

Genetics

What Can Genetics Tell us about the Origins of South and North Ossetians

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ABSTRACT. We have analyzed publicly available mtDNA HV1 sequences, Y chromosome binary genetic markers, and Y chromosome short tandem repeat (Y-STR) variability in the number of North and South Ossetian groups. The mtDNA data suggest a common origin of North and South Ossetians, whereas the Y-haplogroup data indicate that North Ossetians are more similar to other North Caucasian groups, and South Ossetians are more similar to other South Caucasian groups, than to each other. Also, with respect to mtDNA, Ossetians are significantly more similar to Iranian groups than to Caucasian groups. We suggest that a common origin of Ossetians from Iran, followed by subsequent male-mediated migrations from their Caucasian neighbors, is the most likely explanation for these results. © 2008 Bull. Georg. Natl. Acad. Sci.

Key words: *Ossetians, Y chromosome, mtDNA.*

Introduction

Ossetians are unique among the ethnic groups of the Caucasus region in that they are the only group to reside on both the north and south slopes of the central part of the Caucasus Mountains range. They are also of interest in that they speak an Iranian language, belonging to the Indo-European language family, whereas their geographic neighbors all speak Caucasian languages.

There are two main hypotheses concerning the origin of Ossetians. According to the first hypothesis, from the 7th century BC to the 1st century AD, Ossetia came under Scythian-Sarmatian influence, which was succeeded by the Alani, an Iranian-speaking, warrior Sarmatian tribe. The Alani are then believed to be the direct ancestors of Ossetians (Miller, 1992). The second hypothesis describes the origin of Ossetians as descendants of one of the autochthonous groups from the Caucasus. According to this view, Ossetians adopted an Iranian language, most likely from the Alani in the early Middle Ages, or possibly even earlier. It is believed that before this event, Ossetians spoke a Caucasian language (Vinogradov, 1963).

A number of population genetic studies have been carried out on Ossetian groups. Classical genetic markers (blood groups, serum proteins and red cell enzymes) were studied in several groups from South and North Ossetia (Inasaridze *et al* 1990; Salamatina & Nasidze, 1993). Rychkov *et al.*, (1996) also studied classical genetic markers in a number of North Ossetian groups. Eleven polymorphic restriction sites in the first hypervariable segment (HVI) of the mtDNA control region were studied in 40 North Ossetians and in additional groups from Siberia (Rychkov *et al.*, 1995). Eleven bi-allelic loci and 9 short tandem repeat (STR) loci on the Y-chromosome, as well as mtDNA HVI sequence variability, were previously studied in two populations from North Ossetia (Nasidze *et al.*, 2004a). One South Ossetian population, from Georgia, has also been studied for a number of Y chromosome SNPs (Wells *et al.*, 2001) and for mtDNA HVI sequence variability (Kivisild *et al.*, 1999). Three additional North Ossetian groups were analyzed for 11 bi-allelic loci and 9 STR loci on the Y-chromosome, as well as mtDNA HVI sequence variability (Nasidze *et al.*, 2004b).

These data on mtDNA and Y-chromosome variation in Ossetian groups were compiled in order to address the questions concerning a genetic relatedness of North and South Ossetians to each other, their geographic (i.e. Caucasus ethnic groups) and linguistic (i.e. Iranian groups) neighbors; and finally address a question on which of the two prevailing theories concerning Ossetian origins (an Iranian origin, or a Caucasian origin followed by language replacement) receives support from the genetic data.

Materials and Methods

Along with available mtDNA HV1 sequence data from North and South Ossetian groups (Kivisild *et al.*, 1999; Nasidze *et al.*, 2004a,b), we used mtDNA HV1 data from 23 Abazinians, 23 Chechenians, 44 Cherkessians, 37 Darginians, 35 Ingushians, 51 Kabardinians, 42 Armenians, 41 Azerbaijanians, 57 Georgians (Nasidze & Stoneking, 2001), 16 Balkarians, 32 Avarians, 13 Karachaians, 45 Lezginians, 31 Rutulians, 27 Abkhazians, 79 Iranians from Tehran and 46 from Isfahan, 39 Turks (Nasidze *et al.*, 2004a), 50 Adyghe (Richards *et al.*, 1996), 106 Basques (Bertranpetit *et al.*, 1995; Corte-Real *et al.*, 1996), 101 British (Piercy *et al.*, 1993), 69 Sardinians and 42 Middle Easterners (Di Rienzo & Wilson 1991), 72 Spaniards (Corte-Real *et al.*, 1996; Richards *et al.*, 1996), 102 Russians (Orekhov *et al.*, 1999), 18 Slavs (Maliarchuk *et al.*, 1995), 45 Israeli Drusi (Macaulay *et al.*, 1999), and 29 Kurds (Comas *et al.*, 2000).

