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Human Genetic Isolation and Population Structure of Hancock County, Tennessee

James R. Kirkland
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To the Graduate Council:

I am submitting herewith a thesis written by James R. Kirkland entitled "Human Genetic Isolation and Population Structure of Hancock County, Tennessee." I have examined the final electronic copy of this thesis for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Master of Arts, with a major in Anthropology.

Richard L. Jantz, Major Professor

We have read this thesis and recommend its acceptance:

Harry M. Lindquist, William M. Bass

Accepted for the Council:

Carolyn R. Hodges

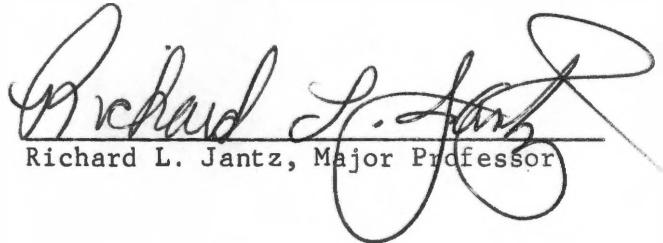
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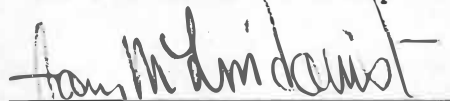
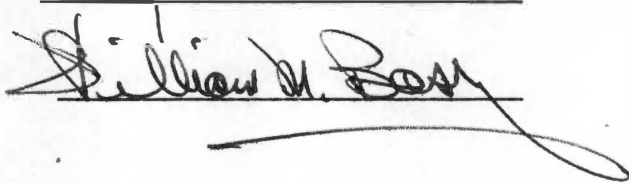
August 19, 1974

To the Graduate Council:

I am submitting herewith a thesis written by James R. Kirkland entitled "Human Genetic Isolation and Population Structure of Hancock County, Tennessee." I recommend that it be accepted in partial fulfillment of the requirements for the degree of Master of Arts, with a major in Anthropology.


Richard L. Jantz, Major Professor

We have read this thesis
and recommend its acceptance:

Accepted for the Council:

Vice Chancellor
Graduate Studies and Research

HUMAN GENETIC ISOLATION AND POPULATION STRUCTURE OF
HANCOCK COUNTY, TENNESSEE

A Thesis
Presented for the
Master of Arts
Degree
The University of Tennessee

James R. Kirkland

December 1974

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The major part of the data for this study was obtained by Dr. Richard L. Jantz and Dr. Harry M. Lindquist, supported by The University of Tennessee Post-Doctoral Fellowships during the period June to September 1972.

ABSTRACT

A study of the population structure of Hancock County, Tennessee, was conducted in order to determine the degree of genetic isolation, and the likelihood of random genetic drift, experienced by the county population. Geneological information for the study was obtained from a random sample of the population utilizing two series of questionnaires. In all, data were obtained for 275 couples from all areas of Hancock County.

Four main analytical steps were taken with these data to determine: (1) the amount of inbreeding, through a surname isonymy study, (2) the effective population size, (3) the patterns of human movement, primarily marital movement, and its main components--distribution, orientation, and diffusion, and (4) the coefficient of breeding isolation, the indicator of human genetic isolation.

The surname isonymy study indicated a much greater amount of inbreeding in the population in the past with a tendency toward breakdown during the last generation due to increased mobility of the population. This increased movement, moreover, was found to exhibit distinct orientations corresponding closely to the main avenues into and out of the county, and also to be limited somewhat in space to an area of approximately 20 miles around Hancock County.

The coefficient of breeding isolation, the product of the effective population size and the effective immigration rate, was found to be in agreement with the indications of the inbreeding study.

Although it was found to be of too great a magnitude during the last generation for the degree of isolation necessary for the development of genetic diversification, all indications are that as recently as only one generation back genetic isolation experienced by the county population was much greater.

When the gene frequencies of the Melungeons, one segment of the Hancock County population, were compared with those of other populations of the United States and England they were found to fall outside the range of these other populations in all but one case. From this it can be concluded that a degree of genetic isolation necessary for random genetic drift was almost assuredly experienced by the Hancock County population in the past, and that this isolation has resulted in altered gene frequencies for this population.

TABLE OF CONTENTS

CHAPTER	PAGE
I. INTRODUCTION	1
II. CONSANGUINITY, SURNAME ISONYMY, AND THE COEFFICIENT OF INBREEDING	9
III. EFFECTIVE BREEDING POPULATION	25
IV. HUMAN MOVEMENT	31
V. COEFFICIENT OF BREEDING ISOLATION	46
VI. DISCUSSION AND CONCLUSIONS	51
BIBLIOGRAPHY	56
VITA	63

LIST OF TABLES

TABLE	PAGE
1. Frequencies of Surnames and Isonymy Among 256 Marriages in the Hancock County Population (Parents' Generation)	15
2. Frequencies of Surnames and Isonymy Among 100 Marriages in the Hancock County Population (Parents' Parents' Generation)	18
3. Isonymy in Different Populations	21
4. Mean Progeny Number (UK) (Adjusted and Unadjusted), Index of Variability (VK/UK), and the Ratio of Effective Number to Actual Number (Ne/N) at Maturity in Various Populations	29
5. Marital Distances for the Hancock County Population	36
6. Coefficient of Breeding Isolation for Various Populations	49
7. Gene Frequencies of the Melungeons and Other Populations . .	55

LIST OF FIGURES

FIGURE		PAGE
1.	Location of Hancock County	4
2.	Spatial Exogamy of the Hancock County Population	39
3.	Orientation of Movement Within Hancock County. Each Concentric Circle Represents an Increment of Five Individuals	42
4.	Orientation of Migration into Hancock County. Each Concentric Circle Represents an Increment of Five Individuals	43

CHAPTER I

INTRODUCTION

Evolution, defined as change in the gene frequencies of a breeding population, can be subdivided into macroevolution and microevolution. Macroevolution consists of all changes which affect man as a species, and through the primary forces of evolution, mutation and natural selection, deals with the development of man's distinctive traits. In similar environmental circumstances, therefore, the processes of macroevolution would act upon breeding populations regardless of their size in order to produce directional change in the gene frequencies. Such processes have not, however, been able to adequately explain the tremendous amount of genetic variability found in man. For this reason factors of a microevolutionary nature, foremost of which, are random genetic drift and determinants of its magnitude, population size, isolation, and admixture, are felt to adequately explain the variations in gene frequencies found in contiguous populations (Lasker. 1954:353; 1960b:684).

The ensemble of factors mediating changes in gene or genotype frequencies, other than mutation or selection, has been referred to variously as the "genetic structure" of a population or "population structure." It represents the limits set to the action of the two primary evolutionary forces upon the human species as a whole taken by the fact that any population is not infinite in size and only approximates the assumption of random mating, which is the basis of the

simplest evolutionary models (Cavalli-Sforza, 1958:389). Consequently, one must view the nature of human variety through the concept of a hierarchy of mendelian populations, each of which is primarily defined by its mating pattern. These patterns are, in turn, determined by the social factors which affect mate selection and the environmental factors which affect the distribution, density and movement of the population (Harrison and Boyce, 1972a:4). Of the environmental factors the parameters of space and distance, combined with the degree of mobility afforded the members of the population, have the greatest effect upon human movement, a primary building block in the genetic structure of the population.

There are many components to human movement, but clearly the only ones of concern genetically are those which lead to an individual of one population contributing his genes to another. Therefore, from the point of view of the genetic composition of a population, gene flow implies the production of offspring in a population other than that in which one or the other parent was born (Harrison and Boyce, 1972b:129). Local genetic structure, however, is determined not only by the amount of gene flow into a population, but also by the size of the geographical area over which the genes are flowing (Harrison and Boyce, 1972b:132). Thus, the genetic structure of an endogamous population is also a function of the geographical distribution of the members of the population and the degree of isolation of the population from other populations. This introduces the concept of the "genetic isolate," which may be defined as a population which forms a more or less closed group, so that its members are less likely than is expected by chance to

exchange genes with members of another group (Birdsell 1951:279). This notion dates back to the Swedish scientist, S. Wahlund, who acknowledged that a large human population is only formed of smaller populations with their extension restricted by factors of different natures: geographical, social, religious, professional, and so on (Sutter and Tran-Ngoc-Toan 1957:379).

In recent years a number of studies have been conducted on the genetic structure of many human populations, especially in the more remote and isolated areas of the world, with the importance of such demographic parameters as population size, density, distribution and migration being recognized (Harrison 1967:352). Although more than 200 American isolates have been identified historically in at least 18 of the states of the eastern United States (Griessman 1972:693), adequate attention has not been placed on the study of such isolates for what they may add to our store of knowledge concerning the effects of such parameters on microevolutionary processes. Such studies would provide data for comparison with other studies of populations possessing different sociocultural systems, comparisons which might display relationships that would be of inestimable contribution to discussions on the evolution of human populations (Morgan and Spuhler 1965:208).

