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Isonymy and repeated pairs analysis: the mating structure of Acceglio, Italy, 1889 - 1968

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Abstract – *Two methods of surname analysis have been commonly employed to study population structure: (1) Isonymy, for estimates of inbreeding and (2) Repeated pairs method (RP) for assessing patterns of subdivision within a population. In this study, both methods are applied to surname data from 793 marriages that occurred between 1889 and 1968 in Acceglio, an isolated Alpine population in Valle Maira, Italy. To observe temporal trends, marriages were divided into four cohorts of approximately 20 years: (1) 1889-1908, (2) 1909-1928, (3) 1929-1948, and (4) 1949 - 1968. The isonymy analysis revealed an overall F value for the first cohort of 0.0432 that decreased through time to a level of 0.0200. RP values were calculated with, and without, isonymous marriages to discriminate the differential contributions of isonymous versus non-isonymous marriages to the RP statistic. Including isonymous marriages, the RP analysis gave a ($RP–RP_r$) value of 0.00280 for the first cohort, which decreased to 0.00041. Excluding isonymous marriages, a ($RP–RP_r$) value of 0.00225 was reported for the first cohort, decreasing through time to 0.00047. The exclusion of isonymous marriages yields a substantial change in the total measure of ($Rp–Rp_r$), suggesting that the same lineages are involved in isonymous marriages and repeated-pairs unions. Overall, the decrease in frequency of isonymous marriages and proportionate decline in repeated-pair marriages suggest an increase in exogamy through time and the breakdown of reproductive isolation in an Alpine community.*

Keywords – *Population structure, Church records, Marriages, Valle Maira.*

Introduction

The term "genetic isolate" has been widely applied to small breeding populations with varying degrees of reproductive isolation and genetic heterogeneity (Benoist, 1973). However, under the impact of increasing urbanization, there has been a recent breakdown of reproductive isolation in populations worldwide (Lasker et al., 1972; Crawford, 1980). The study of population structure offers insight into the process of increased migration and its evolutionary consequences on the gene pool of these small, isolated populations.

The use of surnames as a means of measuring deviations from panmixia is an important tool in studies of population structure. Surname distributions have been used to demonstrate patterns of non-random mating within and between groups and as a proxy measure of reproductive isolation (Crow & Mange, 1965; Morton & Hussels, 1970). Two methods of surname analysis have been applied to the study of population structure: (1) Isonymy, for estimates of inbreeding, and (2) Repeated pairs method *(RP)* for the detection of population substructure.

Isonymy was introduced by Crow & Mange (1965) for the computation of inbreeding coefficients from surname data. This method estimates an index of inbreeding based on the assumption that surnames are transmitted in a patrilineal fashion, i.e., if it were determined by a gene located on the Y chromosome (Wilson, 1981). Crow & Mange (1965) demonstrated that the frequency of marriages between couples with the same surname can be used to estimate inbreeding in a patrilineal society. Since the total number of isonymous marriages in any given population is small, isonymy estimates may underestimate inbreeding levels and produce estimates with high sampling error (Duggirala et al., 1991; Relethford, 1992). To overcome these sampling problems, several matrix and graphical methods have been developed to detect mating structure (i.e., Devor, 1983, Lasker & Kaplan, 1985). One such method proposed by Lasker & Kaplan (1985) is the repeated pairs analysis.

The repeated pairs method *(RP)* attempts to measure the extent of marriages between substructures in a population. This method measures the incidence of repeated pairs of surnames between lineages to determine non-random mating patterns. This is accomplished by comparing the coefficient *(RP)* obtained by measuring the incidence of repeated pairs; to the random expectation (RP_r) developed by Chakraborty (1985). The difference between *RP* and RP_r $(RP–RP_r)$ provides a measurement of the degree of population subdivision.

In this study, both isonymy and repeated pairs analysis have been applied to the marital data of an isolated alpine population from Valle Maira, Italy. Through these analyses, levels of inbreeding and possible population subdivisions or non-random mating patterns have been examined. The present analysis attempts to document the genetic isolation of an Alpine population and how the level of isolation may have changed through time.

