Temporal Trends in Migration in the Åland Islands: Effects of Population Size and Geographic Distance

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Abstract   Using a model developed by Relethford (1992), we as-
sess temporal trends (1750–1949) in marital migration in the Åland
Islands, Finland, in relation to both geographic distance and pop-
ulation size. The 200-year time period was divided into four 50-year
periods. For all time periods both geographic distance and popula-
tion size are important determinants of migration among 15 Lu-
theran parishes. The geographic distance parameter of the model
decreases significantly over time, and the population size parameter
fluctuates slightly but shows no significant change over time. For
all time periods migration is negative density dependent, indicating
that there is greater *relative* flow from larger to smaller subdivisions.
Even though both the geographic distance and population size pa-
rameters are statistically significant, the analysis suggests that geo-
graphic distance has a greater relative effect on migration than pop-
ulation size. There is a clear indication of isolate breakdown during
the last two time periods (1850–1899 and 1900–1949). Residual
analysis indicated that the smallest parish (Sottunga) was a major
outlier that showed greater exogamy (less endemicity) than expected
from the model.

Migration is an important factor in shaping the genetic diversity of pop-
ulations. Although numerous studies of migration among human popu-
lations have focused on the effect of geographic distance on migration
rates among population subdivisions [e.g., see Boyce et al. (1967), Imai-
zumi et al. (1970), and Rogers and Harpending (1986)], few have ad-
dressed the impact of population size (Coleman 1977a,b; Wood et al.
1985; Relethford 1992). Population size, as a factor affecting migration,
has been examined by focusing on either the number of migrants (Lal-

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ouel and Langaney 1976; Relethford 1986) or the rate of migration between populations (Wood et al. 1985). Relethford (1992) recently presented a model using migration rates as a function of population size and geographic distance and suggested that future analyses should include an examination of a single subdivided population over time to explore any temporal effects. This type of analysis would allow examination of the possible effects of demographic shifts (e.g., population growth or decline) and sociocultural changes and would indicate fluctuations in the model's parameter values.

Our purpose here is to employ Relethford's (1992) model using migration data from the Åland Islands, Finland, that extend over a 200-year period. This analysis focuses on possible temporal effects and their interpretation.

Materials and Methods

Materials. Primary data sources for this study are the parish records kept by Åland's Lutheran ministers. In 1686 Swedish ecclesiastical law mandated uniform instructions for maintaining records of baptisms, marriages, burials, and interparish migration (Finland was part of the Kingdom of Sweden at this time). By the mid-1700s the marriage records (*vigsellängd*) included the date of marriage and the name, residence, and occupation of the bride and the groom.

From the marriage records, we obtained residence at the time of marriage of husband and wife to construct matrimonial migration matrices for four 50-year time periods starting in 1750 and ending in 1949. Residence at time of marriage often corresponds to the birthplace of the individual. In fact, based on an extensive genealogy [see O'Brien et al. 1988a,b, 1989], in 83% of the cases in Sottunga parish the residence listed in the marriage records was also the birthplace. In some instances the marriage was recorded only in the parish of the bride, even though the bride moved upon marriage to the parish of the groom. In other cases marriages are recorded in the home parish of both the bride and the groom. Because postnuptial residence is not specified in the marriage records, we made the assumption that the couple remained in the husband's parish of residence. This assumption should pose few problems because nearly identical results were obtained by Pitkänen et al. (1988) for Kitee parish by assuming that the couple resided in either the groom's residence or the bride's residence after marriage. Also, this is a necessary assumption, given that we would otherwise need complete genealogies for all 15 parishes spanning 200 years that are linked to the Parish Main Books or Communion books (*huvudböcker* or *kommunionböcker*), which list the household location and composition. Even with these data we would still

miss a number of individuals whose postmarital residence was outside Åland. Jorde et al. (1982) have shown that the F_{ST} values from parent-offspring migration data compare closely with the F_{ST} values for the matrimonial migration data used in this study. This finding lends support to our assumption and indicates that the matrimonial migration data reflect the patterns of gene flow among the parishes within the archipelago.