The population of Hancock County, Tennessee, can be considered an example of one such isolated American population, one segment of which has received a great deal of attention as a genetic and cultural isolate, the Melungeons (Pollitzer 1972; Pollitzer and Brown 1969). The county is located in the Southeastern Appalachian Region, approximately 70 miles northeast of Knoxville, Tennessee (see Figure 1). It covers 230

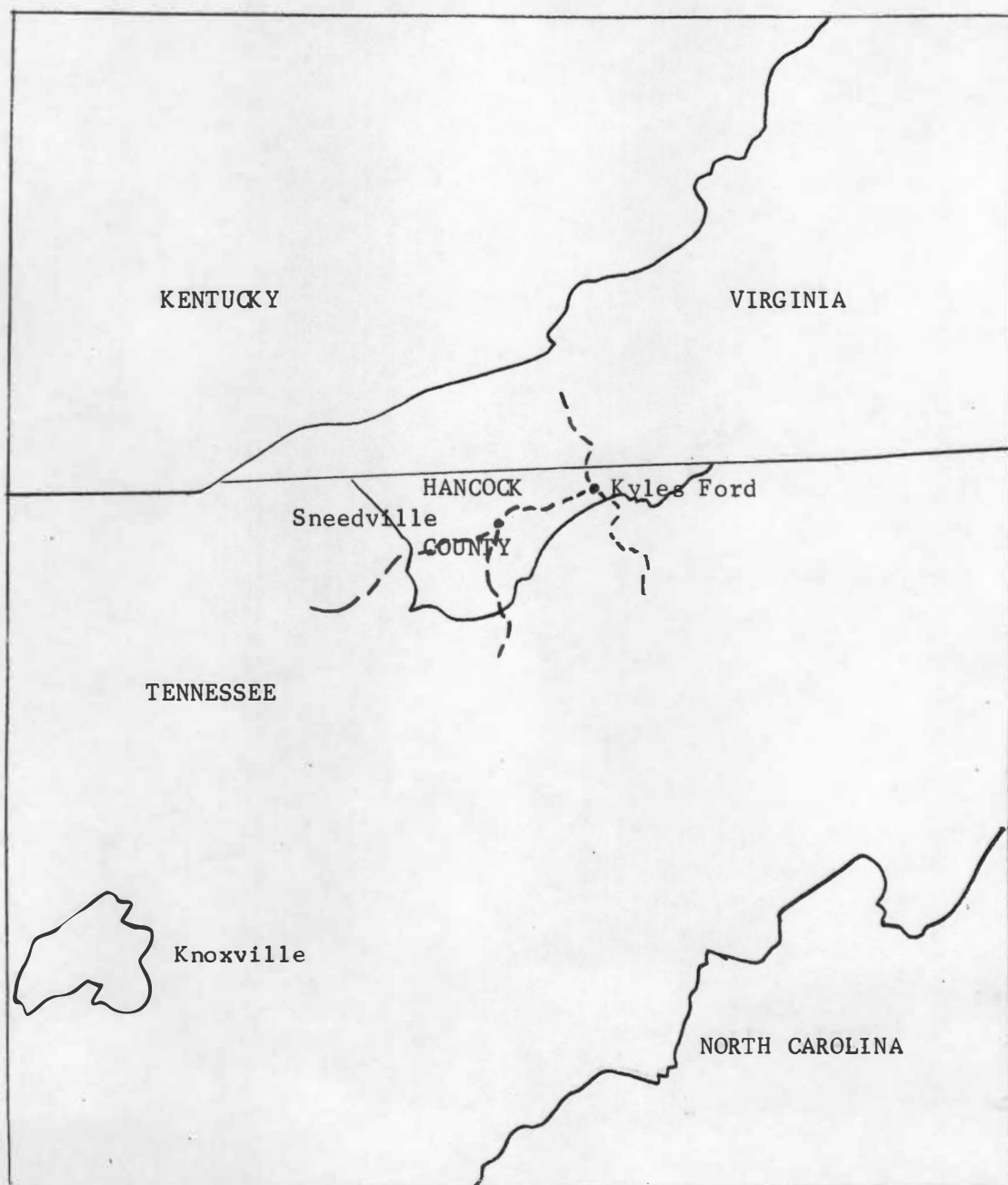


FIGURE 1. Location of Hancock County.

square miles and topographically consists of a series of high ridges, alternated with valleys running from northeast to southwest. Elevation in the county ranges from 1000 to 2500 feet with the valleys being narrow and the ridges steep, allowing only a small portion of the county's land mass to be cultivated or inhabited.

Since it was first settled in 1795 by Euro-American immigrants, Hancock County has supported a traditionally rural population, many segments of which were isolated from each other and the rest of the world by the steep mountain ridges. These ridges also impeded travel across the county and resulted in people who were traveling through the Tennessee Valley or passing through the Cumberland Gap generally bypassing the county all together. Thus, a pattern of isolation developed early in Hancock County which has persisted up to the present.

The communities of Hancock County developed a pattern which is typical of the Appalachian region, a pattern which functioned rather well in meeting the needs of the inhabitants. This included a string of small subsistence farms scattered along the valleys or along the ridges with the communities' basic institutions: a schoolhouse, a store, and a church frequently located at a crossroads, a ford or a gap. This settlement pattern, although still very much in existence in Hancock County today, may be in the process of changing. Because of the lack of satisfactory employment in Hancock County many of the rural people are seeking employment in an industrial setting while continuing to live on these small acreages. There nevertheless still seems to be a real attachment of the people to their ancestral community with many of the members of the population continuing to worship in

the rural church of their childhood while having established residence elsewhere. This behavior coincides with, and undoubtedly contributes to, the continuation of the pattern of ingroup marriage which has been long established in the county. Most of the older families of the county are thus tied to one another through kinship lines, and ancestry continues to play an important role in choice of associates and in social acceptability (Farley and High, 1966).

This study will attempt to evaluate the influence of the aspects of population structure, as exhibited in Hancock County, in an attempt to ascertain in what ways they contribute to the development of human genetic variability through random genetic drift.

During June and July, 1972, Dr. Richard L. Jantz and Dr. Harry M. Lindquist of the Anthropology Department of The University of Tennessee, Knoxville, Tennessee, initiated the collection of demographic and genetic data on the population of Hancock County, Tennessee, for an integrated study of the interaction of the biological and cultural aspects of the population. Hired to assist in the collection of these data were a group of local school teachers working in Hancock County under the auspices of the United States Government's Headstart Program. The selected teachers were provided with questionnaires in order to obtain a random sample from adults of information on families from all areas of the county. In addition, Dr. Jantz and Dr. Lindquist visited each school in Hancock County, obtaining a second set of completed questionnaires from as many school children as possible. The use of both sets of questionnaires taken together was considered to be a random sample of the Hancock County population. The information elicited by

these questionnaires consisted of the names, birthplaces, and birth-dates of the parents and parents' parents of the children who are of school age today, and the number of male and female children in each family. Upon examination of all questionnaires it was determined that 275 provided sufficient data to be useful in an analytical study.

Additional data for the study were collected by the writer from the Hancock County Marriage Registers dating from August, 1930 until July, 1974. Information previous to this period was unobtainable due to the destruction of all records in a courthouse fire in 1929. Data obtained consisted of the age of the spouses at marriage and their birthplaces.

The ultimate aim of the analysis was to determine the degree of isolation and the extent of migration into Hancock County and the concomitant effect these factors have on the possibility of random genetic drift within this population. In order to do this the following related analytical steps were taken to determine:

1. The prevalence of consanguineous marriages through the analysis of surname isonymy from the pedigree data. Using these results it was possible to estimate the amount of inbreeding within the county population.
2. The effective breeding population, defined as the size of an idealized population that would have the same amount of inbreeding or of random gene frequency drift as the population under consideration (Kimura and Crow 1963:279).

3. The pattern of human movement in the county, consisting of:
 - (1) the distribution and orientation of marital movement; i.e., the distances between the birthplaces of spouses (Yasuda. 1968:178), into and within the county, (2) the spatial exogamy of the population of Hancock County, (3) and the correlation, if any, of age at marriage and marital distance.
4. The coefficient of breeding isolation, consisting of the product of the effective population size and the effective immigration rate (Lasker and Kaplan. 1964:327). This in turn is used to estimate the likelihood of random genetic drift taking place within the population of Hancock County.

CHAPTER II

CONSANGUINITY, SURNAME ISONYMY, AND THE COEFFICIENT OF INBREEDING

Two individuals are said to be consanguineous if they have at least one ancestor in common. On the basis of the theory of evolution, all individuals of a species are to some extent consanguineous since all are descended from remote common ancestors. Therefore, in order to feasibly consider its prevalence in any human population, consanguinity, and the level of inbreeding, must be defined as applying only to relationships established after some arbitrary evolutionary point in time, a point after which everyone is considered unrelated (Cavalli-Sforza and Bodmer 1971:341; Crow and Mange 1965:202). In human populations this point is rarely extended back more than four generations. In all cases, however, when progeny are known to come from consanguineous parents they are considered to be inbred (Cavalli-Sforza and Bodmer 1971:341).

No human population is panmictic; that is, considered to be an infinite population in which gametes are combined strictly at random (Spuhler 1972:165; Yasuda and Morton 1967:249). All deviate from panmixia due to a limited number of ancestors, and other barriers imposed by sex, preferences for or against certain types of consanguineous matings, and restricted migration in geographical and social space. All of these deviations from panmixia, including the social customs of the population, constitute population structure. The

frequency with which consanguineous matings occur is therefore a function of the following aspects of population structure: (1) the abundance of relatives, which depends upon the type of relationship and on the growth of the population, (2) the availability of consanguineous individuals in the "mating range" (migration causes a dispersal of relatives whose effect increases as the relationship becomes more remote; i.e., pedigree inbreeding declines with marital distance (Morton and Hussels 1970:77), (3) the age effect, the availability of the consanguineous individuals in the right age group, (4) assortative mating for socioeconomic conditions and physical traits may have to be considered because of the similarity between relatives, (5) traditions for or against some types of consanguineous matings (very close consanguineous matings are usually avoided with practically all societies possessing a taboo against marriages within a certain degree of relationship (Cavalli-Sforza and Bodmer 1971:342)), and (6) other factors of a social or economic nature which would prohibit, inhibit, or encourage consanguineous matings (Cavalli-Sforza et al. 1966:37), such as the practice of monogamy which is found in most populations (MacCluer and Schull 1970:160).

