NATURAL SELECTION FOR WITHIN-GENERATION VARIANCE IN OFFSPRING NUMBER II. DISCRETE HAPLOID MODELS

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ABSTRACT

In the classical model of genetic drift in population genetics theory, use is made of a hypothetical "infinite-gametic pool". If, instead, the gametic pool is determined by the random number of offspring per individual, a new form of natural selection acting on the variance in offspring number occurs. A diffusion model of this selection process is derived and some of its properties are explored. It is shown that, independent of the sampling scheme used, the diffusion equation has the drift coefficient $M(p) = p(1-p) \ (\mu_1 - \mu_2 + \sigma_{e_2}^2 - \sigma_{e_1}^2)$ and the diffusion coefficient $v(p) = p(1-p) \ [p\sigma_{e_2}^2 + (1-p)\sigma_{e_1}^2]$. It is also pointed out that the Direct Product Branching process model of genetic drift introduces a non-biological interaction between individuals and is thus inappropriate for modeling natural selection.

IN a recent paper (GILLESPIE 1974) it was shown that natural selection can change the within-generation variance in offspring number in a natural population. The main properties of this form of selection are: (1) selection favors genotypes with smaller variances in offspring numbers and (2) the strength of selection is inversely proportional to population size. The importance of selection for variances was recently noted by SLATKIN (1974).

The model given in GILLESPIE (1974) was a continuous approximation to a two-dimensional branching process introduced by FELLER (1951). In order to arrive at the results, it was necessary to artificially hold one of the dimensions of the process constant (the population size) while allowing the other dimension (the allele frequency) to move at random, thus arriving at a one-dimensional diffusion process with drift coefficient

$$M(p) = p(1-p) \ [(\mu_1 - \mu_2) + \frac{1}{n} \ (\sigma_2^2 - \sigma_1^2)] \tag{1a}$$

and diffusion coefficient

$$V(p) = p(1-p)n^{-1} \ [\sigma_2^2 \, p + \sigma_1^2 (1-p)] \ . \tag{1b}$$

While the behavior of this model is of obvious biological importance, several people, particularly DRS. JAMES F. CROW and MONTE SLATKIN, have insisted that the method used to arrive at the final diffusion process was not sufficiently justified on mathematical and biological grounds. The former complaint, involving the reduction of the two-dimensional diffusion equation to a one-dimensional

one, is easily handled and is given in APPENDIX I. The second has stimulated the present paper. I will attempt to generalize the clas͏ͥ ͏ͣ͏odel for selection in a finite population to include the effects of variances ͏ͥ͏ͣ offspring numbers. The essential point of the generalization is to drop the assumption of an "infinite gametic pool" (CROW and KIMURA 1970, p. 327) and to substitute the more realistic assumption of a finite, random, gametic pool from which the succeeding generation is sampled. This removes, of course, the binomial nature of the stochastic element. This is foreshadowed in the diffusion coefficient (1b).

KARLIN and McGREGOR (1964) have attempted a similar generalization by introducing a model, the direct produce branching process (DPBP) model, which allows each individual to have a variable number of offspring, but conditions this number on the total number from all individuals being a fixed constant. Although this model reduces to the bionomial sampling model when the offspring numbers are Poisson-distributed, it turns out that the conditioning causes the model to behave in a very non-biological manner when offspring numbers are not Poisson-distributed. This point will be illustrated after the development of the new model.

FINITE GAMETIC-POOL MODELS

In this section a new model for selection in finite populations will be described which generalizes in a meaningful direction the classical model of Wright. Only a theory for selection in haploid species with non-overlapping generations will be presented. The extension to diploidy is straightforward but very cumbersome and will be reserved for a separate paper. It will be useful if the life cycle of the haploid is first described verbally in order to give names to the various segments. The allele frequencies will always be tabulated in a group called young adults. These are individuals which have just been culled from juveniles due to a density-regulating process which works independently of the genotypes of the individuals (this is the binomial sampling step in the classical model). The young adults will die, or live to reproduce according to specified probabilities. If they do reproduce they will produce a random number of juveniles. Some of these juveniles will die due to density-independent factors before they are culled as above. Thus from one tabulation of the allele frequency to the next, the time span of one generation, the population moves from being composed of young adults to mature adults to juveniles back to young adults, with no overlapping in these categories. The juveniles will make up the "gametic pool". This loose usage will allow a certain continuity of description between diploid and haploid models.