Information about 10 Y chromosomal SNP markers: RPS4Y (M130), M9, M89, M124, M45, M173, M17, M201, M170, and M172, and also the YAP *Alu* insertion polymorphism data (Nasidze *et al.*, 2004a,b; Wells *et al.*, 2001) were used in the analysis.

Published Y-SNP data (Semino *et al.*, 2000, Wells *et al.*, 2001) for European, West Asian, and Central Asian populations were also included in some analyses.

Basic parameters of molecular diversity and population genetic structure, including analyses of molecular variance (AMOVA), were calculated using the software package Arlequin 2.000 (Schneider *et al.*, 2000). The statistical significance of F_{st} values was estimated by permutation analysis, using 10,000 permutations. The statistical significance of the correlation between genetic distance matrices based on mtDNA and Y chromosome SNP data was evaluated by the Mantel test with 10,000 permutations. Network analysis for Y-STR data was carried out using the software package NETWORK version 3.1 (Bandelt *et al.*, 1999).

In order to define the geographic regions of large genetic changes (or genetic barriers), spatial analysis of molecular variance (SAMOVA) was used (Dupanloup *et al.*, 2002). SAMOVA determines groups of populations that are geographically and genetically homogeneous and maximally differentiated from each other, based solely

on genetic data. The method is based a simulated annealing procedure that aims at maximizing the proportion of the total genetic variance due to differences between groups of populations; the final number of groups is based on the largest value for this variance component. As a by-product, SAMOVA also leads to the identification of genetic barriers between these groups.

Results

MtDNA HV1 sequence variability

MtDNA HV1 haplotype diversity varied from 0.931 (Alagir) to 0.977 (Digora), which is within the range of haplotype diversity values for other Caucasian groups (Nasidze *et al.*, 2004a). The mean number of pairwise nucleotide differences (MPD) varied from 4.65 (Ardon) to 6.70 (Alagir); these values are at or exceed the upper limit of the range of MPD values for European populations (3.15-5.03; Comas *et al.*, 1997) as well as for the rest of the Caucasus (4.40-5.87; Nasidze *et al.*, 2004a). Tajima's D values were negative in all Ossetian groups.

For overall pairwise comparisons of North and South Ossetians with neighboring populations from the Caucasus, as well as groups from West and East Europe and West and Central Asia, we calculated average pairwise F_{st} values. Pairwise F_{st} comparisons indicate that South and North Ossetians are no closer to each other (average $F_{st} = 0.037$) than to North or South Caucasus groups (average F_{st} values range from 0.020-0.037). These average F_{st} values are not significantly different from one another ($t = 0.976$, $p = 0.332$). Indeed, South and North Ossetians are more distant from each other than are other South Caucasus groups from other North Caucasus groups (average $F_{st} = 0.019$), although the difference between these values is also not significant ($t = 0.817$, $p = 0.460$). North Ossetian populations are more similar to their geographic neighbors from the North Caucasus (average $F_{st} = 0.020$) than South Ossetians are to their neighbors from the South Caucasus (average $F_{st} = 0.033$). The average pairwise F_{st} value between North Ossetians and groups from the South Caucasus (excluding South Ossetians) is lower (0.030) than that between South and North Ossetians (0.037), while the average pairwise F_{st} value for South Ossetians and North Caucasus groups (excluding North Ossetians) is the same (0.037) as that between South and North Ossetians, although these estimates are not significantly different from each other ($t = 0.669$, $p = 0.518$).