Since, by definition, consanguineous mates receive genes from a common ancestor, their progeny have the possibility of receiving, by descent, two copies of a gene that was carried by the common ancestor, the probability of which is referred to as the coefficient of inbreeding, F (Cavalli-Sforza and Bodmer 1971:342-343). This coefficient was defined by Sewall Wright as the "departure from the amount of homozygosis under random mating toward complete homozygosis (Allen, 1954:181).

Such a situation has long been recognized to have effects on populations that are independent of those of selection (Wright, 1969:169), and may even be of such significance as to be considered a fifth evolutionary factor (Lasker, 1954:353). For this reason interest in studying the frequency of consanguinity has arisen from attempts to measure the randomness of matings in human populations in order to determine the amount of inbreeding present and to thereby predict rates of gene frequency change (MacCluer and Schull 1970).

Various methods of measuring the departure from random mating have been devised (Wright, 1969:169). One of these surname isonymy, is based on the fact that in many societies the surname is transmitted in a regular pattern that corresponds closely to the biological ancestry. In such cases, the frequency of marriages between persons of the same name can be used to estimate the amount of inbreeding. This method was first used in 1875 by G. H. Darwin who suggested its utility in calculating the frequency of marriages between first cousins (Darwin, 1875; Lasker, 1969:321; Yasuda and Morton 1967:254). He found that the frequency of isonymous marriages exceeded its expected value under panmixia and used this discrepancy to estimate the frequency of first cousin marriage assuming that all other types of consanguinity could be neglected and that marriages between cousins of the same surname by descent constituted a fraction ($1/4$) of all cousin marriages. Crow and Mange (1965) went on to relax the restriction of consanguinity to first cousins by noting that for common consanguineous unions the proportion of marriages isonymous by descent among all marriages would be one fourth of the actual consanguineous marriages if all six combinations

of intermediate ancestors were equiprobable. For instance, there are four kinds of first-cousin marriage: with mother's sister's daughter, mother's brother's daughter, father's sister's daughter, and father's brother's daughter. Only the last has the same paternal surname. If this type of cousin marriage is one fourth of all cousin marriages in a particular population, the contribution from first cousin marriages to inbreeding can be estimated at four times the inbreeding coefficient of offspring of first cousins (Lasker 1968:250). The same relationship of the inbreeding coefficient of children of a consanguineous mating to the degree of consanguinity of the parents would hold true regardless of whether the parents were siblings, first cousins, half-siblings, uncle and neice, and most other consanguineous matings. Thus for a wide class of relationship an isonymous marriage is found to be indicative of the same amount of inbreeding in a population regardless of the degree of consanguinity of the marriage (Crow and Mange 1965:200).

This principle is true for most situations encountered in human populations, although it cannot be considered completely general. It does not fit situations where one mate is a direct descendant of the other, such as a father-daughter marriage, nor does it hold for certain types of situations where cumulative inbreeding is present, such as two or more generations of sib marriage. Also, this theory rests on the assumption that consanguineous relations occur through male and female ancestors in random proportions and that neither sex is disproportionately represented among migrants (Crow and Mange 1965:200).

Because the method of isonymy is relatively simple it should be evaluated closely for possible sources of error before applying it in the analysis of the Hancock County data. One such source, it may be argued, is that mates having identical surnames are more easily identified as consanguineous and, therefore, may be over-represented in the sample. If this were true, the effect would pertain only to matings in which all common ancestors are males. This is not true, however, since for any given degree of consanguinity an increase in the number of females among the ancestry intermediate between the common ancestors and the consanguineous mates is correlated with a decrease in the observed frequency of the pedigree (Cavalli-Sforza and Bodmer 1971:477).

Another possible source of error is that there may have been duplication of surnames at the time the names were first introduced. It is difficult to evaluate the importance of such an uncertainty, but, since as a general rule duplication of surnames may be postulated to represent common ancestry, the introduction of two identical surnames indicates some degree of common ancestry prior to the date of introduction. However, since the inbreeding coefficient which is calculated from the isonymy has meaning only with respect to some starting point or reference population (Crow and Mange 1965:202), and remote consanguinity has been found to make a very small contribution to the total inbreeding coefficient (Azevedo et al. 1969:17), this situation can be discounted for all practical purposes, except to note that if such a situation did exist, the method of surname isonymy will probably not yield a true estimate of the inbreeding coefficient. Consequently, in

the analysis of the Hancock County data such an error would probably be very small, especially for the inbreeding which has taken place over the last two generations, and therefore, was not taken into account.

The pedigree data obtained from the series of questionnaires from Hancock County yielded a total of 256 marriages for which adequate surname information was available for the parents' generation; that is, those in the sample with children presently in school. In addition, data were obtained on the pedigrees of 100 of the marriages of the parents' parents generation.

Since the use of lists of names alone has been shown to yield calculations of expected isonymy, the random component of isonymy (Lasker, 1969:321), a list of all surnames appearing in the sample and their frequency was prepared with the ones occurring only once being grouped together under the heading "other." Following Lasker (1968:252) and Crow and Mange (1965:200) the assumption was made that surnames occur with approximately equal frequency in both males and females permitting pooling of the sexes in the analysis. For both generations then the probability of isonymy taken as the square of the frequency of each name in the total sample was calculated. From this it was possible to compute the amount of expected isonymy for each surname, the product of the probability times the frequency, and to compare the expected to the amount of observed.

Table 1 gives the expected and observed isonymy for each of the surnames in the parents' generation sample. In this sample, 26 surnames, or 16.31 percent of those represented, accounted for 334, or 65.21

TABLE 1

FREQUENCIES OF SURNAMES AND ISONYMY AMONG 256 MARRIAGES IN THE
HANCOCK COUNTY POPULATION (PARENTS' GENERATION)

Most Common Surnames (Five or more in Sample)	Number in Sample	Frequency Percent	Probability	Expected Isonymy	Observed Isonymy
Fn	7	1.37	.0002	0.05	0.0
Wi	10	1.96	.0004	0.10	0.0
Cs	37	7.24	.0052	1.33	3.0
Sl	32	6.26	.0039	1.00	1.0
Hp	11	2.15	.0005	0.13	0.0
Jn	27	5.28	.0028	0.72	1.0
Hd	10	1.96	.0004	0.10	0.0
We	9	1.76	.0003	0.08	1.0
Kr	17	3.33	.0011	0.28	0.0
Tt	10	1.96	.0004	0.10	0.0
Gn	19	3.72	.0014	0.36	1.0
Rs	10	1.96	.0004	0.10	0.0
Bn	14	2.74	.0008	0.19	0.0
Bl	6	1.17	.0001	0.03	1.0
Ms	10	1.96	.0004	0.10	0.0
Lb	12	2.35	.0006	0.14	0.0

TABLE 1 (continued)

Most Common Surnames (Five or more in Sample)	Number in Sample	Frequency Percent	Probability	Expected Isonymy	Observed Isonymy
Mt	15	2.94	.0009	0.22	0.0
Ge	10	1.96	.0004	0.10	0.0
Dw	8	1.57	.0002	0.05	1.0
Ce	8	1.57	.0002	0.05	0.0
Yt	8	1.57	.0002	0.05	0.0
Dp	6	1.17	.0001	0.03	0.0
Ns	10	1.96	.0004	0.10	1.0
Ln	12	2.35	.0006	0.14	0.0
Bo	9	1.76	.0003	0.08	0.0
Ht	7	1.37	.0002	0.05	0.0
"Other" (Less than Five in Sample)	178	35.28	.0012	0.30	0.0
TOTAL	512	100.67	.0236	5.98	10.0

percent, of the individuals in the sample, while the remaining 134 surnames accounted for only 178 individuals. For this generation the expected isonymy was found to be 5.98 with the observed being 10.

Table 2 gives the expected and observed isonymy for the parents' parents' generation. Here the ratio of expected to observed isonymy was found to differ significantly from that found in the parents' generation, 2.57 expected to 18 observed. Of the seven surnames in the sample which had five or more individuals represented only one had any isonymy observed, while the great majority of isonymous marriages occurred in surnames with only four or less represented. The seven surnames with five or more individuals represented accounted for 1.89 of the expected isonymy, four of the observed and represented 33 percent of the individuals of the sample, while the remaining 134 individuals, or 67 percent of the sample, accounted for .68 of the expected isonymy and 14 of the observed. From these results it is obvious that the number of isonymous marriages has greatly declined over the last two generations.