Let the haploid population be composed of two genotypes, A_1 and A_2. The size of the young adult population will be held constant at n individuals of which i are A_1 and $n-i$ are A_2 in a designated generation. To form the next generation, we require random variables to represent the number of offspring from each individual of the two genotypes. Let X_k be the number of offspring from the kth A_1 individual and Y_k the equivalent random variable for the kth A_2 individual. The X_k and Y_k are all integer-valued, non-negative, and mutually independent.

In addition, the X_k are all identically distributed, as are all the Y_k. Biologically, X_k and Y_k represent a compounding of three events. They incorporate the ability of a young adult surviving to reproduce, the number of offspring it has if it does reproduce, and the density-independent deaths that the offspring experience before being culled for the next generation. The example in the next section will illustrate each of these components.

The total number of A_1 offspring ready for culling will be represented by

$$X = X_1 + X_2 + \ldots + X_i$$

and the total number for A_2 by

$$Y = Y_1 + Y_2 + \ldots + Y_{n-i} \ .$$

Thus $X+Y$ is the total number of juveniles on which the culling process will operate. The quantity $X+Y$ will be loosely called the size of the gametic pool.

The culling process can be any of a number of sampling schemes. We will consider three. Let J be a random variable representing the number of A_1 individuals among the n young adults culled from (X, Y), and let $P(J|x,y)$ be the probability that $J=j$ given that $X=x$ and $Y=y$. The probability that $J=j$ in the new young adults, given that there was i A_1 individuals in the previous generation is

$$p_{ij} = \underset{xy}{\Sigma\Sigma} \ Pr[X=x]Pr[Y=y]P[j|x,y] \ . \tag{3}$$

The matrix $[p_{ij}]$ defines a finite state Markov chain with absorbing barriers at 0 and n. We can write

$$EJ = E_{xy}E[J|X,Y] \tag{4a}$$

$$\text{VAR } J = E_{xy} \text{ VAR}[J|X,Y] + \text{VAR}_{xy}E[J|X,Y] \tag{4b}$$

where

$$E[J|X,Y] = \overset{n}{\underset{j=0}{\Sigma}} \ jP[j|X,Y]$$

$$\text{VAR}[j|X,Y] = \overset{n}{\underset{j=0}{\Sigma}} \ (j-E[J|X,Y])^2 P[j|X,Y] \ . \tag{5}$$

In all of the culling procedures to be considered

$$E[J|X,Y] = n \frac{X}{X+Y} \ . \tag{6}$$

This simply states that the process of culling does not result in any systematic change in the frequency of the A_1 allele in the offspring. Using this we can write for $p' = J/n$

$$Ep' = E_{xy} \frac{X}{X+Y} \tag{7a}$$

$$E\Delta p = Ep' - p \tag{7b}$$

$$\text{VAR}p' = E_{xy}\text{VAR}[\frac{j}{n}|X,Y] + \text{VAR}_{xy} \frac{X}{X+Y} \ . \tag{7c}$$

The expectation of the allele frequency in the young adults is the same as in the gametic pool, while the variance in the frequency can be partitioned into a component due to the culling process and a component due to the variance in $X/(X+Y)$ in the gametic pool. Similar partitionings occur in the theory of effective population size. As n increases, both the mean change in p and the variance in p approach zero (asymptotically) at the rate n^{-1}, providing the difference in the mean number of offspring per individual of the two genotypes also approaches zero at the rate n^{-1}. The limiting diffusion equation arrived at by this procedure depends on the nature of the culling process:

