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Estimation of Inbreeding, Kinship and Genetic Distances from Surnames – Coastal Population of Middle Dalmatia, Croatia

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ABSTRACT

This work was dedicated to the investigation of the population structure of the middle Dalmatia settlements: Jesenice, Mimice, Živogošće and Zaostrog by surname distribution study and applying the isonymous method. The surnames of males and females in marital pairs were analyzed as well as of their first and second-generation ancestors on the sample of a total of 3,024 examinees. The analyses of surnames pointed to the rates of inbreeding, kinship and genetic distances of the populations. Although the values of the inbreeding coefficient are high in all the four settlements, the inbreeding coefficient is exceptionally high in Mimice. A total kinship coefficient for the four settlements speaks also in favor of the high rate of kinship in the examined settlements, i.e. of the high rate of the reproductive isolation of the whole region during the analyzed period. The reasons for such high coefficients are natural features of the examined region (the mountains of Mosor, Biokovo and Rilić), poor traffic connection of this region in the past, the patrilineal mode of inheritance and the demographic specifics of the population. The matrix of genetic distances between examined settlement pairs reveals that Mimice, a settlement with the highest share of isonymous marriages, shows the greatest distances in comparison to the other settlements. On the other hand, Jesenice, Živogošće and Zaostrog are characterized by small genetic distances, which is the fact that speaks in favor of their genetic homogenization and »openness« toward interpopulational migrations, i.e. the gene flow.

Introduction

Contemporary anthropological investigations of human populations deal with the whole range of historical, geographical, demographical, socio-cultural, genetic and many other data in order to offer possible explanations of human variables

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through two basic categories that are space and time. In order to understand the origin and settlement of populations, as well as their migration patterns, biological history, demographic and genetic structure, rates of reproductive isolation, it is necessary to apply the holistic method in following up all the dynamic processes of micro (macro) evolution important for formation of a population structure. Many holistic investigations of the rural populations of the eastern Adriatic islands pointed to these populations' anthropological specifics and so a need arose to undertake the same investigations in the coastal mainland regions of Croatia[1–6].

The aim of this study is to analyze inbreeding, kinship and genetic distances of the populations calculated from surnames, based on the isonymy method, in four settlements of middle Dalmatia. Studies of surname traits are important for determination of population's genetic traits and they offer, as Crow[7] stated, two great possibilities that are not common to the classical genealogical models. The first possibility refers to the estimation of genetic characteristics of ancient ancestors, which were not available prior to the establishment of genealogy as a science, and the other one refers to a separate observation of random and non-random effects on populations. We also have to point out to limitations in interpretation of results obtained by the surname studies. They refer to certain errors which could be made by disturbance of correlations between genetic response and surnames of individuals, which is due to adoption of children, adultery, changes of surnames in the past, polyphyletic origin of surnames, various legal and cultural traits of marriages in different regions etc. One of the best ways to avoid most of the problems arising from isonymy studies and to obtain the most precise assessment of the genetic structure of a population is to investigate smaller populations that are relatively isolated and with a well documented history, as is the case with our population. The settlement models of Dalmatia can be followed from the oldest historical ages, beginning with the high Paleolithic and Neolithic cultures and up to present time. However, the most important modifying factors, directly affecting the formation of the Dalmatian population structure, are two waves of immigration. The first wave refers to the migration of Croats to this region, resulting in the formation of a new ethno-genetic core (from the 6th to the 9th century), while the other refers to the migrations resulting from the Turkish expansion of the Balkan Peninsula in the period from the 15th to the 18th century. The Turks constantly broke through all the Croatian borders causing great migrations of the inhabitants. The greatest migration influx occurred during the Candian war (in the middle and at the end of the 17th century) when many newcomers arrived to settle permanently in Dalmatia and on its islands (a certain number of them moved further on to Italy, Austria)[8–10]. The process of biological and cultural adaptation of the newcomers was relatively fast owing to similarity of their languages and religions, which is best testified by Štokavian-Ikavian language spoken in this region.

The bases of this investigation are the surnames of the inhabitants of Dalmatia. In this sense, it is important to point out that the Trident Council (1545–1563) strictly prescribed that registries of births, marriages and deaths should be kept all over the Christian world, and thus in our regions, as well, while surnames, as found by Šimunović[11], became permanent, inherited and unchangeable. The preservation of the domestic names and surnames of the inhabitants of Dalmatia is proved by numerous documents signed between inhabitants of

Dalmatia and Venice (foreign surnames are found only occasionally[12]. This fact is very important for the interpretation of the results of our studies.