To the extent that inbreeding is correlated with isonymy it can be assumed that all isonymy is a true reflection of common ancestry. Therefore, in principle, the random component, F_r , that which could be expected from random mating, can be separated from the non-random contribution, F_n , to the total inbreeding coefficient F . In accordance with Crow and Mange's (1965) method of determining F the relationship of the random and non-random components to F are as follows:

$$F = F_n + (1 - F_n) F_r . \quad (1)$$

TABLE 2

FREQUENCIES OF SURNAMES AND ISONYMY AMONG 100 MARRIAGES IN THE
HANCOCK COUNTY POPULATION (PARENTS' PARENTS' GENERATION)

Most Common Surnames (Five or more in Sample)	Number in Sample	Frequency Percent	Probability	Expected Isonymy	Observed Isonymy
Sl	13	6.5	.0042	0.42	0.0
Ge	5	2.5	.0006	0.06	0.0
Wn	7	3.5	.0012	0.12	0.0
Gn	5	2.5	.0006	0.06	0.0
Cs	17	8.5	.0072	0.72	4.0
Jn	13	6.5	.0042	0.42	0.0
Ee	6	3.0	.0009	0.09	0.0
"Other" (Less than Five in Sample)	134	67.0	.0068	0.68	14.0
TOTAL	200	100.0	.0257	2.57	18.0

In determining the random component, if x_i is the proportion of the population with a certain surname, then x_i^2 will be the frequency of random marriages between members of the population having this surname, going under the assumption that the frequency of surnames is equally distributed between the sexes. The random contribution to the inbreeding coefficient for members of that surname then would be $x_i^2/4$, and for all surnames in the sample it would equal the sum of these contributions,

$$F_r = \sum x_i^2 / 4 . \quad (2)$$

The non-random component, F_n , is represented by

$$F_n = (P - \sum x_i^2) / 4 (1 - \sum x_i^2), \quad (3)$$

where P is the ratio of the observed isonymous marriages to the total number of marriages in the sample.

For the Hancock County data on the parents' generation $P = .039$ and $\sum x_i^2 = .023$. Using these figures and equations (1), (2), and (3) the following results were obtained:

$$F = .0099$$

$$F_r = .0058$$

$$F_n = .0041$$

For the parents' parents' generation $P = .18$ and $\sum x_i^2 = .0257$ yielding the following results:

$$F = .0456$$

$$F_r = .0064$$

$$F_n = .0395$$

Table 3 illustrates the degree of isonymy in a number of different populations for comparative purposes with the Hancock County results.

In the case of the parents' generation all three figures may be considered negligible. For the parents' parents' generation, however, the average relationship is found to be equivalent to something between first cousins ($F = 1/16$) and half first cousins ($F = 1/32$), with the random component being almost the same as that of the succeeding generation. Thus, it can be seen that the decline in total F from the parents' parents' generation has been limited almost entirely to a decrease in the non-random component, indicating a substantial decrease in consanguineous matings over the last two generations. A similar situation was found for three generations of a Japanese population in a study by Yasuda and Furusho (1971a:314; 1971b:239). They found that the random component was nearly constant over all three generations while the inbreeding coefficient which was due to non-random marriages decreased with time. This decrease was primarily attributed to the increased migration of members of the population.

The decrease in inbreeding noted for Hancock County somewhat mirrors the worldwide tendency for inbred genetic isolates, which have generally been of a rural nature (Beale, 1972:704), to disappear under the impact of modern transportation and other facets of urbanization (Lasker et al., 1972:351). When this tendency is transposed to the local scale it generally represents a trend of rural depopulation which severely affects the size and continued existence of these isolates (Beale, 1972:704).

TABLE 3
ISONYMY IN DIFFERENT POPULATIONS

Population	Random Component of (Fr) Inbreeding Coefficient	Non-random Component (Fn) of Inbreeding Coefficient	Coefficient of Inbreeding (F)	Ratio of Observed Isonymy to Total Number of Marriages (P)
England, 19th ^a Century	.00026	.0029	.0024	.0125
Colonial ^b New York	.00020	.0050	.0055	.0207
Ohio, 19th ^b Century	-----	.0019	.0018	.0084
Loomis ^b Geneology	-----	.0017	.0030	.0076
Burke's Landed ^a Gentry	-----	.0037	.0035	.0151
Hutterites ^c	.04459	.0052	.0490	.1950
Hancock County ^d Parents' Generation	.0058	.0041	.0099	.0390
Hancock County ^d Parents' Parents' Generation	.0064	.0395	.0456	.1800

^aDarwin 1875.

^bArner 1908.

^cCrow and Mange 1965.

^dPresent study.

Other characteristics which have been noted to be general with respect to these isolates and inbreeding are that consanguineous marriages have tended to be concentrated in areas of low population density (Cavalli-Sforza and Bodmer 1971:369) and that inbred children as a whole tend to come from families of lower socioeconomic status as measured by parental occupation and education, density of persons in the household and food expenditures per month (Spuhler 1972:180). These characteristics fit the population of Hancock County in most respects. According to the census definition, Hancock County has remained entirely rural up to the present time, and is considered to be an area of hard core poverty. In 1962, based on per capita income, it ranked the eighth poorest county in the United States (Kolasa 1974:26). This poverty, combined with the limited opportunities for work and/or higher education in the county, is believed to be the cause of a great deal of migration out of the county (Clelland and Lin 1972:1). Furthermore, this migration reflects a decreased dependence on the land and an increase in individual mobility, a fact which Hammel (1964:74) found to correlate with decreased endogamy, and thus decreased inbreeding, in a study of marriage relationships in a coastal Peruvian village.

This out-migration is documented by the fact that one and three-fourth times as many births as deaths have taken place during the last decade, with the population of the county still decreasing. This was in contrast to the rest of the state which experienced a very small out-migration with some increase in total population. An analysis conducted by Clelland and Lin (1972) indicated that out-migrants were principally those young people who had turned 20 to 25 during the

decade, although there were significant numbers in the other age groups as well.

Thus, the increased mobility of a large number of Hancock County's potentially reproducing adults would have had a detrimental effect upon the continuation of the high level of inbreeding of earlier times, and would therefore have resulted in a decrease in the frequency of isonymy noted. These results from Hancock County are in agreement with the negative correlations found by both Lasker et al. (1972:357) and Yasuda and Furusho (1971a:314; 1971b:239) between the rate of isonymy and the frequency of migration.

One aspect of inbreeding which has not received attention in previous studies of this kind and which was noted from the Hancock County data concerns the high frequency of intermarriages observed for certain pairs of surnames, a much higher frequency than would be expected from random mating. In these cases it was found that the frequency of isonymous marriages for each individual surname taken separately was no greater than, and in a number of cases, less than, what could be expected by chance. Upon analysis of one such case it was found that, for the parents' generation the expected intermarriage between individuals with surnames Gi and Jo was 1.0 with the observed being 4.0. For the preceding generation the expected amount was .325 and the observed was 2.0. Thus, although the amount of intermarriage which has taken place between members of these two surnames has apparently decreased over the last two generations it is still high enough to assume that such a practice as this disguises the actual amount of

inbreeding which takes place, causing the results of an isonymy study to yield an underestimation.

CHAPTER III

EFFECTIVE BREEDING POPULATION

In any study of gene frequency change it is the frequency of the genes of a "breeding population" which must be considered. A breeding population, as defined by Lasker (1954:353), is the largest unit within which mate selection takes place. Within this unit, however, are patterns of mate selection and other aspects of population structure which introduce a non-random component, thereby reducing the effective size of the breeding circle (Lasker 1960a:85). Consequently, in order to deal with natural populations in a way which would be practical both for assessing the effect of a small population and for comparative purposes, Wright (1938; 1969) introduced the concept of "effective population number," defined as the number in an idealized population in which each individual has an equal expectation of progeny (Kimura and Crow 1963:279). By calculating the effective size of a breeding population it is then possible to limit it to a finite size, a size which would be directly correlated with the size of a delimited genetic isolate (Birdsell 1951:261). Such a determination is of critical concern in considering stochastic genetic processes which operate in determining the genetic composition of a population (Harrison and Boyce 1972a:9), due to the fact that a population of finite size is subject to two related effects: (1) the inbreeding effect, discussed in the preceding chapter and (2) random gene frequency drift, which occurs because of the sampling variance in the process of gene transmission

from generation to generation. This second effect also leads to an average increase in homozygosity within the population, and eventually to random extinction and fixation of alleles (Kimura and Crow 1963:279; Crow 1954:543).

In order to determine the effective population number one needs to know, (1) the number of reproducing adults, (2) the extent of non-random mating, and (3) the distribution of the surviving progeny per parent. Therefore, if N = total number of offspring of the sample population, and F = the coefficient of inbreeding, used as a measure of the departure from random mating zygotic proportions among the parents, then the effective population number

$$N_e = \frac{2N}{1 - F + (1 + F) (V_k/\mu_k)} \quad (1)$$

where V_k is the variance in the number of surviving offspring per parent and μ_k is the mean number of offspring per parent.

The ratio of variance, V_k , to mean, μ_k , termed the index of variability, is a measure of the degree of departure from idealized conditions. When $V_k/\mu_k = 1$, as would be the case if the progeny numbers had a poisson distribution, all the variance formulae reduce to binominal values and the effective number is the same as the actual number of surviving progeny (Crow and Morton 1955:205). However, when the value of this index, which should be determined at the stage of sexual maturity, is greater than unity, the effective number is less than the true number; and when it is less than unity, the effective number is larger.

In any population which is not expanding or decreasing at a very rapid rate, the average μ_k counted at sexual maturity cannot be far from two, with the index of variability being of the order of unity even if the value was much larger at an earlier stage (Crow and Morton 1955:211). This theory, then, assumes a stage of random survival intervening between the stage of enumeration and sexual maturity. Thus, if one starts out with N families at a certain stage and assumes a constant probability, S , of survival to a certain later stage, with K_{ei} the number of progeny in the i th family at the early stage, e , and K_{ai} the number at the later stage (adult), a , the mean number of survivors per family will be $S\mu_k$, where μ_k is the mean number per family at the early stage. The variance, then, of the number of progeny surviving per family at the later stage, V_k , is represented

$$V_k = S(1 - S)\mu_k + S^2V_e \quad (2)$$

where

$$S = \mu_a / \mu_e \quad (3)$$

and

V_e = variance in number of progeny of
earlier stage =

$$\frac{x_1^2 - \frac{(\sum x_1)^2}{N}}{N-1} \quad (4)$$

where $\sum x_1$ = the total number of progeny in the sample and N = the total number of mating couples (the progeny number is considered the same for both mates).