Population sizes for the 15 parishes were obtained from the census or population tables (*folkmängdstabeller*) that start in 1749. For further details and cautionary notes concerning Finnish-Swedish parish records, see Pitkänen (1977, 1980, 1984, 1986).

Methods. The effects of geographic distance and population size on among-group migration were analyzed using a nonlinear maximum-likelihood model developed by Relethford (1992). The dependent variable is the adjusted migration rate among populations, derived from a standard migration matrix. Let M be an $n \times n$ matrix of migration counts, where M_{ij} is the number of individuals in population j that came from population i and n is the number of populations. This matrix is converted into a column stochastic migration matrix with elements m_{ij} representing the probability that a person in population j came from population i. These elements are computed following the standard method:

$$m_{ij} = M_{ij} \bigg/ \sum_{i=1}^{n} M_{ij}. \tag{1}$$

This matrix is column stochastic; each column sums to unity.

Because the migration rates depend in part on the level of endemicity (m_{jj}), an adjusted migration rate is used as the dependent variable in all analyses (m_{ij}/m_{jj}) (Wood et al. 1985; Relethford 1992). The migration model expresses this adjusted migration rate as a function of the population size of the recipient population (N_j), the population size of the source population (N_i), and the geographic distance between populations i and j (d). That is,

$$m_{ij}/m_{jj} = a(N_i/N_j)^p e^{-bd}, \tag{2}$$

where p is a measure of the effect of population size, b is a measure of the effect of geographic distance, and a is an adjustment factor having no comparative use. The population size parameter p also provides information regarding the average direction of migration flow. If the parameter is positive, then migration is negative density dependent; adjusted migration is greater from large to small populations than from small to large populations. If the parameter is negative, then migration is positive density dependent; adjusted migration is greater from small to large populations than from large to small populations. Full details

and derivation of this model are presented by Relethford (1992). Parameters are estimated from maximum-likelihood estimation using Wood et al.'s (1985) algorithm.

The significance of the parameters p and b are tested using a chi-square test comparing the log-likelihoods of subsets of the full model presented in Eq. (2). The *island model* is the subset where both p and b are set equal to zero; neither population size nor geographic distance affects migration rates. The *density model* is the subset where b is set equal to zero and p is allowed to vary; this model states that population size affects migration but geographic distance does not. The *isolation by distance model* is the subset where p is set equal to zero and b is allowed to vary; this model states that geographic distance affects migration but population size does not. The *full model* allows both p and b to vary. Any two models can be compared, provided that one is a subset of the other. For each model the log-likelihood is computed as

$$\ln(L) = \sum_{i=1}^{n} \sum_{j=1}^{n} M_{ij} \ln(\hat{m}_{ij}), \tag{3}$$

where M_{ij} is the observed *number* of migrants in population j from population i and m_{ij} is the estimated migration *rate* for a given model. Given log-likelihoods for two models, the two models can be compared using the chi-square statistic:

$$\chi^2 = 2[\ln(L_1) - \ln(L_2)], \tag{4}$$

where $\ln(L_1)$ and $\ln(L_2)$ are the log-likelihoods of models 1 and 2, where model 2 is a subset of model 1. The degrees of freedom are the difference in the number of independent parameters between the two models.

Four model comparisons were performed here: density versus island, isolation by distance versus island, full versus density, and full versus isolation by distance. The first two tests examine the single effects of population size and geographic distance, respectively. The last two tests examine the effect of one variable given inclusion of the other variable in the model. As such, these tests are analogous to testing for partial correlations. For example, the comparison of the full and density models tests for the significance of geographic distance given the inclusion of population size in the model. Although other comparisons are possible [see Wood et al. (1985)], these four tests provide the most useful information on the relative influence of population size and geographic distance.