1. *Culling with replacement:* This is perhaps the easiest to visualize but the least biological. In this case

$$P[j|x,y] = \binom{n}{j}\left(\frac{x}{x+y}\right)^j\left(1-\frac{x}{x+y}\right)^{n-j} . \tag{8}$$

For this case $E\Delta p$ is given by (7b) while

$$\mathrm{VAR}\, p' = \frac{1}{n}E\left[\frac{X}{X+Y}\right]\left(1-E\left[\frac{X}{X+Y}\right]\right) + \mathrm{VAR}\left[\frac{X}{X+Y}\right]\left(1-\frac{1}{n}\right) . \tag{9}$$

In order to approximate this case with a diffusion equation as $n \to \infty$, we must assume that the difference in the mean number of offspring per individual for the two genotypes approaches zero at the rate n^{-1}. To do this let $EX_i = a(1+\mu_1 n^{-1})$ and $EY_i = a(1+\mu_2 n^{-1})$.

Let $\mathrm{VAR}\, X_i = \sigma_1^2$ and $\mathrm{VAR}\, Y_i = \sigma_2^2$:
Then, as $n \to \infty$

$$E\Delta p = n^{-1}M(p) + 0(n^{-2}) \tag{10a}$$
$$\mathrm{VAR}\Delta p = n^{-1}V_B(p) + 0(n^{-2}) \tag{10b}$$

where

$$M(p) = p(1-p)\left[\mu_1-\mu_2+a^{-2}(\sigma_2^2-\sigma_1^2)\right] \tag{11a}$$

$$V_B(p) = p(1-p)\left[1+a^{-2}(p\sigma_2^2+(1-p)\sigma_1^2)\right] \tag{11b}$$

(For more details on this calculation see APPENDIX II.)
If time is measured in units of n generations, the limiting process will satisfy the stochastic differential equation

$$dp(t) = M(p)dt + \sqrt{V_B(p)}dW \tag{12}$$

where $W(t)$ is normalized Brownian motion. The only problem arising in this scheme will occur if $X=0$ and $Y=0$ in some generation. If $a\geq 1$ and n is large, the probability of this event is extremely small; and as $n\to\infty$ becomes so small as to be irrelevant to the limiting process. To make the process well defined for the finite n case, adopt the convention that if $X+Y=0$ in some generation, new experiments are performed in sequence until $X+Y>0$ for the first time, at which time the gametic pool is culled with replacement.

2. *Culling without replacement:* This is clearly the most realistic culling

procedure. The problem with this procedure, however, is that there may be a non-zero probability that $X+Y<n$, in which case the culling cannot be carried out. Any model incorporating a variable offspring distribution will suffer some such difficulty and in each case an artificiality must be introduced to overcome the problem. It is only necessary that whatever artificiality is introduced, it does not imply a non-biological interaction as was present in the DPBP model. The simplest method to overcome the possibility that $X+Y$ may be less than n is to assume that $Pr\,[X_k = 0]=0$, and $Pr\,[Y_k = 0]=0$. Other techniques could be used.

For the culling without replacement

$$P\,[j|x,y] = \binom{x}{j}\binom{y}{n-j}\Big/\binom{x+y}{n}\,. \tag{13}$$

A somewhat tedious calculation shows that in this case the drift coefficient of the limiting diffusion is the same as the previous case, but that the diffusion coefficient is

$$V_H\,(p) = p(1-p)\,[1-\alpha^{-1}+\alpha^{-2}(p\sigma_2^2 + (1-p)\sigma_1^2)]\ . \tag{14}$$

As one would expect, $V_H(p) \leq V_B(p)$.

