.63	0.67
5	0.50	0.65	0.71	0.74	0.75
10	0.50	0.70	0.73	0.74	0.75
∞	0.50	0.75	0.75	0.75	0.75

two genotypes the third generation will occur as 0.5 $Aa + 0.5$ aa. This represents the equilibrium condition under which A has a frequency of 0.25 and a of 0.75, regardless of their initial values. But since complete negative assortative mating occurs rarely if at all in nature, a more general method of calculating is needed if the effects of such a mating system are to be conveniently assessed.

Let the genotypes AA, Aa, aa have the respective frequencies α, β, γ; let the alleles A, a have respective frequencies p, q; let the phenotypes $A-$, aa have respective frequencies D $(=\alpha+\beta)$ and R $(=\gamma)$; and let the mating types $A-\times A-$, $A-\times aa$, $aa\times aa$, have the respective frequencies x, y, z $(\alpha+\beta+\gamma = p+q = D+R = x+y+z = 1)$. Finally, let the coefficient of assortative mating c be measured on the usual correlation scale. Since panmixis occurs at $c = 0$ and since only negative values of c are of interest here, we may set up the definition

$$c = \frac{x_- - x_0}{x_0} = \frac{y_- - y_0}{y_0 - 1} = \frac{z_- - z_0}{z_0}$$

where the − subscript indicates negative assortative mating and the 0 subscript indicates panmixis.

Then, with $c = 0$,

$$x = x_0, \qquad y = y_0, \qquad z = z_0$$

and

$$(\alpha+\beta+\gamma)^2 = D^2 + 2DR + R^2 = \alpha' + \beta' + \gamma' = 1$$

where primes indicate the subsequent generation. Collecting the indicated segregation classes according to genotype, gives

$$\alpha' = p^2, \qquad \beta' = 2pq, \qquad \gamma' = q^2. \tag{1}$$

And if gene frequencies remain constant,

$$\alpha' = \alpha, \qquad \beta' = \beta, \qquad \gamma' = \gamma.$$

Similarly, with $-1 \leqslant c \leqslant 0$,

$$x = x_- = x_0 + cx_0 = (1+c)x_0, \qquad y = y_- = y_0 - c(x_0 + z_0) = (1+c)y_0 - c, \qquad z = z_- = z_0 + cz_0 = (1+c)z_0$$

and

$$(\alpha+\beta+\gamma)^2 = (1+c)D^2 + 2DR(1+c-c/y_0) + (1+c)R^2 = \alpha' + \beta' + \gamma' = 1.$$

Proceeding as for (1),

$$\alpha' = (1+c)p^2, \qquad \beta' = [2q(1+c) - c/D]p, \qquad \gamma' = (1+c)q^2 - c\beta/2D. \tag{2}$$

But when $-1 \leqslant c < 0$,

$$\alpha' \neq \alpha, \qquad \beta' \neq \beta, \qquad \gamma' \neq \gamma.$$

When $c = 0$, (2) reduces to (1).

Genotype frequencies for any desired generation may be calculated by (2), used iteratively. Then, since $q = 0.5\beta + \gamma$, under any mating system, the effect of negative assortative mating upon q may readily be determined (Table 1). The determination of the limiting values of q (Table 1), together with the equilibrium properties of negative assortative mating, will be discussed elsewhere. From the present discussion it is clear that the mating system in question necessarily results in changed gene frequencies and that no selective action, as it is customarily defined, is at all involved in the change.

References

1. HALDANE, J. B. S. *Proc. Cambridge Phil. Soc. (Biol. Sci.)*, **1**, 158 (1924).
2. HOGBEN, L. *An Introduction to Mathematical Genetics.* New York: Norton, 1946.
3. JENNINGS, H. S. *Genetics*, **1**, 53 (1916).
4. LI, C. C. *An Introduction to Population Genetics.* Peiping: Natl. Peking Univ. Press, 1948 (lithoprint reproduction by Oregon State College Press, Corvallis).
5. WENTWORTH, E. N., and REMICK, P. *Genetics*, **1**, 608 (1916).
6. WRIGHT, S. *Ibid.*, **6**, 144 (1921).

Manuscript received August 4, 1953.

Weather Influence in Blue Comb in Chickens[1]

Glenn Van Ness[2]

Department of Veterinary Science, University of Florida, Gainesville

Blue comb in poultry is a pathological complex resembling shock in the early phase, with enteritis and nephritis in less acute cases. Accumulated data on field outbreaks in Florida indicated that climatic stress might be a contributing factor in the development of the disease. A maximum temperature exceeding 85° F was found to occur 3 or 4 days before cases were presented to the laboratory for diagnosis. Cold weather stress was an insignificant factor in the development of outbreaks, probably on account of the low humidity.

The possibility that the climatic stress was a local factor encouraged the study of climatic stress in another weather province. The New England states were selected because they have had experience with blue comb. Several diagnostic laboratories are available, and geographic variability is less than in many other service areas.

During 1951, the maximum temperature recorded at Boston was used to provide the state diagnostic laboratories with a prediction of blue comb. They were asked to report the days when cases were presented to the laboratory. Several factors enter into this comparison. A less observant poultryman might delay presenting the problem to the laboratory. Some cases of blue comb not due entirely to climatic factors may

[1] Florida Agricultural Experiment Station Journal Series, No. 173.

[2] The cooperation of G. Snoyenbos, G. P. Faddoul, E. Jungherr, F. E. Allen, and B. Wasserman is gratefully acknowledged.