Furthermore, demographic investigations of the inhabitants of the settlements of Jesenice, Mimice, Živogošće and Zaostrog[13] revealed that there were no major oscillations in term of the population size and that it did not significantly change during the 19th and 20th century, so that it conforms to the following anthropogenetic analyses.

Material and Methods

Sample

This investigation includes names and surnames of males and females from a total of 1,513 marital pairs from the settlements of Jesenice, Mimice, Živogošće and Zaostrog, along with names and surnames of their first and second-generation ancestors. The examined sample was made by interviewing the examinees during field researches in 1997. A total of 3,024 examinees, born between 1837 and 1976, were included in the investigation.

Inbreeding studies

The inbreeding coefficient of some populations was computed as follows:

$$F = F_n + F_r\,(1–F_n) \qquad (1)$$

where F represents inbreeding coefficient for the whole population. It consists of two components: a random one (F_r), which estimates the amount of inbreeding occurring simply due to panmixia in a finite population; and a non-random one (F_n), measuring a possible positive or negative behavior towards isonymous marriages. The aforementioned coefficients were calculated as follows:

$$F_r = (\Sigma p_k q_k) / 4 \qquad (2)$$

where p_k is the frequency of the k-th surname in males, and q_k is the frequency of k-th surname in females; summation is over all surnames[14] :

$$F_n = (P – \Sigma p_k q_k) / 4\ (1 – \Sigma p_k q_k) \qquad (3)$$

where P is the proportion of isonymous marriages in the population.

Kinship studies

The kinship coefficient for each pair of subpopulations of the whole population (village, city, region, island, family...) was computed as follows:

$$\Phi_{ij} = r_{ij} + (1 – r_{ij})\,\Phi_r \qquad (4)$$

where Φ_{ij} is the unreduced covariance of subpopulations i and j (relative to the founding population); r_{ij} is the reduced covariance of subpopulations i and j (relative to the contemporary population), and Φ_r is the unreduced variance of the whole population (relative to the founding population). The term formerly used for »unreduced (co) variance« was »a priori kinship«, and for »reduced (co)variance« it was »conditional kinship«[14].

This author suggested the following computation of the aforementioned coefficients based on isonomy:

$$\Phi_r = R / 4 \qquad (5)$$

$$r_{ij} = (I_{ij} – R) / [4\ (1 – R)] \qquad (6)$$

where I_{ij} is the random isonomy between subpopulations i and j, and R is the random isonomy of the contemporary population relative to the founding population. The following methods were applied for computation of I_{ij} and R:

$$I_{ij} = (\Sigma n_{ik} n_{jk}) / (N_i N_j) \qquad (7)$$

$$R = \Sigma\ N_i\,(\Sigma N_i–1)] \qquad (8)$$

where n_{ik} and n_{jk} are the numbers of individuals with surname k in subpopulations i and j, respectively; N_i and N_j are the total number of surnames in subpopulation i and subpopulation j, and R represents an unbiased estimate of population random isonomy.

Measures of genetic microdifferentiation for our population were computed as follows:

$$F_{st} = R_{st} + (1 - R_{st})\,\Phi_r \qquad (9)$$

where F_{st} refers, according to Relethford[14], to the average within-group unreduced variance, R_{st} refers to the average within-group reduced variance and Φ_r is the unreduced variance of the whole population. R_{st} was computed as follows:

$$R_{st} = \Sigma(w_i\; r_{ii}) \qquad (10)$$

where w_i, F_i and r_{ii} in studies where differential migration by sex is of interest, should be computed as:

$$w_i = n_i \,/\, \Sigma n_i \qquad (11)$$

$$r_{ii} = (I_{ii} - R) \,/\, [4\,(I - R)] \qquad (12)$$

$$I_{ii} = (\Sigma m_{ik} f_{ik}) \,/\, (M_i F_i) \qquad (13)$$

where n_i is the size of the subpopulation i, R is the random isonomy in the contemporary population, I_{ii} is the within-subpopulation random isonomy, m_{ik} and f_{ik} are the numbers of males and females with surname k in subpopulation i, M_i and F_i are the total numbers of males and females in subpopulation i[14].