Overall, Ossetians are more distant from the other Indo-European-speaking population from the Caucasus (Armenians; average $F_{st} = 0.030$) than from Caucasian-speaking populations (average $F_{st} = 0.026$), although these values are not significantly different ($t = 1.430$, $p = 0.212$). However, Ossetians are significantly closer to Ira-

nian-speaking populations from Isfahan and Tehran (average $F_{st} = 0.019$) than to Caucasian-speaking populations (average $F_{st} = 0.027$; $t = -2.564$, $p = 0.026$). The same trend holds when South and North Ossetians are compared separately. However, South Ossetians show greater similarity with other Indo-European-speaking populations in the Caucasus and West Asia (average $F_{st} = 0.020$ and 0.015 respectively) than do North Ossetians (average $F_{st} = 0.032$ and 0.024 respectively), although these differences are marginally non-significant ($t = 3.823$, $p = 0.062$).

Y-SNP haplogroups

Overall, ten Y-SNP haplogroups were found in Ossetians, with the number of haplogroups in each individual Ossetian group ranging from 4 to 7. Haplogroup DE (YAP) was found only in South Ossetians (Wells *et al.*, 2001), and haplogroup C (RPS4Y) was completely absent. The most frequent haplogroup was G(M201) among North Ossetians. Haplogroup I(M170) was found in substantial frequencies in North Ossetian groups from Digora and Ardon, whereas this haplogroup is absent from the rest of the groups. Haplogroup J2(M172) was found in all groups, with frequencies ranging from 0.03 in the Digora group to 0.29 in the Ardon group. Haplogroup K(M9) was found in all groups except for South Ossetians and the Digora group. The remaining haplogroups were found at low frequencies in one or two groups.

Pairwise F_{st} values indicate substantial differences between South and North Ossetians. The average F_{st} value between these groups was 0.330, significantly higher than between the other North and South Caucasus groups (average $F_{st} = 0.190$; $t = 4.687$, $p = 0.009$); by contrast, the average F_{st} value between South Ossetians and other North Caucasian populations (excluding North Ossetians) was only 0.101 and the average F_{st} between South Ossetians and the other South Caucasus groups was 0.126. North Ossetian populations were almost as distant from South Caucasian groups as from South Ossetians (average F_{st} value, excluding South Ossetians, was equal to 0.298), while the average F_{st} value between North Ossetians and other North Caucasian populations was significantly lower (average $F_{st} = 0.231$; $t = 3.48$, $p = 0.001$). Despite the fact that North Ossetians showed greater similarity with other North Caucasian populations compared with South Ossetians, the difference in F_{st} values is not significant ($t = -0.734$, $p = 0.503$).

Pairwise F_{st} comparisons between Ossetians and Armenians (the other Indo-European speaking group from the Caucasus) showed that Ossetians are closer to this group (average $F_{st} = 0.144$) than to the Caucasian-speaking groups (average $F_{st} = 0.213$). However, the difference in average F_{st} values is not statistically-significant ($t = 0.559$, $p = 0.583$). Also, Ossetians are about as

distant from their direct linguistic relatives, Iranian-speaking groups from Isfahan and Tehran (average $F_{st} = 0.204$), as from non-Indo-European speaking West Asian groups (average $F_{st} = 0.215$; $t = 0.103$, $p = 0.920$).

Y chromosome STRs

A median network of Y-STR haplotypes against the background of haplogroup G(M201) revealed two clearly separated clusters (data not shown). One of them contains almost exclusively haplotypes found in the Digora group. The second cluster contains the remaining North Ossetian groups, suggesting either different sources of introduction of haplogroup G(M201) or isolation and genetic drift in the Digora group.

Comparison of mtDNA and Y-chromosome data

The geographic and linguistic structure of Ossetians, other Caucasus groups, and European, West and Central Asian groups, as assessed by mtDNA and Y chromosome variation, was investigated by the AMOVA procedure. For both the mtDNA and the Y-SNP data, the geographic classification of populations gave a slightly better fit to the genetic data (in terms of higher among-group variance and lower among-populations-within-groups variance) than did linguistic classifications.

The correlation between pairwise F_{st} values based on mtDNA and Y-SNP data in Ossetians was high but not significant (Mantel test, $Z = 0.531$, $p = 0.084$). The correlation between pairwise F_{st} values based on mtDNA and geographic distances between Ossetian groups was significant ($Z = 0.651$, $p = 0.013$), whereas the correlation between pairwise F_{st} values based on Y-SNP haplogroups and the geographic distances between Ossetian groups was not significant ($Z = 0.659$, $p = 0.149$).