3. *Non-random culling:* If the population size of the gamete pool is adjusted back to n with no change in p,

$$E_{xy}\,\text{VAR}\,[j/n|x,y] = 0 \tag{15}$$

and the limiting diffusion, with the same drift coefficient as the preceding cases, has the diffusion coefficient

$$V_{NR}(p) = p(1-p)\,\alpha^{-2}(p\sigma_2^2 + (1-p)\sigma_1^2)\ . \tag{16}$$

In all three culling schemes, the drift and diffusion coefficients are in the same functional form as (1); their differences simply involve reparameterizations reflecting the nature of the culling schemes. Since the culling scheme is non-genetic, it seems natural to relate all cases to the non-random culling case. Notice that in this case the coefficient of p in the linear portion of the diffusion coefficient is $\alpha^{-2}\sigma^2$. This will be called the effective variance in offspring number for genotype A_1 and will be notated $\sigma_{e_1}^2$. Similarly $\sigma_{e_2}^2$ will be the effective variance in offspring number for A_2. By using the coefficient of p and $(1-p)$ in the linear term in the diffusion coefficient for the three cases as the definition for the effective variance in offspring number in the other two cases, we arrive at the following:

Culling $\sigma_{e_i}^2 =$	Non-random $\alpha^{-2}\sigma_i^2$	With replacement $1+\alpha^{-2}\sigma_i^2$	Without replacement $1-\alpha^{-1}+\alpha^{-2}\sigma_i^2$.

All three cases may now be said to satisfy the stochastic differential equation

$$dp(t) = M(p)\,dt + \sqrt{V(p)}\,dW \tag{17}$$

with

$$M(p) = p(1-p)\,[\mu_1-\mu_2 + (\sigma_{e_2}^2-\sigma_{e_1}^2)] \tag{18a}$$

$$V(p) = p(1-p) \ [p\sigma_{e_2}^2 + (1-p) \ \sigma_{e_1}^2] \ . \tag{18b}$$

The fact that all three culling schemes yield equations of the same form suggests that this equation is the most general one for describing selection in a finite population in a constant environment. The models pioneered by WRIGHT and KIMURA (see CROW and KIMURA 1970, for a summary of their properties) must be regarded as special cases which are appropriate only if one of the following conditions are met:

1. *Random sampling from an infinite gametic pool:* In the above parameterization, a is a measure of the size of the gametic pool. As $a \to \infty$ the average number of juveniles does also and $\sigma_{e_i}^2 \to 1$ in both the with- and without- replacement schemes. As this occurs at the limit the process satisfies

$$M(p) = p(1-p) \ (\mu_1 - \mu_2) \tag{19a}$$

$$V(p) = p(1-p), \tag{19b}$$

which is the WRIGHT-KIMURA model.

2. *Poisson offspring distribution:* If X_k and Y_k are Poisson, then their variances equal their means; so the difference

$$\sigma_{e_2}^2 - \sigma_{e_1}^2 = \frac{1}{n} \ (\mu_2 - \mu_1) \ {}_{n \to \infty} \ 0 \tag{20}$$

and the sum

$$p\sigma_{e_2}^2 + (1-p)\sigma_{e_1}^2 = a + \frac{1}{n} \ (p\mu_2 + (1-p)\mu_1) \to a; \tag{21}$$

so in the limiting diffusion

$$M(p) = p(1-p) \ (\mu_1 - \mu_2) \tag{22a}$$

and

$$V(p) = p(1-p) \ (1+a^{-1}) \tag{22b}$$

or

$$V(p) = p(1-p)a^{-1} \tag{22}$$

depending on the culling scheme.

3. *Equal variances in offspring number:* In this case

$$M(p) = p(1-p) \ (\mu_1 - \mu_2) \tag{23a}$$

$$V(p) = p(1-p) \ \sigma_e^2 \tag{23b}$$

where $\sigma_e^2 = \sigma_{e_1}^2 = \sigma_{e_2}^2.$

It almost goes without saying that each of these conditions is seldom, if ever, realized in nature. Although it would seem that gametic pools are frequently large, it must be remembered that the relevant size is after, not before, the density-independent deaths occur. It is the size at the time of the density-dependent culling process that matters. The Poisson assumption has often been proposed for species producing lots of eggs, but with few survivors, (e.g., FISHER 1958). In the next section this kind of thinking will be explored more completely in an

example which will argue for this situation leading to a non-Poisson offspring distribution. Finally, we would expect there to be as much genetic variation in variances as there is in means; hence the arbitrary assumption of equal variances between genotypes is unwarranted.