Genetic distances

Genetic distances could be computed in terms of unreduced and in terms of reduced variance. Let d^2 be the distance between populations i and j based on random isonomy:

$$d^2 = I_{ii} + I_{ij} - 2\,I_{ij} \qquad (14)$$

Then for »a priori« (unreduced variance) and for »conditional« kinship (reduced variance) D^2 equals to:

$$D^2 = [d^2\,(4 - R)] \,/\, [16\,(1- R)] \qquad (15)$$

$$D^2 = d^2 \,/\, [(4(1 - R)] \qquad (16)$$

Relethford[14] suggests the computation of D^2 in term of unreduced variance, i.e. the equation (15) because that estimation of kinship is more applicable for analyzing of population structure.

Results

Table 1 presents the basic distribution of samples by settlements taking into consideration the number of examinees (n), the number of examined marital pairs (m), the number and proportion of marriages with the same surname of both spouses (the so-called isonymous marriages) (P), the number of surnames in the settlement (N), the number of »frequent« surnames (more than 3 persons) in the settlement (N_{fi}), the number of persons with one of the »frequent« surnames (n_{fi}), the number of »frequent« surnames

TABLE 1
BASIC DISTRIBUTION OF THE EXAMINEES AND CHARACTERISTICS OF SURNAME DISTRIBUTION BY SETTLEMENTS

Settlement	n	m	P (%)	N_i	N_{fi}	n_{fi}	N_{fi}/N_i	n_{fi}/n
Jesenice	1,120	560	34 (6.3%)	210	54	856	0.257	0.764
Mimice	576	288	88 (29.9%)	118	22	422	0.186	0.732
Živogošće	602	301	17 (5.3%)	177	42	392	0.237	0.651
Zaostrog	726	363	34 (9.3%)	196	29	458	0.147	0.631
Total	3,024	1,512	34 (2.2%)	606	151	2,128	0.249	0.703

n = number of examinees; m = number of marital pairs; P(%) = number and proportion of marriages with the same surname of both spouses (the so-called isonymous marriages); N_i = number of surnames in the settlements; N_{fi} = number of »frequent« surnames (more than 3 persons) in the settlements; n_{fi} = number of examinees with one of the »frequent« surnames; N_{fi}/N_i = proportion of »frequent« surnames in the total number of surnames; n_{fi}/n = proportion of examinees with »frequent« surnames in the total number of examinees.

in the total number of surnames (N_{fi}/N_i), and the proportion of examinees with »frequent« surnames in the total number of examinees (n_{fi}/n).

Before analyzing the aforementioned table, let's give an example of the most frequent surnames by settlements. The most frequent surname in Jesenice is Vuković (6.3%) of the whole population of the settlement, then comes Tomaš (5.7%), Marasović (2.6%) and Klarić (2.6%); the most frequent surname in Mimice is Mimica (the top value of 44.2%), then comes Medić (4.7%) and Kuzmanić (3.3%); in Živogošće it is Franićević (3.7%) and Perić (3.5%), and in Zaostrog it is Banović (5.1%).

From Table 1, showing the basic distribution of the sample by settlements and the surname distribution, it can be seen that the number of examinees in some settlements ranged from 576 (Mimice) to 1,120 (Jesenice) so that the number of examined marital pairs was between 288 and 560. In the examined settlements, Mimice stands out with the top value of 29.9% of isonymous marriages in the total number of marriages. The number of isonymous marriages in other examined settlements ranged from 5.35% in Živogošće and 6.3% in Jesenice to 9.4% in Zaostrog.

The proportion of »frequent« surnames in the total number of surnames per settlement ranged from 14% to 25%, meaning that only every fourth to sixth surname was a »frequent« one (carried by more than three persons in the settlement). However, the fact is that the share of the inhabitants with some of the »frequent« surnames was a large one in all the settlements, ranging from 63% (Zaostrog) to 76% (Jesenice)

Let us remember that, according to Relethford[14], inbreeding coefficient of the whole population computed by surname distribution consists of two components: a random one (F_{ri}), which estimates the amount of inbreeding occurring simply due to panmixia in a finite population, and a non-random one (F_{ni}) measuring a possible positive or negative behavior towards isonymous marriages due to various reasons (sociocultural, economic). Furthermore, F_{st} is the average within -group unreduced variable; R_{st} refers to the average within-group unreduced variable of the whole examined population (these values used to be called »a priori« and »conditional« inbreeding). All the aforementioned coefficients are generally known as »measures of genetic (micro) differentiation« of examined population.