Population

Acceglio is located in an Alpine valley, Valle Maira, Italy, 40 kilometers to the northwest of the Piedmontese city of Cuneo, and 100 kilometers to the south of Torino (Fig. 1). The valley is 43 kilometers long, narrow, and has only one road transecting the valley. It is a valley carved by the Po river with several settlements located off the road that are inaccessible during the winter. The valley is subdivided into 9 communes, or towns. Acceglio is one of these communes located at the west end of the valley, near the French border. Acceglio is subdivided into 7 fraziones or hamlets (Crawford, 1980).

This valley is historically, geographically, and culturally distinct from the surrounding Piedmont area and the rest of Italy (Crawford, 1980). The valley has remained undisturbed throughout history, as most invasions and population movements followed the major passes into the Piedmont area, towards Rome, thus avoiding this Valley. Additionally, only a few exogamous marriages take place with residents of the surrounding valleys, individuals usually mate with spouses from greater distances, migrating from industrial cities of Italy and France.

According to Crawford (1980), the population of Acceglio declined numerically during the last 50 years. Moreover, it was illustrated that during this 50 year period there was a preponderance of females in the population, due to differential male out-migration. In particular, distinct age cohorts were identified where there was a large reduction in population size, corresponding roughly to the time periods of the two world wars.

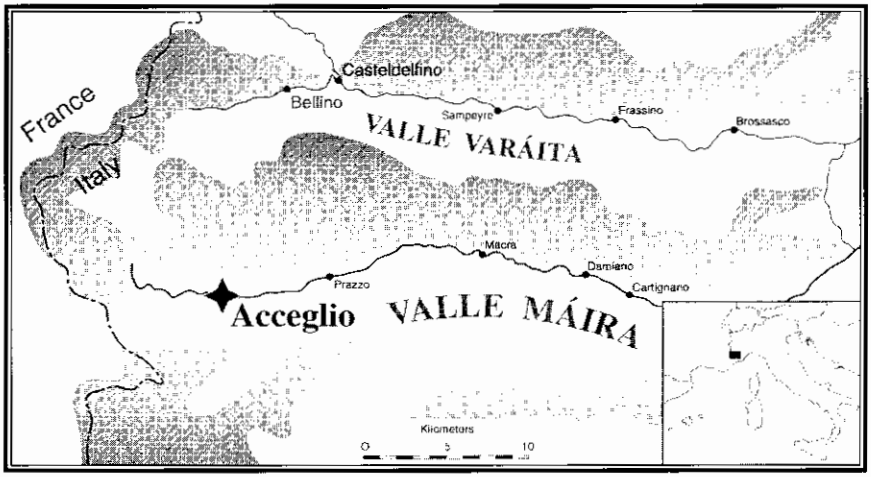

Fig. 1 - A Map Showing the Location of Acceglio, Italy, the Alpine Community Described in this Study.

Methods

Church records were available from the nineteenth century to the present (1889-1968) and provided a demographic continuum with few gaps. The marriage surname data used in this analysis were from church records, transcribed directly by Crawford and four students.

Marriages were recorded only when the exact date of marriage (in years) was provided. The first twenty years of data were excluded because of incomplete records.

To chronologically observe trends in mating patterns, the marriages were divided into four time cohorts (approximating generations), each representing twenty years: (1) 1889-1908, (2) 1909-1928, (3) 1929-1948, and (4) 1949-1968. A total of 793 marriages were recorded for the 4 cohorts.

Following Crow & Mange (1965), the total inbreeding coefficient *(F)*, its random component *(F_r)*, and non random component *(F_n)* have been computed as:

$$F_r = \sum P_i Q_i / 4$$

$$F_n = (P - \sum P_i Q_i) / 4(1 - \sum P_i Q_i)$$

$$F = F_n + (1 - F_n)F_r$$

in which P_i = frequency of males with ith surname; Q_i = frequency of females with ith surname; and P = frequency of marital isonymy.