AN EXAMPLE

The ideas of the previous section may be well summarized and illustrated by a particularly simple example. We will construct a sequence of events to generate the random variables X_k and Y_k. Suppose the probability that a young adult of genotype A_i survives to reproduce is α_i. If it does reproduce, it produces a large number, M_i, of offspring each of which has a small probability P_i of surviving the density-independent death processes. Thus the number of surviving offspring may be approximated by a Poisson density with mean $= m_i = M_i P_i$. The distribution of X_k is thus

$$Pr\cdot [X_k = 0] = (1-\alpha_1) + \alpha_1 e^{-m_1} \tag{24a}$$

$$Pr\cdot [X_k = j] = \alpha_1 e^{-m_1} m_1{}^j/j! \tag{24b}$$

and that of Y_k is

$$Pr\cdot [X_k = 0] = (1-\alpha_2) + \alpha_2 e^{-m_2} \tag{24c}$$

$$Pr\cdot [Y_k = j] = \alpha_2 e^{-m_2} m_2{}^j/j! \tag{24d}$$

Obviously

$$EX_k = \alpha_1 m_1 \qquad EY_k = \alpha_2 m_2$$

$$\text{VAR } X_k = \alpha_1 m_1 + \alpha_1 m_1{}^2 (1-\alpha_1)$$

$$\text{VAR } Y_k = \alpha_2 m_2 + \alpha_2 m_2{}^2 (1-\alpha_2) \ .$$

Although there is a Poisson distribution buried in the model, the relevant distribution is very non-Poisson in character. Also, the average broad size M_i enters only through the product $M_i P_i$ and, therefore, the temptation to regard M_i as the size of the gametic pool must be resisted in favor of $M_i P_i$. The importance of the proper stochastic description of this model is most dramatically illustrated if we assume both genotypes have the same mean number of offspring, i.e., that

$$\alpha_1 m_1 = \alpha_2 m_2 = \beta.$$

The relevant diffusion equation in the binomial culling scheme has coefficients

$$M(p) = p(1-p) \beta (m_2-m_1) \tag{25a}$$

$$V(p) = p(1-p) [1+\beta (1-\beta) + \beta(pm_2+(1-p)m_1)] \ . \tag{25b}$$

Thus allele A_1 has an advantage when $m_2 > m_1$, i.e., when allele A_2 has more offspring per reproducing individual. This would seem paradoxical at first, but the reason lies strictly with variance effects. The statement that $EX_k = EY_k$ and $m_2 > m_1$ implies that genotype A_2 has a smaller probability to survive to reproduce than A_1, but more offspring if it does. This causes A_2 to have a larger variance in its overall offspring production (compounding the survival probability)

and thus a selective disadvantage. Such situations are undoubtedly common in nature. This analysis indicates that simply examining the means of all fitness components and applying the classical ideas of selection in finite populations will not be sufficient to make decisions regarding the relative fitnesses of genotypes.

DIRECT PRODUCT BRANCHING PROCESSES

Consider a haploid species made up of two genotypes, A_1 and A_2. Let p_i be the probability that an individual of genotype A_1 has i offspring and let q_i be the equivalent probability for A_2. To illustrate the biological flaw in the DPBP model assume that

$$p_i = \tfrac{1}{3}(1-\delta) \ , \quad i = 0,1,2$$

$$p_3 = \delta$$

$$p_{3+i} = 0 \qquad\qquad i = 1,2,\ldots$$

and $\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad$ (1)

$$q_i = \tfrac{1}{3}(1-\delta) \ , \quad i = 0,1$$

$$q_2 = \tfrac{1}{3}(1+2\delta)$$

$$q_{2+i} = 0 \qquad i = 1,2,\ldots$$

Genotype A_1 has on the average $1+2\delta$ offspring while genotype A_2 has fewer, $1+\delta$. Common sense and the theory of selection in infinite populations both suggest that genotype A_1 is superior to A_2. If we apply the theory of DBPB to a population of size 2, we arrive at the transition matrix