The significance of temporal changes in model parameters was tested using a Z test of parameters of adjacent time periods. The standard error of the difference of parameter estimates was derived using traditional

Table 1. Chi-Square Tests Comparing Migration Models[a]

	χ^2			
Time Period	Density vs. Island Model	Isolation by Distance vs. Island Model	Full vs. Density Model	Full vs. Isolation by Distance Model
1750–1799	65.36	866.45	863.38	62.29
1800–1849	56.78	1035.85	1017.50	38.42
1850–1899	108.59	1088.35	1061.79	82.75
1900–1949	163.61	1040.23	1002.88	126.27

a. All chi-square values are highly significant ($P < 0.001$), d.f. = 1.

methods as the square root of the sum of the squared standard errors for the two time periods.

Results

The chi-square tests comparing model subsets are reported in Table 1 for all four time periods. All the chi-square values are highly significant ($P < 0.001$). These results indicate that both population size and geographic distance are significant predictors of adjusted migration, both by themselves and together. The relative fit of the models was assessed using Akaike's information criterion, computed as $2[k - \ln(L)]$, where k is the number of model parameters (Blangero 1990). For each time period Akaike's information criterion (not shown) was lowest for the full model, followed by the isolation by distance model, the density model, and the island model. These results show that the full model provides the most parsimonious fit, indicating that both geographic distance and population size are significant predictors of adjusted migration rates. Comparison of the chi-square values within each time period suggests that geographic distance has a greater influence on adjusted migration rates than does population size, because the chi-square values comparing the full model to the isolation by distance model are smaller than the chi-square values comparing the full model to the density model.

The parameter estimates and standard errors for the full model are reported in Table 2 for all four time periods. In each case the population size parameter p is positive, indicating negative density dependence (Relethford 1992). The geographic distance parameter b declines over time, particularly during the most recent time period, suggesting breakdown of isolation. The population size parameter fluctuates over time but within a narrow range [see Relethford (1992) for comparative values].

Table 2. Parameter Estimates (and Standard Errors) for the Full Model

Time Period	p	b
1750–1799	0.526 (0.067)	0.107 (0.005)
1800–1849	0.393 (0.064)	0.116 (0.005)
1850–1899	0.522 (0.058)	0.095 (0.004)
1900–1949	0.424 (0.038)	0.057 (0.002)

Z tests comparing parameter values in adjacent time periods are reported in Table 3. None of the comparisons for the population size parameter p are significant; the density-dependent effect is therefore constant over time. The last two comparisons for the geographic distance parameter b are significant ($P < 0.001$), showing that the reduction in distance decay occurred after 1850 and was particularly noticeable after 1900.

Discussion

Although numerous models of human population structure incorporate the effects of geographic distance on migration rates, few studies have dealt with the influence of population size. In a previous paper Relethford (1992) extended Wood et al.'s (1985) migration model and applied it to 13 samples from the literature. That study showed three generalities that held across a wide range of ecological settings: (1) Geographic distance limits human migration, (2) population size affects human migration patterns, and (3) most populations show negative density-dependent patterns of migration, where adjusted migration rates are greater from large to small populations than from small to large populations. One of the recommendations made by Relethford was to apply the migration model to temporal subsets in order to look at possible relationships between model parameters and demographic change.

Table 3. Z Tests Comparing Population Size p and Geographic Distance b in Adjacent Time Periods

Time Periods Compared	p		b	
	Z	Probability	Z	Probability
1750–1799 & 1800–1849	1.44	0.150	1.27	0.204
1800–1849 & 1850–1899	1.49	0.136	3.28	0.001
1850–1899 & 1900–1949	1.41	0.159	8.50	0.000

We fill that need here by presenting results for four time periods in the Åland Islands. Demographic and sociocultural changes in the Åland Islands between 1750 and 1949 could affect the relationship of migration to both geographic distance and population size. Changes in the parameters of the migration model might reflect these changes. For example, the Åland Islands experienced both population growth and decline during the past few centuries. Differential growth of population subunits combined with changes in the economic base might lead to changes in the influence of population size on migration over time. Likewise, changes in ease and availability of transportation and other related sociocultural changes might affect the relationship of migration to geographic distance.