The statistic repeated pairs *(RP)* was calculated by the method of Lasker & Kaplan (1985) as follows:

$$RP = \sum [S_{ij}(S_{ij} - 1)] / N(N - 1)$$

in which S_{ij} = number of couples with a husband of the ith surname and a wife of the jth maiden name, and N = number of marriages.

The random expectation is computed using Chakraborty (1985):

$$RP_r = [\sum S_i^2 / N(N - 1) - 1 / N - 1] [\sum S_j^2 / N(N - 1) - 1 / N - 1]$$

in which S_i = number of husbands with ith surname, S_j = number of wives with jth maiden name, and N = number of marriages.
Relethford (1992) measured the significance of the RP results by computing a Z score testing the null hypothesis $RP = RP_r$ as follows:

$$Z = (RP - RP_r) / \mathrm{SE}(RP_r)$$

in which $\mathrm{SE}(RP_r)$ = standard error of RP_r as computed by Chakraborty (1985). Additionally, using Relethford (1992), the percentage of excess RP above that expected at random was computed as follows:

$$RP\ \% = 100(RP - RP_r) / RP_r$$

Results

Table 1 reports the number of marriages and the frequency of isonymous marriages for each cohort, respectively. The frequency of marriages increases during the second period, and subsequently decreases in the following two periods. The frequency of isonymous marriages decreases through time. Table 2 and Table 3 display an increase in exogamous marriages and emigration rates through time as reported by Crawford (1980).

Tab. 1 - Number of marriages and frequency of isonymy and repeated pairs marriages (*RP*) by marriage cohorts (Crawford, 1980).

	Marriage Cohorts	Number of Marriages	Frequency of Isonymy (%)	Frequency of RP
1.	1889-1908	233	13.73	29.61
2.	1909-1928	274	13.50	21.53
3.	1929-1948	158	10.13	10.76
4.	1949-1968	128	5.47	10.94

Tab. 2 - Frequencies of exogamous marriages in Acceglio (Crawford, 1980).

Generation	Frequency of Exogamous Marriages (%)
1890-1910	7.91
1911-1930	4.32
1931-1950	20.00
1951-1968	50.49

Tab. 3 - Emigration rates from Acceglio, Italy based on 100 interviews (Crawford, 1980).

Generation	Number of Cases	Emigration %
— -1890	278	5.75
1891-1910	329	18.54
1911-1930	480	22.90
1931-1950	292	24.65

Tab. 4 - Isonymy estimates for Acceglio, Italy 1889-1968.

Marriage Cohorts	Number of Marriages	Number of Isonymous Marriages	P	F_r	F_n	F
1. 1889-1908	233	32	0.1373	0.0199	0.0317	0.0432
2. 1909-1928	274	37	0.1350	0.0122	0.0311	0.0429
3. 1929-1948	158	16	0.1013	0.0092	0.0232	0.0322
4. 1949-1968	128	7	0.0547	0.0085	0.0117	0.0200
Total Time	793	92	0.1160	0.0109	0.0266	0.0372

Abbreviations P = Frequency of marital isonymy; F_r = Random component of inbreeding coefficient; F_n = Non random component of inbreeding coefficient; F = Total inbreeding coefficient.

Table 4 depicts the frequency of isonymy and the inbreeding coefficients *Fr*, *Fn*, and *F* by marriage cohort. The overall *F* for the population ranged from 0.0432 to 0.0200. The proportion of isonymous *(P)* marriages range from 0.1373