Table 2 presents the values of genetic (micro) differential measures for the total population of the four examined settlements computed from surname distribution. The first fact which should be noted is relatively high inbreeding coefficient of the whole population (F_i) which amounts

TABLE 2
MEASURES OF GENETIC MICRODIFFERENTIATIONS COMPUTED FOR THREE GENERATIONS OF INHABITANTS OF JESENICE, MIMICE, ŽIVOGOŠĆE AND ZAOSTROG BY SURNAME DISTRIBUTION

Measures of microdifferentiation	R	F_{ST}	R_{ST}
Results (total population of four settlements)	0.0038	0.0151	0.0114
	Inbreeding coefficient (Fi)		
Jesenice		0.015	
Mimice		0.113	
Živogošće		0.013	
Zaostrog		0.023	

to 2.2% and fits right into the range (from 1% to 5%) which was recorded during examinations undertaken on the islands of middle Dalmatia[15-16].The main reason for such a high value of inbreeding coefficient was an exceptionally high value of the non-random component of this coefficient (F_{ni}), which was always several times higher than the random kinship component (F_{ri}), which is probably because of the positive relationship towards marriages in family lineages based on the ethnohistorical and cultural interests. However, this was apparently not the case with the entire population of Jesenice, Mimice, Živogošće and Zaostrog.

The unreduced variance of the whole population (F_r), i.e. of the kinship coefficient is significantly higher than the inbreeding coefficient, and it amounts to 0.38%. This can be explained by the generally high kinship rate of the population, which is due to the homogeneity of the founding population (the founder effect) in regard to the unique hereditary potential, uniform migration patterns and marriages in family lineages and all these within the frame of the unique ecological niche, which reduces the value of inbreeding coefficient.

R_{st} or an average within-group »reduced« variance is a better indicator than an »unreduced« variance (F_{st}) when the isonymous method is applied, so that it should be noted that it amounted to 1.1%. Such a result is expected and it fits right into the values of kinship and inbreeding coefficients.

Genetic distances are computed according to the equations (14, 15) for each pair of the settlements in the three examined generations. Table 3 shows those results.

TABLE 3
MATRIX OF GENETIC DISTANCES BETWEEN SETTLEMENT PAIRS ESTIMATED FROM SURNAME DISTRIBUTION

	1.	2.	3.	4.
1. Jesenice	---			
2. Mimice	0.2118	---		
3. Živogošće	0.0355	0.2053	---	
4. Zaostrog	0.0726	0.2407	0.0604	---

The review of Table 3 confirms one of previously set hypotheses: the settlement with the high rate of isonymous marriages (Mimice) indicates the high values of genetic distances (ranging from 0.20 to 0.24) in comparison to the rates in other settlements (Jesenice, Živogošće and Zaostrog), which, on the other hand, show genetic homogeneity and very small genetic distances (0.04 to 0.07).

The results obtained in this way can be more clearly shown by a linkage and by formation of a two-dimensional space between two vectors with the largest discriminatory value of the examined structure of variables. Figure 1 shows the results of such an analysis of matrix of genetic distances (presented on Table 3) by generations, using the method of UPGMA (unweighted pair wise group mean).

From Figure 1 it can be more precisely seen what has already been presumed during the basic surname distribution analyses by settlements.

The surname distribution analysis reveals that genetically the closest settlements are Jesenice and Živogošće; then comes Zaostrog and the most distant is Mimice. Such a result is due to the higher isolation, reproductive isolation and significantly lower rate of genetic homogenization of the inhabitants of Mimice compared to the inhabitants of other examined settlements.

Figure 2 indicates (in another way) the matrix of genetic distances between the analyzed settlements computed by surname distribution analysis, using the two-dimensional scheme of two vectors with the largest discriminatory value of

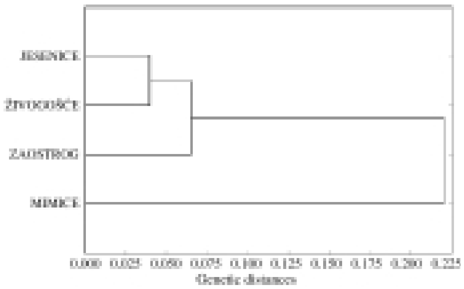

Fig. 1. Linkage of genetic distances between the examined settlements computed by surname distribution of marital pairs.

the examined components of variables. It can also be noted that Jesenice and Živogošće are closest to each other, while Mimice is isolated by its genetic structure from the other three analyzed settlements.