$$
\begin{matrix}
1 & 0 & 0 \\
(1-\delta)/3 & (1-\delta)/3 & (1+2\delta)/3 \\
0 & 0 & 1
\end{matrix}
\qquad (2)
$$

which suggests that A_2 is at a selective advantage. This is most dramatically illustrated when $\delta \to 1$, in which case allele A_2, if segregating, becomes fixed in a single generation. The reason for this behavior is simple; by conditioning on the population size being constant, genotypes producing a large number of offspring per individual will often violate the conditioning, or at least make their appearance in the conditioned sample of offspring unlikely. The particular case chosen shows this most dramatically because genotype A_1 can have more offspring per individual than will appear in the total population in the next generation. In more realistic models, the discrepancy between the infinite population prediction and the DPBP theory will probably be reduced, but the point being made here is that the DPBP model introduces an interaction between individuals which is non-biological and runs counter to the ideas of natural selection. Certainly no such forces have ever been described in the ecologic literature. KARLIN and McGREGOR (1964) introduced the DPBP as a technique for investigating the influence of variable offspring distributions on the behavior of alleles in finite populations. Although the technique may give correct answers in certain

instances, it should not be trusted in any situation involving alleles with different distributions of offspring numbers.

DISCUSSION

Most of the important properties of selection for variances in offspring number were given in GILLESPIE (1974). That paper used the parameterization of (1) rather than (18), but the results are easily reparameterized using the obvious equivalencies. It is interesting to compare the limiting operations used to arrive at (1) *vs.* (18). In the former, the mean difference between genotypes was assumed to approach zero at the same rate as the variances, but the population size was held constant. In the latter, the means behaved in the same way as n^{-1} went to zero while the variances did not. The method presented in this paper is probably preferable since it involves an explicit formulation whose biological assumptions are easily assessed.

In the theory of selection in temporally fluctuating environments, there are certain analogies to selection for within-generation variances in offspring numbers. Most importantly, both models favor genotypes with lower variances in offspring numbers. It has already been pointed out that in selection in temporally fluctuating environments the mean fitness of the population will often decrease (GILLESPIE 1973). There seems to be no biologically motivated function of the state of the population $\phi(p)$, say, which has the property that $Ed\phi(p) > 0$. It is natural to inquire whether a similar situation exists in the case of selection for the within-generation variance in offspring number. Here the situation is more clear-cut. If we define the mean fitness of the population corresponding to the diffusion model as

$$\phi(p) = p(\mu_1 - \sigma^2_{e_1}) + (1-p)\ (\mu_2 - \sigma^2_{e_2})\ ,$$

then

$$Ed\phi(p) = p(1-p)\ [\mu_1 - \mu_2 + (\sigma^2_{e_2} - \sigma^2_{e_1})]^2$$

and thus the stochastic form of the fundamental theorem of natural selection holds for both moments of the offspring distribution.

LITERATURE CITED

CROW, J. F. and M. KIMURA, 1970   *An Introduction to Population Genetics Theory.* Harper and Row, N. Y.

FELLER, W., 1951   Diffusion processes in genetics. Proc. 2nd Berkeley Symp. on Math. Stat. and Prob. 227–246.

FISHER, F. A., 1958   *The Genetical Theory of Natural Selection.* Dover, N. Y.

GILLESPIE, J. H., 1973   Natural selection with varying selection coefficients—a haploid mode. Genet. Res. **21:** 115–120. ——, 1974   Natural selection for within-generation variance in offspring number. Genetics **76:** 601–606.

KARLIN, S. and J. McGREGOR, 1964   Direct product branching processes and related Markov chains. Proc. Nat. Acad. Sci. U.S. **51:** 598–602.

SLATKIN, M., 1974   Hedging one's evolutionary bets. Nature **250** (5469): 704–705.

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APPENDIX I

The problem is to go from the two-dimensional process defined by equation (3) of GILLESPIE (1974) to equation (1) of this paper. One procedure to accomplish this is as follows:

(1) Let the process begin evolving at time $t=0$ at the point $(p(0),\hat{n})$ and continue until $t=\tau$.