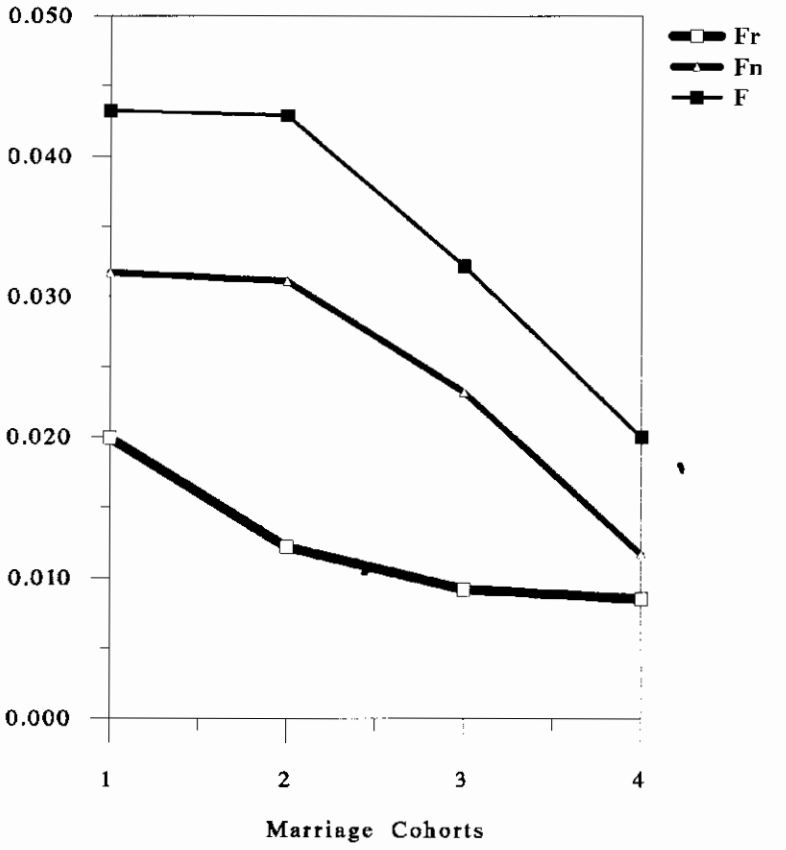

Fig. 2 - Temporal Trends in Estimates of Isonymy for Acceglio, Italy. Marriage Cohorts: 1=1889-1908; 2=1909-1928; 3=1929-1948; 4=1949-1968. *Fr*, *Fn*, and *F* are measures of isonymy as defined in the text.

Tab. 5 - Repeated Pairs (*RP*) of surnames in married couples and Random Expectation (RP_r) of repetition in Acceglio, Italy.

Marriage Cohort	*N* of Mar	*N* of Rep	*RP*	RP_r	$RP–RP_r$	SE(RP_r)	%	*Z* value
1.1889-1908	233	272	0.00503	0.00223	0.00280	0.0002658	126.60	10.53**
2.1909-1928	274	250	0.00334	0.00236	0.00098	0.0002969	41.53	3.30*
3.1929-1948	158	58	0.00234	0.00125	0.00109	0.0002183	87.20	4.99**
4.1949-1968	128	24	0.00148	0.00107	0.00041	0.0002533	38.32	1.62
Total Time	793	1586	0.00252	0.00171	0.00081	0.0001328	47.37	6.10**

Abbreviations *N* of Mar = Number of Marriages; *N* of Rep = Number of Repeated pair marriages; SE(RP_r) = Standard Error of RP_r; % = Percentage of excess *RP* above that expected at random; *Z* Value = Measure of the significance of the *RP* results.
* $p < 0.05$; ** $p < 0.001$.

to 0.0547 and decrease through time. *Fr*, *Fn*, and *F* follow this trend without interruption. Figure 2 displays this temporal trend through time. For comparison, published isonymous rates (overall *F*) range from a high of 0.0495 in the Hutterites to a low of 0.0034 in Vindalhaven Island, Maine (Crow & Mange, 1965; Sorg, 1983). Moreover, published isonymous rates (overall *F*) from various Italian populations range from a high of 0.0296 in S. Paolo Albanese to a low of 0.0009 in Ferrara (quoted in Biondi et al., 1993).