The chi-square tests show that both geographic distance and population size have a significant effect on migration rates among Åland parishes, with geographic distance having the greater relative effect. In all time periods migration is negative density dependent, which, given the available information (Relethford 1992), might be typical of most human populations. Statistical comparison of model parameters between adjacent time periods shows that the population size parameter p has not changed significantly over time. Closer analysis of changes in population size suggests that this lack of change is related to relative constancy of subdivision population sizes over time. Although the population sizes of all parishes increased over time (and then decreased), their rank-order relationship did not vary (all the rank-order correlations of parish population sizes across time periods exceed 0.96). Also, the degree of variability in population size remains relatively constant: The coefficients of variation range from 46% to 52%, which is a narrow range. It appears that the differential population growth over all time periods was not sufficient to alter the basic relationship of migration and population size.

We have excluded the only urban parish (the city of Mariehamn) from these analyses because it was designated as a separate parish in 1905 and started to exert major influences on demographic characteristics after this date. [Mariehamn was established in 1861 (Mead and Jaatinen 1975) and became a separate parish in 1905.] However, incorporating Mariehamn parish into the model does not substantially change the general patterns or conclusions. With Mariehamn added to the analysis, the change in the distance parameter for 1900–1949 is slight ($b = 0.057$), and the population size parameter p increases to 0.525, still indicating that migration is negative density dependent. The full model still provides the best fit. We had suspected, based on earlier results showing Mariehamn as a population sink (Mielke 1982) and as a centrally plotting parish based on genetics (Jorde et al. 1982) and migration (Mielke et al. 1976), that migration would become positive density dependent with the incorporation of this town. A probable explanation for the lack of change is the relatively slow growth of Mariehamn from 1905 to 1950 and the

fact that it started to exert a major influence on population structure only after 1920 (Mielke et al. 1976; Jorde et al. 1982). [By 1910 only 5.1% (1090 individuals) of Åland's population resided here. Mariehamn slowly increased in size until it reached 4635 inhabitants (21.4% of the resident population of Åland) in 1950. Major growth occurred after 1950, and by 1980 the town had 9553 inhabitants (41.9% of Åland's population) (Statistisk Årsbok för Åland 1982).] Apparently, this effect was not great enough to change the parameters for the whole 50-year period that we examined.

The effect of geographic distance on migration does change over time. The parameter value does not change significantly over the first two time periods but does decrease significantly after 1850. The decrease is particularly noticeable after 1900, when the distance parameter b drops to roughly half the previous value. This finding is in agreement with previous studies of marital migration, parent-offspring migration, and patterns of genetic variation in the Åland Islands, which have also documented changes after 1850 with extensive breakdown in local isolation after 1900 (Mielke et al. 1976, 1982; Jorde et al. 1982). This change is probably related to a number of factors, including improvements in transportation (a fleet of steamboats started to serve Åland after 1890, and private motorboats started to facilitate transportation and communications in the 1920s and 1930s), the abandonment of many outer islands (60 of Åland's inhabited islands were abandoned between 1905 and 1960), and the shift of the population to the Main Island or Fasta Åland (de Geer 1960; Jaatinen 1960; Pipping and Pipping–van Hulten 1961; Mead and Jaatinen 1975).

It is useful to examine residuals from the full migration model to determine population-specific influences on migration patterns that may not be detected otherwise. We computed the mean square residual for each parish in each time period. The results are reported in Table 4. For all four time periods the parish of Sottunga is a major outlier, as judged by the high mean square residual values. Closer examination shows that Sottunga's outlier status is due mostly to a lower level of endemicity (m_{jj}) than expected in each time period. The full model consistently predicts greater endemicity than observed. Sottunga is a small parish, but it has considerably lower endemicity rates than would be expected on the basis of any linear function of population size. Part of the lower endemicity rates may be due to Sottunga's location on a major shipping route between Finland and Sweden (Jorde et al. 1982) and thus its potential for more contact with peoples from other parishes in the Baltic region. Along these same lines, it is also interesting to note that genealogical studies of Sottunga indicate that genetic drift (including a true founder effect) rather than inbreeding is probably responsible for the el-