(2) At $t=\tau$ begin the process again at the point $(p(\tau),\hat{n})$ and allow it to continue until $t=2\tau$; at $t=2\tau$ begin at $(p(2\tau),\hat{n})$ and so forth.

(3) This procedure results in a one-dimensional discrete-time Markov process: $\{p(0), p(\tau), p(2\tau) \ldots\}$. Using the original equation, it is obvious that

$$\lim_{\tau \to 0} E\,p[\,(i+1)\tau] - p(i\tau)$$

$$= \lim_{\tau \to 0} E\Delta p = M(p)$$

$$\lim_{\tau \to 0} E\Delta p^2 = V(p) \ .$$

(4) If time is measured in units of τ^{-1} in the $p(i\tau)$ process, as $\tau \to 0$ the limiting diffusion is clearly (1).

APPENDIX II

In this APPENDIX, derivation of the drift coefficient (11a) will be given. An analogous calculation will yield the diffusion coefficient (11b).

To obtain an approximation to $E(X/X+Y)$, we introduce the notation

$$\frac{X}{X+Y} = \frac{\dfrac{X}{n}}{\dfrac{X}{n}+\dfrac{Y}{n}} = \frac{\bar{X}+\delta X}{\bar{X}+\delta X+\bar{Y}+\delta Y} \tag{II-1}$$

where $\bar{X} = pEX_i$, $\bar{Y} = (1-p)EY_i$. Obviously:

$$E\delta X = E\delta Y = 0$$

$$E(\delta X)^2 = p\sigma_1^2\, n^{-1}$$

$$E(\delta Y)^2 = (1-p)\sigma_2^2\, n^{-1} \tag{11-2}$$

$$E(\delta X\delta Y) = 0$$

II-1 may be expanded as a geometric series:

$$\frac{X}{X+Y} = \frac{\bar{X}}{\bar{X}+\bar{Y}} \left[\left(1+\frac{\delta X}{\bar{X}}\right)\left(1-\frac{\delta X+\delta Y}{\bar{X}+\bar{Y}}+\frac{(\delta X+\delta Y)^2}{(\bar{X}+\bar{Y})^2}+\ldots\right)\right]$$

$$= \frac{\bar{X}}{\bar{X}+\bar{Y}}\left[1+\frac{\bar{Y}\delta X-\bar{X}\delta Y}{\bar{X}(\bar{X}+\bar{Y})}+\frac{\bar{Y}\delta X^2+(\bar{X}-\bar{Y})\delta X\delta Y-\bar{Y}\delta X^2}{X(\bar{X}+\bar{Y})^2}+\ldots\right] \ .$$

The expectation of $X/X+Y$, using (II-2) is

$$E\left(\frac{X}{X+Y}\right) = \frac{pEX_i}{pEX_i+qEY_i} = \left(\frac{p(1-p)}{n}\right)\frac{EX_i\sigma_2{}^2-EY_i\sigma_1{}^2}{(pEX_i+qEY_i)^3} + \cdots$$

Using $EX_i = a(1+\mu_1 n^{-1})$, $EY_i = a(1+\mu_2 n^{-1})$, we get

$$E\Delta p = E\left(\frac{X}{X+Y}\right) - p = \frac{1}{n} \cdot \frac{pq(\mu_1-\mu_2)}{1+n^{-1}(\mu_1+\mu_2)} + \frac{p(1-p)}{n} \cdot$$

$$\times \frac{a[\sigma_2^2-\sigma_1^2+\dfrac{\mu_1}{n}\sigma_1^2-\dfrac{\mu_2}{n}\sigma_2^2]}{a^3[1+\dfrac{p}{n}\mu_1+\dfrac{q}{n}\mu_2]^3} + \cdots$$

$$\xrightarrow[n\to\infty]{} \frac{pq(\mu_1-\mu_2)}{n} + \frac{pq}{a^2 n}(\sigma_2^2-\sigma_1^2) + 0\left(\frac{1}{n^2}\right)$$