Conclusion

The results of this investigation have shown that the inbreeding coefficient (F_i) in Jesenice amounts to 0.015, in Mimice 0.113, in Živogošće 0.013 and in Zaostrog 0.023. The coefficient of 0.113 indicates the high isolation of Mimice compared to the other settlements of this region. If we compare the inbreeding coefficient in Mimice with the investigation results of some other populations of the world (Table 4), we shall conclude that such a high coefficient could be found only in the population of Nebraska Amish, USA 0.112[17]. This can be explained by the specific impact of the strict religious rules regarding the selection of a marital (reproductive) partner.

The most recent investigations of inbreeding coefficient in the populations of Croatian islands also point to its high values. The highest values have been found on the islands of Pag (0.0466)[18] then on the island of Korčula (0.0243)[16] and Hvar (0.0228)[19], while somewhat lower values have been found in the population of the islands of Silba (0.0068) and Olib (0.0053)[15]. My feeling is that the inbreeding coefficient data of the inhabitants of our islands, as shown above, are based on the extremely high values of the so-called non-random component of this

TABLE 4
VALUES OF INBREEDING COEFFICIENT CALCULATED BY ISONYMOUS METHOD IN SOME POPULATIONS OF THE WORLD

Author	Population	Kinship coefficient
Lasker (1977)	Peru	0.0040
Lasker et al. (1979)	Reading, England	0.0003
Kayshap & Tiwari (1980)	Kashmir	0.0400
Wilson (1981)	Bhatia	0.0427
Hurd (1983)	Nebraska, Amish	0.1129
Sujoldžić (1989)	Island Silba, Croatia	0.0068
Sujoldžić (1989)	Island Olib, Croatia	0.0053
Sujoldžić (1993)	Island Korčula, Croatia	0.0243
Roguljić et al. (1997)	Island Hvar, Croatia	0.0228
De Guerra et al. (1999)	Ganga, Venezuela	0.0026
Rudan (1999)	Island Pag, Croatia	0.0466
Malnar (2001)	Jesenice, Croatia	0.0150
Malnar (2001)	Mimice, Croatia	0.1130
Malnar (2001)	Živogošće, Croatia	0.0130
Malnar (2001)	Zaostrog, Croatia	0.0230

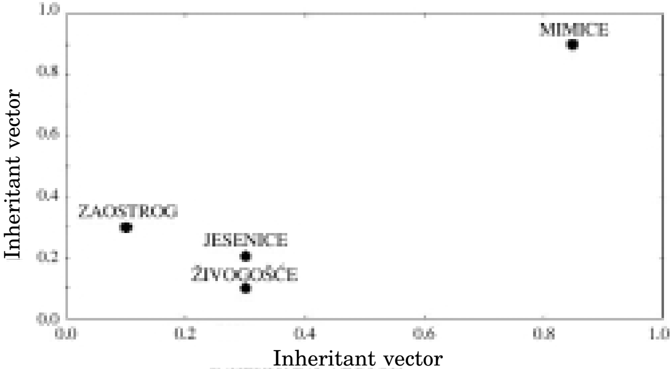

Fig. 2. Matrix of genetic distances between the examined settlements computed by surname distribution of marital pairs shown within two-dimensional space between two vectors with the highest discriminatory value of the examined components of variables.

coefficient, which were as much as several times higher than random component. This fact is due to the positive relationship towards marriages in family lineages owing primarily to such interests as are the historical and cultural characteristics of the population[16]. Since the case is about the populations tending toward reproductive and distinct geographical isolation, it can be concluded that in this investigation the populations of the settlements of middle Dalmatia showed similar characteristics in the past as the populations of the Adriatic islands, which were investigated up to now.

Total kinship coefficient of the populations of Jesenice, Mimice, Živogošće and Zaostrog amounting to 4% again confirms the high rate of isolation, fitting into the results obtained for island populations of Silba and Olib, which ranged from 1% to 5% in the period from 1861 to 1980[15]. The inbreeding coefficient on the island of Korčula determined from surname distribution amounted to 2.4% and in the settlements of Lumbarda and Račišće it amounted to 3.4%. More convincing results were obtained by surname studies on the island of Hvar[19] showing that the inbreeding coefficient in some villages reached the value of 39%.