RP was calculated with and without isonymous marriages. The results from the repeated pairs analysis including and excluding isonymy are reported in Tables 5 and 6 respectively. The exclusion of isonymy yields a substantial change in the total measure of $RP–RP_r$. This implies that the same lineages or surnames are involved in isonymous marriages and repeated pairs unions. Including isonymous marriages, the total $RP–RP_r$ value obtained was 0.00081, excluding isonymy the value obtained was –0.00004. *RP* values decrease through time, with the exception of cohort 4, after exclusion of isonymous marriages (Fig. 3 and 4). For comparison, various published $RP–RP_r$ rates range from –0.00020 reported for Tarpa, Hungary to a higher value of 0.00058 reported for the Protestants of Fogo Island, New Foundland (Duggirala et al., 1991; Koertvelyessy et al., 1988). Moreover, RP statistics reported for Italian populations range from a high of 0.05497 for a Greek Italian population of Reggio Calabria Province to a lower of 0.01394 from a Greek Italian population of Lecce Province (Biondi et al., 1996).

Tab. 6 - Repeated Pairs (*RP*) of surnames in married couples and Random Expectation (RP_r) after exclusion of Isonymous marriages in Acceglio, Italy.

Marriage Cohort	*N* of Mar	*N* of Rep	*RP*	RP_r	$RP–RP_r$	SE(RP_r)	%	*Z* value
1.1889-1908	201	144	0.00358	0.00133	0.00225	0.0001905	169.00	11.81**
2.1909-1928	237	120	0.00215	0.00185	0.00030	0.0003228	16.22	0.93
3.1929-1948	142	18	0.00090	0.00078	0.00012	0.0001536	15.38	0.78
4.1949-1968	121	20	0.00138	0.00091	0.00047	0.0002241	51.65	2.10*
Total Time	701	586	0.00119	0.00123	–0.00004	0.0001018	–3.25	–0.39

Abbreviations *N* of Mar = Number of Marriages; *N* of Rep = Number of Repeated pair marriages; SE(RP_r) = Standard Error of RP_r; % = Percentage of excess *RP* above that expected at random; *Z* Value = Measure of the significance of the *RP* results.
* $p < 0.05$; ** $p < 0.001$.

Relethford's (1992) comparative statistic measuring the percentage of excess RP above that expected at random confirms this reduction through time. When including isonymous marriages, there is a gradual reduction through time, with a slight increase in the third cohort. However after exclusion of isonymous marriages, there is a decrease in the percentage excess in cohorts 2 and 3.

Additionally, the *Z* score test for the significance of *RP* was calculated for *RP* with and without isonymous marriages. Including isonymous marriages, the first three cohorts and the total time period have observed *RP* above that expected at random (Tab. 5). Excluding isonymous marriages, both cohort 1 and cohort 4 have observed *RP* values significantly greater than expected at random (Tab. 6). In contrast, the total time estimate was non significant when excluding isonymous marriages.