The correlation between the geographic distances and the mtDNA F_{st} values for all Caucasus groups was not statistically significant ($Z = -0.216$, $p = 0.751$). A similar result was obtained for the correlation between geographic distances and the Y-SNP haplogroup F_{st} values (Mantel test, $Z = -0.107$, $p = 0.718$). Moreover, the correlation between the F_{st} distances among pairs of Caucasus groups based on mtDNA and Y-haplogroups was not statistically significant ($Z = 0.063$, $p = 0.297$), suggesting differences in the genetic structure of these groups based on mtDNA and the Y chromosome.

We also carried out a spatial analysis of molecular variance (SAMOVA) to look for regions of large genetic change between Ossetian groups, as well as among Ossetians and other neighboring populations from the Caucasus, West Asia and East Europe, that might define genetic barriers. This analysis follows the same principle as used in the AMOVA analysis to define groups of samples that are best supported by genetic data. SAMOVA applied to mtDNA data for Ossetians alone suggests the genetic isolation of North Ossetian groups from Alagir and Zamankul. The Y-chromosome data un-

derline the genetic isolation of the North Ossetian samples from Ardon and Zamankul.

Discussion

North and South Ossetians are the only ethnic group found on both slopes of the Caucasus Mountains. They speak a language which belongs to the Iranian branch of the Indo-European language family; hence, Ossetians are a linguistic enclave, surrounded by Caucasian-speaking populations. By surveying mtDNA and Y-chromosome variation in Ossetians, we sought answers to several questions concerning the origins and genetic relationships of Ossetians. First, how different groups are related within North Ossetia? Comparing different North Ossetian groups, we found substantial genetic differentiation between these groups comparable with the rest of the Caucasus. How could remarkable genetic differentiation among North Ossetian groups be explained? High level of genetic differentiation of North Ossetians observed in pairwise F_{st} comparisons finds obvious explanation in the relatively recent history of Ossetians. Before the 14th century North Ossetians mainly inhabited the piedmont of the central part of the North Caucasus. During the 14th and the 15th centuries Ossetians moved into valleys of the Central Caucasus, forming territorial units isolated from one another. There were five such units in North Ossetia: Tagaur, Kurtatin, Alagir, Tual and Digora. Separated by deep valleys, these units were under strong isolation which possibly led to the enforcement of the effect of genetic drift. This assumption is confirmed by the fact that haplotype diversity of Y-STRs analyzed against the background of M201 Y-SNP haplogroup is dramatically reduced compared with those for other Caucasus populations (Nasidze et al., 2003). Moreover, unusually high frequencies of haplogroups G(M201) observed in Ossetians could be explained by the effect of genetic drift as well. Second, are North and South Ossetians more similar genetically to each other, or to their geographic neighbors (i.e., Caucasian-speaking populations in the North and South Caucasus, respectively)? The results are somewhat different for mtDNA vs. the Y-chromosome. North and South Ossetians do show quite close genetic affinity, which may indicate a common origin. However, the mtDNA genetic distance between North and South Ossetians is not smaller than the distance between either and other Caucasian groups. Whereas for the Y-chromosome, North Ossetians are more similar to other North Caucasian populations, and South Ossetians to other South Caucasian populations, than to each other. The SAMOVA analysis also identifies a boundary between South Ossetians and other groups for the Y chromosome, but not for mtDNA. Thus, there is no indication in the Y-chromosome of a particularly close genetic relationship between North Ossetians and

South Ossetians. If they did have a common origin in the past, it has apparently become obscured by subsequent gene flow with their geographic neighbors on the same sides of the Caucasus Mountains.