A total inbreeding coefficient of the inhabitants of the examined settlements amounted to 3.8%. The same coefficient on the island of Hvar amounted to 4%[19], on the island of Pag it was 8%, and in some isolated populations of the world it had the following values: in the Cashmere Valley – 2%[20], among Leuts of Bhatia – 2.3%[21] and among Amish of Nebraska and Pennsylvania – above 9%[17]. In some other examined populations these coefficients were lower than 2%[22-27].

The matrix of genetic distances between examined settlement pairs reveals that the settlement of Mimice, with the highest share of isonymous marriages, shows the greatest genetic distance in comparison to the settlements of Jesenice, Živogošće and Zaostrog (between 0.04 and 0.07) which clearly speaks in favor of their genetic homogenization, but also of their »openness« towards interpopulational migrations.

Although we follow almost the same migration and settlement patterns of very similar newcomers to all the four examined settlements, it can be concluded that the so-called share of the founding population is the first significant fact that affected the formation of the population structure. The founding population structure changed due to various influences over time. Furthermore, it can be supposed that the tendency toward kinship, which, according to our survey, was the highest in the settlement of Mimice, has given its share to the preservation of the existing genetic distances between the analyzed settlements. Under such conditions, the effect of genetic drift was strengthened, tending to increase the discrepancies among subpopulations by fixation of some traits, which are uniform for some settlements.

The results of surname distribution (taking into consideration the high inbreeding and kinship coefficients, as well as the high values of genetic distances between populations of Mimice and other settlements), led us to try to find causes of such isolation and of the specific location of the settlement of Mimice in this investigation.

The crucial reason for such high tendency toward the reproductive population isolation is, in the first place, the natural barrier to the gene flow represented by the Dinaric mountain chain. The other reason is the traffic isolation, which lasted up to the second half of the 20th century. Namely, at the beginning of the 19th century the French administration which ruled Dalmatia built the so-called »Mediterranean road«, which stretched from Knin and Sinj, further on to Ugljane, Šestanovac and Zagvozd, but bypassing, by some 10 kilometers, the region settled by the inhabitants of Mimice leaving this region in further isolation. The same happened with the road from Šestanovac to Makarska, which was built during the Austrian administration which ruled Dalmatia. A road, which finally connected Mimice with the rest of Dalmatia, was not built before 1964[28].

This traffic isolation, as well as the impossibility to expand the agricultural and cultivable soil (limiting ecological factors) were the reasons for the migration of the inhabitants of Mimice to the North and South America contributing to the further genetic homogenization of the population and to the preservation of hereditary characteristics brought during the great migrations from Bosnia and Herzegovina. In addition, the population showed a high tendency toward marriages in family lineages in order to preserve even such a modest properties and the patrilineal mode of inheritance.

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ISTRAŽIVANJE UROĐENOSTI, SRODSTVA I GENETIČKIH UDALJENOSTI ANALIZOM PREZIMENA U KOPNENIM NASELJIMA SREDNJE DALMACIJE

SAŽETAK

U ovom radu istraživana je populacijska struktura stanovništva naselja srednje Dalmacije: Jesenica, Mimica, Živogošća i Zaostroga studijom raspodjele prezimena primjenom metode izonimije. Analizirana su prezimena bračnih parova, muškaraca i žena, te njihovih predaka prve i druge generacije na uzorku od ukupno 3.024 ispitanika. Analizom prezimena procijenjeni su stupanj urođenosti i srodstva, te genetičke udaljenosti populacija. Premda vrijednosti koeficijenta urođenosti u sva četiri naselja ukazuju na visok stupanj urođenosti isti je ipak najnaglašeniji u Mimicama. Visoki koeficijent srodstva za sva naselja zajedno također govori u prilog visokog stupnja srodstva proučavanih naselja, tj. o visokom stupnju reproduktivne zatvorenosti cijelog područja. Uzroci ovako visokih vrijednosti su prirodne osobitosti istraživanog područja (planine Mosor, Biokovo i Rilić), slaba prometna povezanost ovog kraja kroz prošlost, patrilinearni način nasljeđivanja i demografske specifičnosti populacije. Matrica genetičkih udaljenosti između parova istraživanih naselja pokazuje da Mimice, naselje s najvećim brojem izonimičnih brakova, pokazuje najveće udaljenosti u odnosu na ostala naselja. S druge strane, Jesenice, Živogošće i Zaostrog odlikuju se malim genetičkim udaljenostima koji govore u prilog genetičkoj homogenizaciji i »otvorenosti« prema međusobnoj migraciji tj. toku gena.