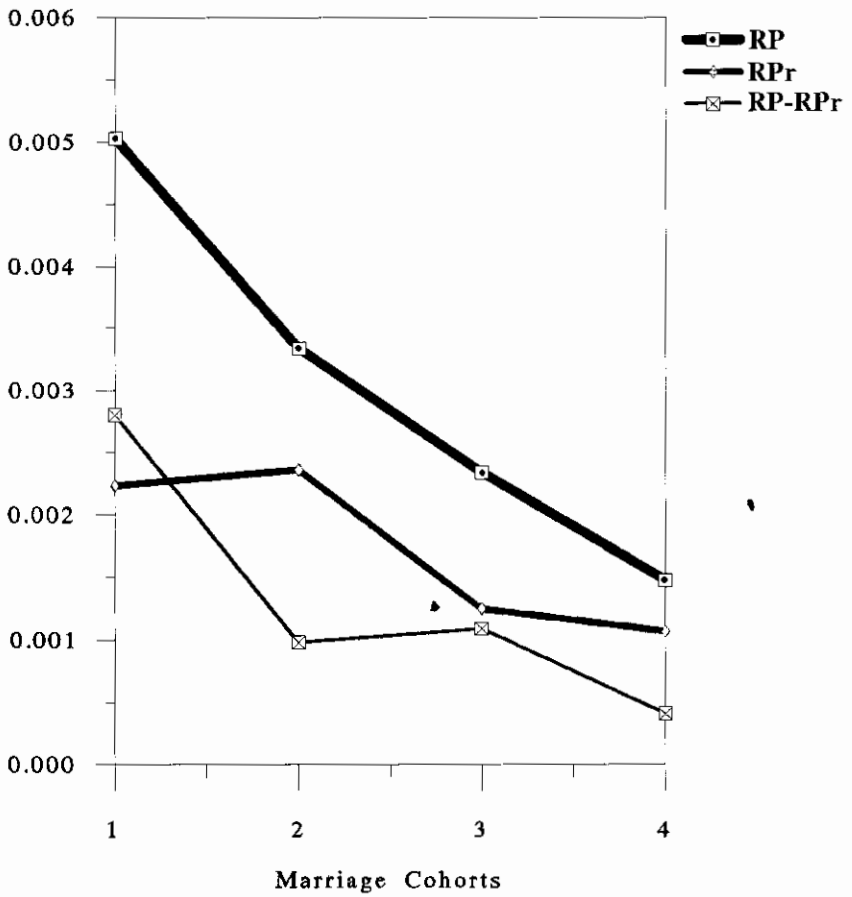

Fig. 3 - Temporal Trends in *RP*, RP_r, and $RP–RP_r$ for Acceglio, Italy. Marriage Cohorts: 1=1889-1908; 2=1909-1928; 3=1929-1948; 4=1949-1968. *RP*, RP_r, and $RP–RP_r$ are measures of repeated pair marriages as defined in the text.

