

12-2-2008

Chapter 5, Summary and Conclusion

Alan C. Swedlund
Prescott College

Follow this and additional works at: https://scholarworks.umass.edu/anthro_res_rpt7



Part of the [Anthropology Commons](#)

Swedlund, Alan C., "Chapter 5, Summary and Conclusion" (2008). *Research Report 07: The Genetic Structure of an Historical Population: a Study of Marriage and Fertility in Old Deerfield, Massachusetts*. 7.

Retrieved from https://scholarworks.umass.edu/anthro_res_rpt7/7

This Article is brought to you for free and open access by the Anthropology Department Research Reports series at ScholarWorks@UMass Amherst. It has been accepted for inclusion in Research Report 07: The Genetic Structure of an Historical Population: a Study of Marriage and Fertility in Old Deerfield, Massachusetts by an authorized administrator of ScholarWorks@UMass Amherst. For more information, please contact scholarworks@library.umass.edu.

CHAPTER V
SUMMARY AND CONCLUSIONS

Introduction

The evidence from Deerfield which is presented in the foregoing chapters would tend to confirm the observation of Sutter and Tran-Ngoc-Toan (1957), that the departure of human populations from genetic models may often be great. This has been demonstrated particularly in regard to population numbers and the problems of fertility and migration. As Neel (1958) pointed out and Spuhler has reiterated (1959) there is very little information on selection in human populations, yet selection is a very significant and relevant departure from the conditions normally assumed in human populations. Observations and conclusions concerning the evidence from Deerfield may be summarized as follows:

Population Numbers

1. Although the "effective population size" is a useful parameter in concept, it is extremely difficult to actually quantify in man. The nature of internal population growth, migration, and generational overlap in human beings makes estimates subject to a variety of errors. The Deerfield sample demonstrates that if constant population size is assumed, the tendency is to overestimate the effective population size. Further, a failure to include the effects of migration will introduce errors in estimating the size of the breeding population and ultimately the effective population size.

2. The importance of knowing population numbers, in regard to genetic structure, is primarily for an understanding of the possibilities of non-random mating in the subject population. In the present study estimates of inbreeding, and the opportunities for drift, are based on an analysis of isonomy, or the tendency for people of like surname to marry. Observations for Deerfield include: (a) inbreeding tends to be low and mating is essentially random during the period studied; (b) there may be a tendency for exogamous marriages to commonly occur between related individuals; (c) close consanguineous marriages are less fertile than non-consanguineous marriages; and, (d) inbreeding tends to increase through time. This may confirm previous observations concerning effective population size, namely, that large family size increases the likelihood of relatives to marry each other, which subsequently decreases relative effective population size.

3. It would appear from the evidence from Deerfield and other communities studied (e.g. Alström and Lindelius, 1966; Küchemann et al, 1967) that migration is the most significant variable in attempting to define population numbers and that measurement of migration is very important in community studies.

Migration

1. Exogamous marriages occurring in time and space form the basis for a study of migration in Deerfield. The frequency of outside marriages increases relatively and absolutely in time, and the mean marriage distance increases only very slightly in time. By far the majority of exogamous marriages occur with members of nearby

neighboring communities.

2. The Deerfield population tends to be patrilocal but this is by no means an exclusive pattern. The general implications of the effect residence patterning has on sex-linked loci is discussed. If only females are exchanged between populations in gene flow, then the equilibrium frequency of newly introduced alleles will be achieved faster than if only males are exchanged, or if migration is equal with respect to sex.

3. The migration in Deerfield is plotted with respect to frequency over space and related to the geometric and exponential curves. The exponential curve provides a slightly better fit and is probably most often the best approximation of human migration. Several past studies have found migration to show a leptokurtic distribution over space, as is true of Deerfield.

4. The nature of migration observed for Deerfield compares closely with that found for historic English villages (Küchemann et al, 1967). The concept of "neighborhood knowledge" provides a formal explanation of the nature of migration and both population density and settlement pattern are important variables affecting migration.

Selection

1. Crow (1958) has defined the Index of Total Selection which measures the maximum possible amount of selection. Evidence from most studies (e.g. Spuhler, 1962; Kirk, 1966) suggests that the component of fertility is greater than that of mortality in the total selection intensity. However, in the Deerfield example and others (e.g. Hutterites), where family size is large and the ratio of mean family

size to variance is small, the mortality component is likely to be greater. As the ratio of family size to variance increases, as with many modern populations, the total index of selection will tend to increase.

2. In an analysis of selection and heterosis it is found that endogamous marriages in Deerfield are more fertile than exogamous marriages. However, if mean family size is measured at maturity, differences in fertility become non-significant. Speculation in regard to these results is as follows: (a) Adaptation to local selective factors and maximum compatibility of all polymorphic alleles in the local population select positively for a large mean family size at birth among native marriages; (b) incompatibility of new allelic combinations and lower fitness to local conditions tend to increase fetal and neo-natal deaths among migrant matings, so that mean family size at birth is lower than for native matings; and, (c) certain new alleles or allelic combinations are favorably selected for and the viability of offspring of migrant matings who survive birth is greater than that of native offspring, who may carry greater segregation loads and who do not possess favorable new alleles. This results in a tendency for mean family size at maturity to be closer than at birth for native and migrant matings.

3. Past studies on heterosis in man and animals are somewhat equivocal in regard to expected results. This suggests that no single outcome from outcrossing is predictable, and that the outcome in any specific situation will depend on the fitness of the two parent populations to the selective environment in which the offspring are produced

and raised. Although this may appear to be a simplistic and obvious statement, it is seldom made by human geneticists.

The study of Deerfield has brought to light an important recurring factor, this is the effect cultural patterns may have on population structure and ultimately genetic structure. In the present study evidence on human migration, residence practices, settlement patterns, and other aspects of mating behavior suggests significant non-random occurrences. These events can have a definite effect on the distribution of genotypes and the microevolution of a breeding population. This brings to the attention of physical anthropologists who are working on a population at a specific point in time, the importance of having knowledge of the demographic and ethnographic history of the subject population.

I have attempted, by using Deerfield as an example, to demonstrate the way in which actual populations may differ from the conditions commonly assumed in genetics models. It would be overstating my case to imply that geneticists are not aware of the way in which actual populations depart from the "simplifying assumptions," for much of the recent literature in human genetics is concerned with this very problem (see Schull and MacCluer, 1968; Morton, 1969). It is, however, very clear that the need for comprehensive studies of local populations, including historic ones, is great. The expansion and refinement of mathematical-genetical models is dependent upon a better empirical base from which generalizations may be made.