When considering the probability of survival of progeny it is taken that individuals migrating out of a population without having contributed their genes to the gene pool are considered not to have survived.

From the Hancock County data

$$N = 275$$

$$\sum x_1 = 1123$$

and $V_{Ke} = 6.617.$

Due to the fact that the population is neither increasing nor decreasing rapidly the mean progeny number at sexual maturity in accordance with Crow and Morton (1955) is adjusted to $\mu K_a = 2.$

Therefore

$$S = \mu K_a / \mu K_e = 2 / 4.08 = .49,$$

$$V_{K_a} = 2.608$$

and the adjusted index of variability

$$V_{K_a} / \mu K_a = 2.608 / 2 = 1.304.$$

Using these numbers in equation (1), $N_e = 973.56$ with the effective to actual, N_e/N , number being .867. Table 4 presented for comparative purposes, illustrates the unadjusted and adjusted values for the Hancock County population and various other populations taken from Crow's and Morton's study (1955:206).

According to Lasker and Kaplan (1964:335) the ratio of the effective population to the total population will vary, although not greatly, with the form of the population pyramid. He found that for the communities he considered the figure of 29 percent of the total population was an adequate estimate of the size of the effective

TABLE 4

MEAN PROGENY NUMBER (\bar{K}) (ADJUSTED AND UNADJUSTED), INDEX OF VARIABILITY (VK/\bar{K}), AND THE RATIO OF EFFECTIVE NUMBER TO ACTUAL NUMBER (N_e/N) AT MATURITY IN VARIOUS POPULATIONS

Population Sample	Unadjusted		Adjusted ($\bar{K}=2$)	
	\bar{K}	VK/\bar{K}	VK/\bar{K}	N_e/N
New South Wales ^a Women	6.2	2.61	1.52	.79
English Women ^a	3.5	2.54	1.88	.69
U. S. Women, ^a born 1839	5.5	1.28	1.10	.95
U. S. Women, ^a born 1866	3.0	1.93	1.63	.76
Hancock County, ^b Men and Women taken together	4.08	1.62	1.30	.87

^aCrow and Morton 1955.

^bPresent Study.

breeding population. In order to determine if this proposition would hold for the Hancock County population the population pyramid of the county was obtained from the United States Census for 1970. The use of these data, however, presented a complication due to the fact that a census estimate includes people from roughly three successive generations, roughly one third of which belong to the same generation on an average (Cavalli-Sforza and Bodmer 1971:418). Therefore, in order to take account of this fact the "breeding generation" for the county was taken to be the sum of individuals between the ages of 18 and 45, since very few progeny would come from matings of individuals below or above these age limits. The total number of individuals within this age range was 2195, which, when adjusted to the effective size ($2195 \times .87$) yielded 1903 individuals, or 28.3 percent of the total county population.

CHAPTER IV

HUMAN MOVEMENT

It has long been recognized that gene flow between contiguous populations has been of critical importance in determining the genetic structure of, and maintaining the integrity of, the human species (Boyce et al. 1967:335; Hiorns et al. 1969:237), and since gene flow occurs through the movement of people and the choice of mates (Harrison 1967:351) the analysis of movement patterns is important in understanding the dynamics of genetic interchange between human populations. All patterns of human movement, however, are not genetically significant; that is, the only components of human movement which are of concern are those which lead to an individual of one population contributing his genes to another. In such cases movement of any magnitude may be regarded as human migration (Lasker 1960a:81; Spuhler and Clark 1961:223).

A universally important component of human migration is the widespread practice of exogamy, two aspects of which have evolutionary importance for any particular population: (1) the amount of exogamy practiced, which determines the amount of gene flow into a population and (2) the distribution of distances over which individuals obtain their mates; i.e., the distribution of distances between birthplaces of paired persons (Boyce et al. 1967:335; Yasuda and Kimura 1973:313). This aspect, which is important for understanding the pattern of human migration and the geographical range of marriages (Yasuda 1968:178),

determines the size of the geographical area over which gene flow takes place and serves to delimit the breeding population.

Because of the discrepancy noted between the limited migration distance of individuals as compared to the total geographical area over which the individual would have to be able to migrate if panmixia was to be a reality, the situation of breeding units more or less isolated from each other by distance exists (Kimura and Weiss 1964:561). The concept of such a situation, termed "isolation by distance," was first proposed by Sewall Wright in 1943 who made the assumption that distance alone is a barrier to migration and gene flow, whether or not geographical or other barriers are present (Clarke 1972:29). He went on to develop a model, termed the "Island Model," in order to illustrate the microevolutionary effects of this isolation upon subdivisions of a population. In this model a population was considered to be subdivided into random breeding "islands" with populations of size N of which a proportion m consisted of immigrants that could be considered a random sample of the total species. Since the islands could be expected to become differentiated from each other a correlation between uniting gametes was implied, based on the proportion of cases $(1 - m)^2$ in which both were of local origin. For the model the standard case of a completely random union of gametes within each breeding unit was assumed (Wright 1969:291).

This model represents a situation which would be rarely realized in nature in pure form. In most cases immigrants come largely from neighboring groups with geographical propinquity being an important factor in mate selection (Spuhler and Clark 1961:233). Consequently,

most immigrants would be expected to differ little in gene frequencies from the populations into which they migrated (Wright 1969:292).

In contrast to this "continuous" type of isolation by distance was proposed a "discontinuous" type, referred to as the "Stepping Stone Model" of population structure. This model was developed to analyze the situation often found in natural populations where individuals are distributed more or less discontinuously to form numerous colonies or clusters (Kimura and Wiess 1964). In this model these "colonies" are considered to be of equal size at the point of an infinite regular lattice and to have a given rate of exchange depending on the number of steps apart (Bodmer and Cavalli-Sforza 1968:565).

Both types of isolation by distance, the continuous and the discontinuous, suffer from several limitations. Neither can cope with the fact that real populations are almost always irregular in their geographical distribution and that population size, density, and mobility are not constant with respect to space and time. Nevertheless, either model can provide a satisfactory theoretical framework for assessing the effects of a variety of migration patterns on random genetic drift (Bodmer and Cavalli-Sforza 1968:587).

In considering the relationship of human movement to isolation by distance it is convenient to distinguish between long-range and short-range movement, although this distinction is clearly an arbitrary one. Long-range movement is of special concern in considering macro-evolution of the species, since with such movement, gene flow would technically encompass all species members. This movement can occur either by the migration of a group of people during their own lifetime

over a considerable distance, or by the continual movement of a population through many generations over an equivalent distance. Such movement, except in recent times, is difficult to quantify in amount and effect, and tends not to follow any single pattern or show adherence to rigid migration laws (Harrison and Boyce 1972b:130).

Short-range movement, on the other hand, is seen to be of paramount importance in the microevolution of the species, in determining local genetic structure and differentiation, and is broadly dictated by routine daily activity patterns and certain general characteristics: (1) the tendency to move only during daylight hours, (2) the tendency to have a home base, particularly in sedentary communities, and (3) the tendency for individuals to restrict their travel to predetermined routes are of prime genetic concern since they structure that human movement which directly or indirectly leads to the choice of a mate (Harrison and Boyce 1972b:130). All such movement as this can be referred to as marital movement and can be thought of as having four possible components: distance, magnitude, orientation, and direction (Harrison and Boyce 1972b:131). Each of these components, with the exception of direction, will be analyzed for the Hancock County population. Because of the fact that the direction component refers primarily to the exchange of individuals between any two populations and since no other single population is considered with respect to migration into or out of Hancock County it was not considered in this study.

An analysis of marital distance, the distance between the birthplaces of spouses, provides a measure of the movement of genetic

importance and supplies additional information for the evaluation of the probability of consanguineous marriages and the effective size and heterogeneity of a population (Yasuda 1968:178). With respect to such an analysis of the Hancock County data it was found that of the 275 pairs of mates in the sample, 242 yielded adequate birthplace data for both mates. For this study the marital distances for each pair was measured on a map along the straight line between birthplaces of husband and wife, and the angle between the line and the longitude which passed through the county seat, Sneedville, was also measured for a survey of the orientation of migration. These data were then divided into three parts depending on whether one, both, or neither of the partners were natives of Hancock County. The marital distances for the first two parts of the data were then calculated (see Table 5).

In the sample, 13, or 16 percent, of the 81 couples which contained one mate from outside the county migrated from distances greater than 100 miles. The marital distance for these couples accounted for 5710, or 80.5 percent, of the sum of the marital distances for this part of the sample. Thus, those few occasions where marriages were contracted over very large distances are seen to have an effect on the mean distance which is out of proportion to the genetic effect, as witnessed by the discrepancy between the mean and median distances for this group. This fact can be further illustrated by discounting these distances altogether in computing the mean and median distances, thereby reducing them to 20.4 miles and 18 miles, respectfully. Both these figures are very similar to the median distance for this part of the sample.

TABLE 5
MARITAL DISTANCES FOR THE HANCOCK COUNTY POPULATION

Sample	Total Number of Couples	Total Marital Distance	Mean Marital Distance	Median Marital Distance
When both mates are native to Hancock County	141 (89 with Ø marital distance)	594.8	4.2	Ø
When one mate comes from outside Hancock County	81	7094.4	87.6	20
When both of the above are taken together	222	7689.2	34.64	10

Magnitude of marital movement is typically measured in terms of the amount of spatial exogamy, defined here as the geographical range over which all the married members of the population of Hancock County have moved in obtaining a mate, disregarding whether or not one, both, or neither, are native to the county. From the 242 pairs in the sample the following data were obtained:

Total Marital Distance = 9663.7 miles;

Mean Marital Distance = 39.9 miles; and

Median Marital Distance = 7 miles.