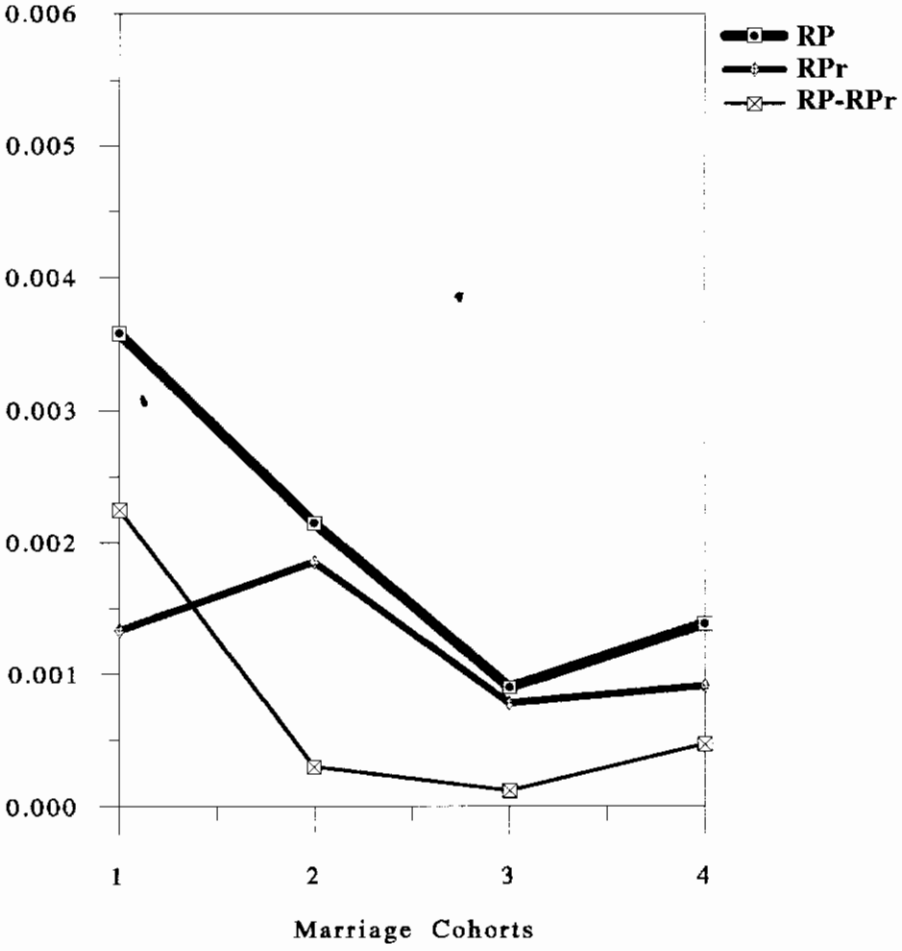

Fig. 4 - Temporal Trends in *RP*, RP_r, and $RP–RP_r$ Excluding Isonymous Marriages for Acceglio, Italy. Marriage Cohorts: 1=1889-1908; 2=1909-1928; 3=1929-1948; 4=1949-1968. *RP*, RP_r, and $RP–RP_r$ are measures of repeated pair marriages as defined in the text.

Discussion

Despite certain caveats, the use of surnames to determine population structure can be an invaluable tool (Weiss et al., 1983). For the purpose of this study, population subdivision was examined using two tools, isonymy as a measure of inbreeding, and repeated pairs analysis.

The isonymy statistic is interpreted by examining the contribution of *Fr* (random component) and *Fn* (nonrandom component) to *F* (the total inbreeding level). The overall *F* reported for Acceglio shows a clear decline through time due to the reduction in frequency of isonymous marriages. The two world wars sparked migration out of Acceglio and after world war two migration to industrial

centers continued, thus reducing the number of eligible mates, and removing much of the population substructure. Therefore, the marital isonymy findings suggest that inbreeding, potentially causing genetic differentiation, was a factor which has become less influential through time.

Lasker et al. (1972) report a similar trend in isonymous marriages in the next valley, Valle Varaita, in which they examined two isolated communities: Bellino and Casteldelfino. In their study, both populations in the valley showed decreases in the frequency of isonymous marriages through time. Like this study, Lasker and colleagues detected an increase in exogamous marriages and an increase in emigration through time. In fact, they report that Valle Varaita was experiencing this decline around the same time as Acceglio.

The second measure used to investigate population subdivision was the repeated pairs analysis. *RP* is not a direct measure of inbreeding, yet it measures an important aspect of population subdivision, preferential interlineage mating. Indeed, *RP* values vary from population to population because of the extent of preferential interlineage mating, population size, and the number of different surnames (Duggirala et al., 1991). According to Lasker (1985), an excess of *RP* over RP_r implies subdivision in a population and a probable reduction in genetic heterogeneity. A correlation between *RP* and heterogeneity has been reported by Koertvelyessy et al., (1988).

The high *RP* values in Acceglio confirm the findings from the isonymy analysis; there was considerable population substructure which has declined through time. Cohorts 1, 2, and 3, and the total time period exhibit an observed *RP* value greater than expected at random. In contrast, when excluding isonymous marriages, these results suggest that the significant values found in cohort 2 and 3 were inflated by isonymous marriages. Therefore, only cohort 1 and cohort 4 show the presence of patterned subdivision. However, note that there still is a reduction in *RP* values through time. The test measuring the relative excess of $RP–RP_r$ are in accordance with the previous findings, in that the combined cohorts implied subdivision when including isonymous marriages, and suggested no subdivision when excluding isonymous marriages. However, patterned subdivision of preferential inter-lineage mating was suggested when considering the four cohorts separately. In this case, the four cohorts are more informative than the total time period because historic changes in the population through time can be isolated.

Together, the results from the marital isonymy and repeated pairs analyses suggest the presence of population substructure in Acceglio which has declined through time. These patterns are directly related to the changes in patterns of mating and migration that occurred in this population. As previously stated, in Acceglio, there was an increase in emigration rates and an increase in the frequency of exogamous marriages through time. According to Crawford (1980), the generation born at the turn of the century experienced an increase in emigration and exogamous marriages because of an acceleration of movement to surrounding industrial centers in search of jobs and a higher standard of living.