Table 4.   Mean Square Residuals from the Full Migration Model ($\times 10^5$)

Parish	Time Period			
	1750–1799	*1800–1849*	*1850–1899*	*1900–1949*
Eckerö	5.36	5.13	2.28	4.15
Hammarland	20.16	1.72	4.49	15.87
Geta	12.50	9.40	11.06	13.46
Finström	7.92	3.95	3.98	14.24
Saltvik	1.52	0.83	0.98	7.32
Sund	6.20	3.26	1.49	17.91
Vårdö	26.68	8.02	3.70	25.72
Jomala	4.59	0.99	0.49	36.07
Lemland	6.88	3.44	1.79	5.61
Lumparland	16.35	2.59	8.61	35.88
Föglö	3.92	4.13	4.56	4.75
Sottunga	121.84	61.50	35.54	34.34
Kökar	0.46	2.48	0.32	2.33
Kumlinge	27.82	16.37	0.89	6.73
Brändö	1.11	6.12	2.23	3.24

evated frequencies of rare disorders, such as von Willebrand and Wolman's diseases (O'Brien et al. 1988a,b; Röyttä et al. 1992).

The observation that small populations often have lower endemicity rates has been made for historical Sweden (Beckman 1961), Bundi clans (Malcolm et al. 1971), twentieth-century Britain (Coleman 1977a,b), historical Massachusetts (Relethford 1986), and Åland (Mielke 1980; Workman and Jorde 1980; Mielke et al. 1982). The lack of suitable potential mates in such small populations may lead to higher immigration rates and, as a consequence, lower rates of endemicity. Thus far we have not been successful in incorporating this type of demographic behavior into the full migration model. Because the migration model used here was designed primarily for examining migration *among* populations, a separate analysis of endemicity may be necessary in cases such as this (Relethford and Mielke, 1994).

In any case, the inclusion of Sottunga does not affect parameter estimation to any great extent. When Sottunga is removed from the analysis, the population parameter p values are 0.517 for 1750–1799, 0.448 for 1800–1849, 0.554 for 1850–1899, and 0.398 for 1900–1949. These values are close to those reported from all populations (Table 2). The geographic distance parameter b changes even less when Sottunga is removed: 0.110 for 1750–1799, 0.118 for 1800–1849, 0.095 for 1850–1849, and 0.056 for 1900–1949.

The residual analysis for the last time period (Table 4) shows that in addition to Sottunga two other parishes are relatively large outliers:

Jomala and Lumparland. Here, predicted endemicity in Jomala is greater than expected and predicted endemicity in Lumparland is less than expected.

Jomala is one of the few parishes that experienced net population gains from 1881 to 1950 (de Geer 1960), and it has also maintained a comparatively normal age-sex structure (Jaatinen 1960). Jomala is the rural parish surrounding the only urban center, Mariehamn, in the archipelago. Thus one would expect this parish to be an outlier given the growth of Mariehamn during the twentieth century.

Lumparland, on the other hand, is the second smallest parish after Sottunga. At the turn of the century the number of children decreased in both Sottunga and Lumparland and mates in the 20–30-year age range were deficient, according to Jaatinen (1960). Also, Lumparland's population size in 1910 was 564, and it decreased to 448 individuals in 1950 (*Statistik Årsbok för Åland* 1979). Individuals in both Sottunga and Lumparland found the local mating pools shrinking in size and were compelled to look outside the parish for mates. Thus relatively low endogamy in Sottunga and Lumparland and high endogamy in Jomala are consistent with the argument that reduced mate availability leads to higher exogamy.

In sum, this study has shown the utility of Relethford's (1992) migration model in assessing temporal changes in determinants of migration. Comparison of model parameters over time combined with residual analysis provides succinct descriptions of migration trends and a framework for hypothesis testing. Future studies of human migration should focus on similar temporal analyses, particularly among populations that have experienced rapid demographic and economic shifts.

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