Taking the county seat at the point of origin of a circle with the radius equal to the mean marital distance it was found that for 89.7 percent of the couples, both mates came from within this circle. Of the remaining couples (25) where one or both mates came from outside this circle, three were located within a fifty-mile radius of the county seat, three others within a fifty to one-hundred mile radius, and nineteen came from greater than one hundred miles. If these latter nineteen couples are discounted the percentage of couples who found their mates within this circle increases to 97.3 percent.

Since a circle of radius 20 miles, taking Sneedville as point of origin, encompasses the entire county with the exception of a very small area of the northeastern section which is virtually uninhabited, it was felt that by applying the same data and methods as before to this case would provide a test for the assumption that there is an exponential relationship between the frequency of marriages and distance (Boyce et al. 1967:336; Kuchemann et al. 1974:20); in other words, an exponential decline with distance of the number of mates found

migrating into a breeding population. The results of this analysis showed that 193, or 79.8 percent, of the couples in the sample obtained their mates from within this 20-mile radius of Sneedville. Thus, although the area encompassed by a circle with a 20-mile radius from Sneedville is only one-fourth of that area encompassed by a circle with a radius equal to the mean marital distance, it was found to account for all but about 10 percent of the couples who found their mates within the larger circle (see Figure 2). Consequently, as far as these conclusions go, the previous assumption is supported.

The third component of marital movement, spatial orientation, has received relatively little attention up to the present (Harrison and Boyce 1972b:135). Two studies which have been conducted in this area, one by Boyce et al. (1968) and one by Yasuda and Kimura (1973), have arrived at the same general conclusion although from different tacks and with somewhat conflicting results. Both agree that distinct orientations are almost assuredly present and that these orientations are probably introduced by such factors as geographical patterns and roadway patterns. When all is said and done, however, they both conclude that marital movement, as a rule, can be considered to be isotropic. In their study, Yasuda and Kimura found a tendency for long-range movement to be directional; that is, oriented to the main roads, while movement on the local scale was essentially isotropic. Boyce et al., on the other hand, found that orientation of marital movement was probably present on a very local scale with the long-range movement being isotropic. Since both of these studies dealt primarily with the movement between population concentrations and/or between population

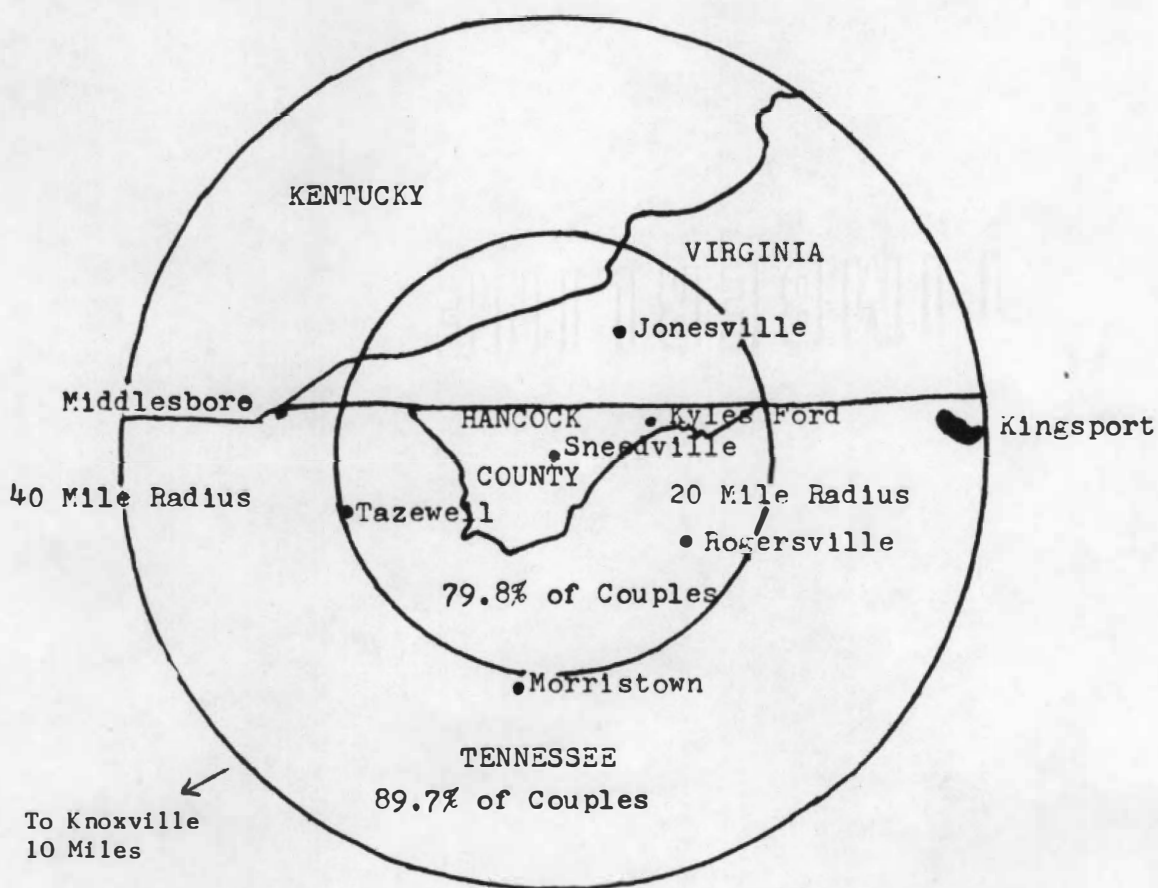


FIGURE 2. Spatial exogamy of the Hancock County population.

concentrations and rural populations, it was felt that an analysis of the movement into and within the entirely rural population of Hancock County from the surrounding rural populations might throw some light on this problem.

The analysis of the orientation of this marital movement was approached in two parts: (1) the orientation of movement within Hancock County was determined for couples where both mates came from within the county, and (2) the orientation was determined for the migrants marrying into the Hancock County population. In conducting the analysis, Sneedville was taken as the point of origin with all movement transposed in order that it appeared to be directed toward or away from Sneedville. Angles measured from the longitude passing through Sneedville to the lines of marital movement were taken and subdivided into 36 components, each corresponding to a 10 degree segment of a circle with Sneedville as point of origin and the longitude passing through Sneedville as the orientation of the circle to true north. Upon completion of the tabulation of these data the Chi Square Test for Homogeneity was applied to part one ($\chi^2_3 = 21.4$, $p < .001$) and part two ($\chi^2_{35} = 126$, $p < .001$) in order to insure that results obtained from further analysis could not be attributed to sampling error. Also, all movement in the sample was taken together, irrespective of whether it was the male or female who actually migrated.

From the analysis of the within county movement it was found that for the 23 couples considered the vast majority of movement was between the two towns in Hancock County, Sneedville and Kyles Ford, and was oriented with the road which connects these two towns. Most of

the remaining movement also appeared to be oriented with the major roads although the data were not extensive or complete enough to warrant a final determination (see Figure 3).

The analysis of the orientation of the migration into Hancock County proved more interesting. Figure 4 illustrates three main orientations of movement, two of which coincided closely with the roadways into the county from the larger towns located in adjacent counties. The third major orientation coincided with the direction of the larger towns to the northeast and with the geographical orientation of the ridges and valleys of this area, although no major roads run in this direction. A fourth, but smaller and slightly scattered orientation, was noted for the northwest. Upon closer analysis of the source of the movement from this direction it was found that it all came from an area immediately adjacent to the county with no migration coming from a distance greater than 10 miles from the county boundary.

Both parts of this analysis would fall within what is termed short-range movement since only 13, or 12.5 percent, of those considered came from a distance of over 100 miles from Sneedville. Owing to the fact that no orientation was found for the movement of these 13, and since distinct orientations do appear to be present with respect to both groups considered, this study tends to support Boyce et al.'s (1968) contention that the orientation of marital movement is particularly limited to the local scale while at the same time disagreeing with his conclusion that marital movement is generally isotropic.