Interestingly, these changes in patterns of mating and migration were similar to patterns reported in two nearby populations, Bellino and Casteldelfino, in the Valle Varaita (Lasker et al., 1972). In accordance with the findings from these analyses, Lasker and colleagues report an increasing rate of exogamous marriages through time to industrial centers in Italy and other countries. In fact, Lasker and colleagues suggest that Bellino and Casteldelfino, much like Acceglio, were genetically isolated populations (characterized by high rates of isonymy and high rates of inbreeding) which have become less isolated through time.

Conclusion

In conclusion, the gradual decrease in number of marriages, the increase in exogamy through time, the decrease in frequency of isonymous and repeated pairs marriages all are suggestive that Acceglio was a reproductively isolated population that has experienced changes and declined numerically through time. The population is geographically isolated, and this possibly influenced the nature and structure of marriage patterns in combination with other factors, such as subdivision into hamlets, their geographic locations, and had an influence on non-random mating. Through time, Acceglio demographics experienced changes. With the introduction of improved transportation to the industrial centers of France and Italy, in combination with the two world wars, there was a large increase in emigration from the population. These factors help explain the gradual decrease in the inbreeding coefficient measured by isonymy and the level of repeated pairs marriages. This study demonstrates the influence of changing cultural and historical events that shape the genetic structure of an isolated population, such as Acceglio.

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In honour of Gabriel W. Lasker and his numerous contributions to the field of anthropological genetics. We would like to first acknowledge the residents of Acceglio. Without their participation, this study would not have been possible. Additionally, we would like to thank Professor Brunetto Chiarelli for his administrative assistance and four of his former students (Chiara Bullo, Anna Vidili, Anna Imasi, and Lorenzo Grosspietro) who helped transcribe the records. We also recognize Dr. Koertvelyessy and Dr. Duggirala for their critiques of this manuscript and suggestions for the analyses of this research.

ABSTRACT

Analisi dell'isonimia e delle coppie ripetute: la struttura matrimoniale di Acceglio, Italia, 1889-1968

Riassunto – Due metodi di analisi dei cognomi sono stati comunemente impiegati per studiare la struttura delle popolazioni: (1) l'isonimia, per l'analisi della consanguineità e (2) il metodo delle coppie ripetute (*RP*), per evidenziare andamenti di suddivisione all'interno di una popolazione. In questo studio sono applicati entrambi i metodi ai cognomi relativi a 793 matrimoni celebrati tra il 1889 ed il 1968 in Acceglio, una popolazione alpina isolata in Valle Maira, Italia. Per osservare andamenti temporali, i matrimoni sono stati suddivisi in quattro coorti di circa 20 anni: (1) 1889-1908, (2) 1909-1928, (3) 1929-1948 e (4) 1949-1968. L'analisi dell'isonimia ha rivelato un valore di F per la prima coorte pari a 0,0432 che decresce nel tempo fino a 0,0200. I valori di *RP* sono stati calcolati con e senza i matrimoni isonimici, per evidenziare i contributi differenziali dei matrimoni isonimici e non isonimici alla statistica *RP*. Includendo i matrimoni isonimici, l'analisi *RP* ha dato un valore $RP–RP_r$ pari a 0,00280 per la prima coorte, che decresce a 0,00041. Escludendo i matrimoni isonimici, è stato trovato un valore $RP–RP_r$ pari a 0,00225 per la prima coorte, che decresce nel tempo a 0,00047. L'esclusione dei matrimoni isonimici porta a cambiamenti sostanziali del valore $RP–RP_r$ e suggerisce che le stesse linee sono coinvolte nei matrimoni isonimici e nelle unioni a coppie ripetute. In definitiva, la diminuzione della frequenza dei matrimoni isonimici ed la corrispondente diminuzione nei matrimoni a coppie ripetute suggerisce un aumento dell'esogamia nel tempo e la rottura dell'isolamento riproduttivo nella comunità alpina.

Parole chiave – Struttura di popolazione, Archivi parrocchiali, Matrimoni, Valle Maira.

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