Another aspect of this in-migration, that of whether there were a disproportionate number of males to females who migrated, was

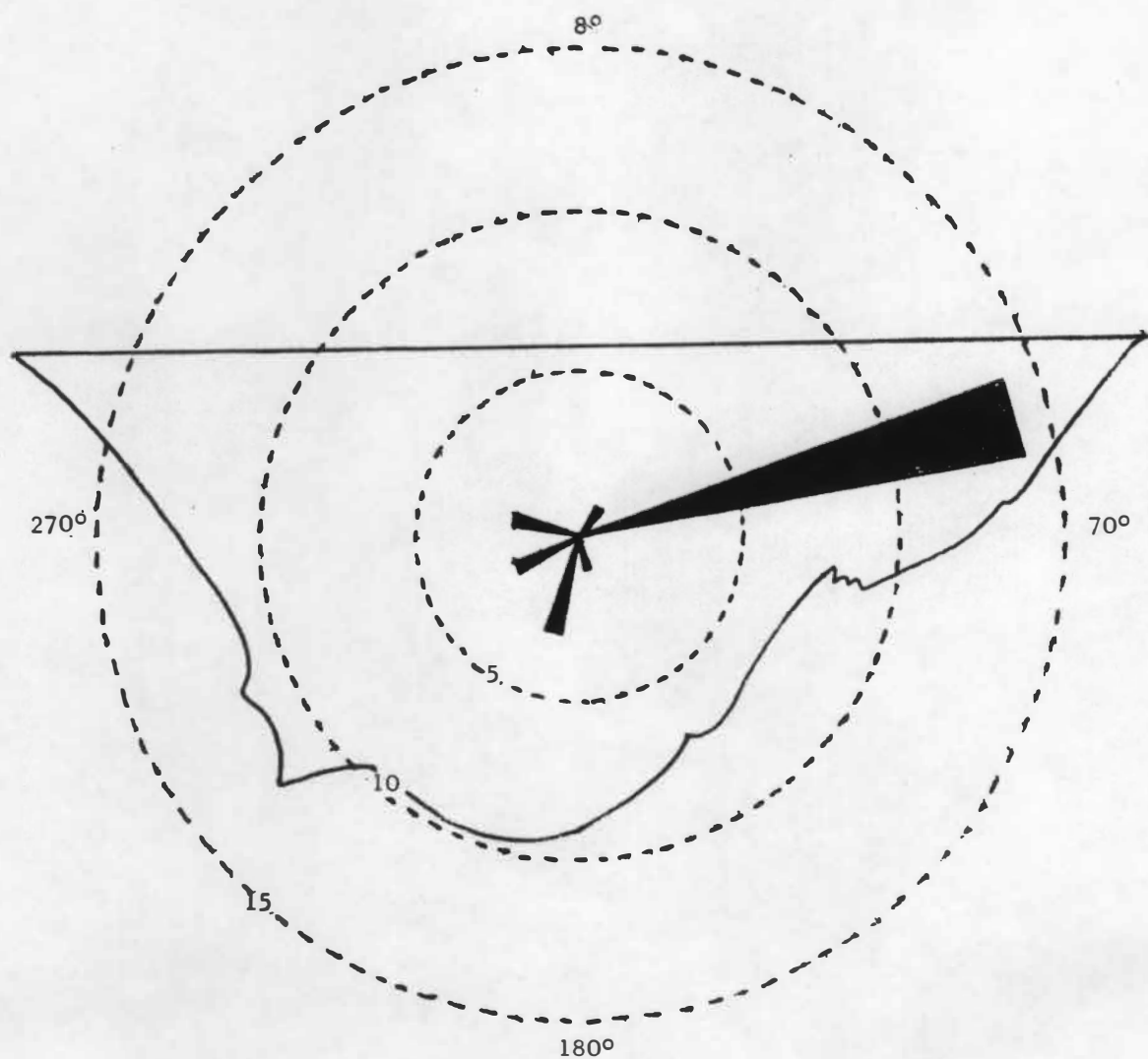


FIGURE 3. Orientation of movement within Hancock County. Each concentric circle represents an increment of five individuals.

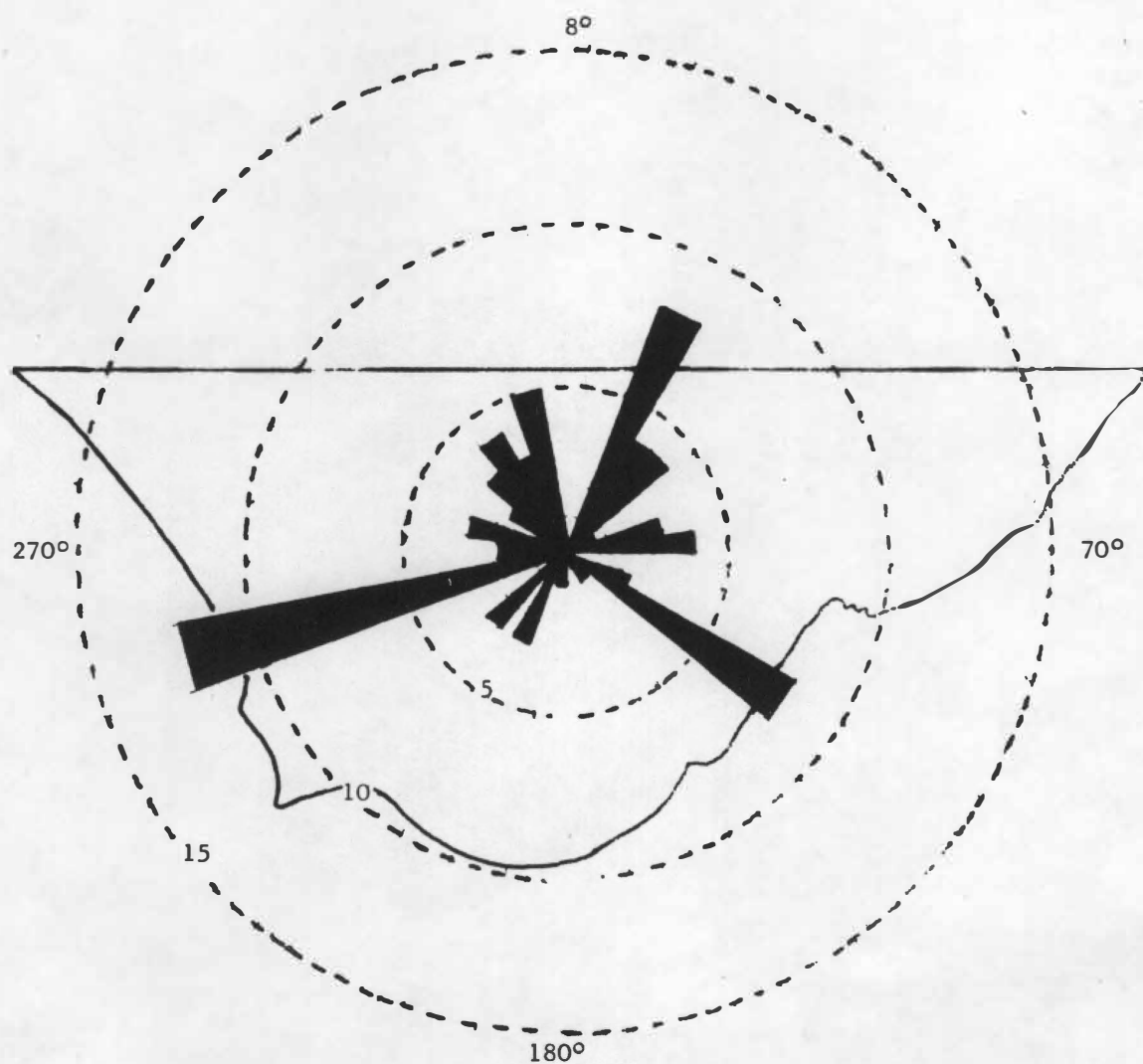


FIGURE 4. Orientation of migration into Hancock County. Each concentric circle represents an increment of five individuals.

considered. Of the 81 couples in the sample, 54, or 66.7 percent, had the wives coming from outside the county with a mean migration distance of 46.5 miles, while that for the in-migrating husbands was 169 miles. Upon calculation of the median distances for both these groups it was found that the difference in magnitude between the distances traveled by the husbands and wives, as indicated by the mean distances, is more apparent than actual; i.e., the median distance for the wives was 20 miles and that for the husbands was 24. These results are, nevertheless, in line with the findings of Spuhler and Clark (1961) for the population of Ann Arbor, Michigan, where the median migration distance for males was found to exceed that of females. Spuhler and Clark, whose data were obtained from marriage licenses, felt this situation was a reflection of the well known fact that marriages usually take place near the home of the female and that females tend to be less migratory than males (Spuhler and Clark 1961:228).

The Hancock County data exhibit a somewhat different situation in that it appears that women are actually more migratory than males, although in reality the pattern may be the same as that found by Spuhler and Clark. It is highly probable that because of the occupational limitations combined with the poverty situation of the county very few individuals from outside the county would have established residence there before finding a mate. Consequently, it could be assumed that mates from outside the county were probably obtained by individuals who had migrated out of the county for one reason or another, later returning to establish residence in the county.

The fifth, and last, aspect of marital movement which will be analyzed here pertains to the correlation of age at marriage of the mates and marital distance, a phenomenon which has been referred to as "diffusion" (Harrison and Boyce 1972b:137). Cavalli-Sforza (1958:397), in his study of the Parma Diocese in Italy, examined the correlation between age at marriage and marital distance and found an effect, significant but small, which suggested that the older the spouses at marriage the greater the distance between their birthplaces since they have had more time to move around. Such a trend was later found by Kuchemann et al. (1974:22-23) for Oxford City parishes.

For such an analysis of the Hancock County population the age of both husbands and wives at time of marriage were obtained from the marriage registers located in the Hancock County Court House in Sneedville. Of the 275 couples in the questionnaire sample, only 92 were found to have had marriages recorded in Hancock County. To ascertain if indeed a correlation did exist between these two aspects the Pearson Correlation was used. The results of this analysis yielded a correlation of $r = -.028$ for the husbands of the sample and $r = -.00123$ for the wives. Neither correlation was significantly different from zero.

CHAPTER V

COEFFICIENT OF BREEDING ISOLATION

The coefficient of breeding isolation, the product of the effective immigration rate times the effective size of a breeding population, gives a good indication of the relative degree of reproductive isolation experienced by a breeding population. The smaller the coefficient, the more the isolation, and the greater the probable effect of sampling "error" on gene frequencies; i.e., the greater the likelihood of random genetic drift. Therefore, estimates of the two variables, size and immigration rate, and the calculation of the coefficients for different human communities should help in understanding the changes from generation to generation which constitute human microevolution (Lasker and Kaplan 1964:327).

Before considering the Hancock County situation, an explanation of the relationship of migration to isolation is needed if the true significance of the coefficient of breeding isolation is to be understood. Both migration and isolation affect the gene frequencies of a population, although the effect of one is the converse of the other. Migration tends to increase intragroup genetic variability while reducing the intergroup differences in frequencies of genes. Isolation, on the other hand, tends to lead to the diversification of groups, and, through natural selection under local conditions, makes for the development of local subgroups. It also permits local diversification of groups on the basis of traits that have no adaptive significance, even

to the point of enhancing the chances of survival of a group that may be handicapped in comparison with other subgroups from which it has become genetically isolated. Such a situation occurs through the accidental selection of genotypes through random genetic drift (Lasker 1960a:80). Since the effective size of Hancock County's breeding population has already been determined (see Chapter III), it is only necessary to calculate the effective immigration rate before the coefficient of breeding isolation can be determined. From a genetic point of view the proportion of foreign to domestic gametes in a breeding population is considered to be the "effective immigration rate" (Lasker 1960a:81).

By this definition Lasker is making the assumption that all immigrants in a population are contributors to the gene pool of that population, which in reality may or may not be the case. In a later paper (Lasker and Kaplan 1964) this definition is refined somewhat by including only the immigrants who have children residing in the population. Here again, however, this improvement falls one step short. Lasker and Kaplan fail to take into account that in cases where both mates are immigrants their genes will not enter the gene pool of the population unless, and until, their children mate with a native of the population and reproduce in that population. Consequently, by using their method inflated results may be obtained.

The method proposed here is to consider only those immigrants who have contributed to the population's gene pool; i.e., mated with a member of the population and reproduced, as being genetically significant. The ratio of the number of these individuals to the number of individuals in the sample, discounting those individuals of couples

where both mates are immigrants, yields the effective immigration rate for the population. In the analysis of the Hancock County data both methods were applied and the results compared to coefficients derived from a variety of other populations (see Table 6).

Using Lasker's method, of the 484 individuals considered in the sample, 121 were immigrants yielding an effective immigration rate of 25 percent, and a coefficient of breeding isolation of 476. Applying the writer's method the 20 couples where both mates came from outside the county were discounted, leaving a sample of 444, 81 of which were considered immigrants. This yielded an effective immigration rate of 18.24 percent and a coefficient of breeding isolation of 347. Both of these coefficients, although considered of such magnitude as to negate any possibility of genetic diversification taking place due to random genetic drift, are probably much smaller in reality. This is due to the fact that in this study the Hancock County boundaries were taken to delimit the population, with anyone moving into the county being considered a migrant irrespective of whether he moved one mile or one thousand miles. In reality, as shown in the preceding chapter, the majority of immigrants came from the immediate vicinity of the county and could in most respects be considered members of the breeding population of the Hancock County area. In addition, when the results of the inbreeding obtained for the previous generation are taken into account, it can be assumed that these coefficients were, and have been, a great deal smaller during previous generations. Consequently, differentiation very probably did occur and was maintained during an earlier period of somewhat greater genetic isolation. The size of these coefficients

TABLE 6
COEFFICIENT OF BREEDING ISOLATION FOR VARIOUS POPULATIONS

Group	Total Population	Effective Breeding Population	Effective Immigration Rate (%)	Coefficient of Breeding Isolation
Ramah ^a Navaho	614-634	205-211	6	12.3-12.7
Dunkers, ^b Penn.	298-350	99-117	10-22	9.9-25.7
Ulithi Atoll ^c Pacific	421	140	15-20	21-28
Tzintzuntzan ^d Mexico	1231	410	12	49.2
Australian ^e Aborigines	100-1500	33-500	4-10	1.3-50
Hopewell, N. C. ^f Parish	250-330	83-110	12	10.0-12.0
Reque, ^g Peru	1200	348	26.3	92
San Jose, ^g Peru	1500	435	24.7	107
Monsefu, ^g Peru	10000	2900	13.0	377
Hancock County ^h Tennessee (Lasker's Method)	6719	1903	25	476
Hancock County ^h Tennessee (Writer's Method)	6719	1903	18.24	347

^aSpuhler and Kluckhohn 1953.

^bGlass et al. 1952.

^cLessa 1955.

^dFoster 1948.

^eBirdsell 1951.

^fDudley and Allan 1942.

^gLasker and Kaplan 1964.

^hPresent Study.

today, however, indicate a breakdown of any such isolation and a tendency toward population amalgamation.

CHAPTER VI

DISCUSSION AND CONCLUSIONS

The conditions necessary for the formation, and at least temporary maintenance, of human diversity are: (1) small size of the breeding group, and (2) relatively low admixture rate. Both these factors affect the degree of reproductive isolation experienced by the population and thus determine the extent to which random genetic drift will take place. This "sampling process," by which a subsequent generation may differ by chance in the proportion of its heredity traits from some previous generations (Lasker 1952:433) is a prime force which brings about a reduction in the heterozygosity of a population's gene pool. For example, in a small isolated population which is mating at random heterozygosity in respect to a pair of alleles would decrease at the rate of $1/(2N)$ per generation, when N = the effective breeding population size (Kimura 1955). This eventually leads to random extinction and fixation of the alleles (Kimura and Crow 1963:279) through the cumulative effects of this sampling (Wright 1969:211), and thus brings the population to a gene frequency equilibrium (Crow 1954:543).

Birdsell (1951), Kluckhohn and Griffith (1951) and others have pointed out that contemporary human tribes and communities are small enough so that genetic variability could decrease rapidly, and Lasker (1960b) has shown that degrees of isolation adequate to fix facial types have been recorded for a variety of populations. These conditions, though now somewhat rare in the world, may be presumed to have been

more pronounced in past times (Lasker 1960b:689) and similar to those that have occurred throughout the major phase of human evolution (Kuchemann et al. 1967:251). Therefore, it seems valid to assume that such conditions did undoubtedly play a critical part in the development of the local racial differences in man (Lasker 1960a:87).

A simple estimate of the rate of decrease in heterozygosis as a result of random genetic drift does not, however, take into account the contrary effect of admixture which would tend to bring about intra-group diversification (Hirons et al. 1969:237). Both the processes of diminishing relatedness with isolation of populations and increasing relatedness of populations through gene flow interact simultaneously and therefore should be considered together (Hirons et al. 1969:240). Roberts (1956) applied Sewall Wright's criteria to the estimation of this interaction, determining that when the product of the effective population size by the admixture rate; i.e., the coefficient of breeding isolation, is less than five, changes in gene frequencies due to random genetic drift are likely to be marked, and when the product is between five and fifty, the changes will still be appreciable. Such a rule of thumb depends, of course, on the assumption that the product of the effective population size by the admixture or immigration rate is a true measure of the degree of reproductive isolation experienced by the population.

Glass et al. (1952) used such a criteria to analyze a contemporary community which was isolated by religious beliefs--the Dunker population of Pennsylvania. In this analysis they showed that the gene frequencies for the Dunker population differed significantly from

both the general populace of the region and from the German state from whence their ancestors had come. This random genetic drift had occurred within a few generations in a group which consisted of 300 to 350 people at the time of the study.

Although the coefficient of breeding isolation for the parents' generation in Hancock County did not fall within the range where random genetic drift would be expected to have an effect in differentiating the population from surrounding populations, the evidence for inbreeding from the previous generation gives a good indication that this coefficient was indeed a great deal smaller during that period and previous to that time. If this were truly the case, one would expect to find a significant difference in the gene frequencies of the people in the county as compared to people in the surrounding areas.

From a study of one portion of the Hancock County population, the so-called Melungeon isolate, Pollitzer and Brown (1969:399), who assumed that inbreeding within this group was common in the past, saw the marked tendency toward out-migration and out-marriage--as indicated by birthplaces, isonymy, and differential gene frequencies by generation--as the apparent cause of the isolate losing its identity by blending into the surrounding population. In their analysis of this group, commonly considered a remnant of a once extensive population of tri-racial origin, it was found that they were a predominantly Caucasoid people with some Indian and possibly Negroid admixture, but not enough admixture, however, to account for the variation in gene frequencies found between the Melungeons and other white populations in the Southeast.

A comparison of the gene frequencies of the Melungeons with those of another county in the Southeast and with the frequency range for other United States and English whites (see Table 7) pointed out that in all but one case the gene frequencies for the Melungeons fall outside the range of the other populations. This indicates that, although the Melungeon sample is not considered a random sample of the Hancock County population it does point up the probability of reproductive isolation of the county in the past and illustrates the effects of this isolation on the gene frequencies of the population.

Most studies of human populations have tended to concentrate either on demographic parameters or on genetic ones with little attention being paid to the inter-relationship between the two types of parameters (Kuchemann et al. 1967:251). Furthermore, the studies which have been conducted in this area have for the most part been done on populations located outside of the United States. The present study, although concentrating primarily on the demographic parameters of a population, has illustrated the fact that there are abundant opportunities for such research in this area in the United States, opportunities which have been overlooked up to the present time.

TABLE 7
GENE FREQUENCIES OF THE MELUNGEONS AND OTHER POPULATIONS

Gene	Melungeons ^a	Claxton ^b Whites	Other U. S. and English Whites ^b
O	.0549	.704	.66-.70
A	.3423	.246	.23-.29
B	.0728	.050	.057-.09
M	.6102	.508	.533-.547
S	.2254	.281	.327-.377
R ¹	.3606	.426	.408-.420
R ²	.1881	.148	.141-.150
R ^o	.0839	.037	.026-.028
Fy ^a	.2869	.422	.414-.434
Hp ¹	.3853	.41	.43

^aPollitzer and Brown 1969.

^bWorkman et al. 1963.

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