There is no general agreement between historians and archaeologists regarding the origin of Ossetians (for overview see Isachenko and Kuchiev, 1995). However, there are archaeological finds indicating a long-standing complex process of formation of Ossetians and multiple migration events in the North Caucasus, which could leave genetic footprints in North Ossetians. There are archaeological finds assigned to so-called "proto-Alanian" tribes dated back to 8th-7th cc BC in the central part of the North Caucasus (Berezin and Vinogradov 1988). Followed by archaeological cultures with Sarmato-Scythian features and which are dated back to 7th-3th cc BC (Zhdanovski, 1990). Archaeologists assign these two periods (8th-3th cc BC) to an early stage of formation of Ossetians. At the later stages archaeologists recognize two major migration events in the central part of the North Caucasus: so-called Savromato-Scythian and Sarmato-Alanian who presumably brought the Iranian language (Isachenko, Kuchiev, 1995). These migrations, originated in the Southern Russian steppes, could leave recognizable genetic footprints in North Ossetians but not in South Ossetians.

Putting together the archaeological and genetic data, and assuming a common origin of South and North Ossetians (which is supported by the mtDNA data), a plausible scenario is that "alteration" of the initial Ossetian Y-chromosome gene pool took place in North Ossetians from other North Caucasus groups and/or groups from the Southern Russian steppes. This assumption is enforced by the fact that the genetic distances between North Ossetians and South Caucasus groups is similar to that between North Ossetians and South Ossetians, but the genetic distances between North Ossetians and other North Caucasus groups are much smaller. Moreover, there are differences in genetic structures based on Y chromosome and mtDNA, as the correlation between F_{st} distances among pairs of Caucasus groups based on mtDNA and Y-haplogroups was not statistically significant. The different patterns observed between South and North Ossetians for the Y chromosome may also have been reinforced by the traditional patrilineal social structure of this population, leading to a higher degree of differentiation for the Y chromosome than for mtDNA.

The Ossetians speak an Iranian language; is this because they are directly descended from the Alani (an Iranian-speaking group), or is it rather that genetically the Ossetians resemble their geographic neighbors in the Caucasus, and hence replaced their ancestral Caucasian language with an Iranian language, after contact with the Alani (or another group)? Average pairwise F_{st} values are smaller between Ossetians and Iranians than

between Ossetians and Caucasians for both mtDNA and the Y chromosome, significantly so for mtDNA, which suggests an Iranian origin of Ossetians. The subsequent, largely male-mediated migrations between Ossetians and neighboring groups in the North and South Caucasus, respectively, would explain the greater similarity between Ossetians and Caucasians for the Y-chromosome, as discussed previously.

In conclusion, the genetic results find support in the archaeological record in that they reflect a common Iranian origin of South and North Ossetians, as well as the genetic footprint of ancient migrations in the North Caucasus that mostly involved male individuals. Thus, genetic studies of such complex and multiple migrations as the Ossetians can provide additional insights into the circumstances surrounding such migrations.

გენეტიკა

რას გვეუბნება გენეტიკა ჩრდილოელი და სამხრეთელი ოსების წარმომავლობაზე

ი. ნასიძე

მაქს პლანკის ევოლუციური ანთროპოლოგიის ინსტიტუტი, ლაიფციგი, გერმანია

(წარმოდგენილია აკადემიის წევრის ნ. ალექსიძის მიერ)

ოსები ერთ-ერთი ეთნიკური ტომია, რომელიც კავკასიის ქედის ჩრდილო და სამხრეთ ტერიტორიაზე ცხოვრობს, მეტყველებს ოსურ ენაზე, რომელიც ირანულ ენათა ოჯახს მიეკუთვნება, და აქვს გენეტიკური თვისობა მეზობელ კავკასიელ ეთნიკურ ტომებთან. აღნიშნულთან დაკავშირებით პრობლემური გახდა ჩრდილო და სამხრეთელი ოსების წარმომავლობისა და გენეტიკური მსგავსება-განსხვავების საკითხი.

დღეს ლიტერატურაში არსებობს ორი ჰიპოთეზა: პირველი, ოსები ჯერ კიდევ ჩვენს წელთაღრიცხვამდე VII საუკუნეში განიცდიდნენ ალანების წინაპრების – სარმატების – გავლენას და მეტყველებდნენ ირანული ოჯახის ენაზე (ისფაჰანი, თეირანი). აქედან, სწორედ ალანები უნდა მივიჩნიოთ ოსების წინაპრებად. მეორე ჰიპოთეზის თანახმად ალანები კავკასიის ავტოქტონური ჯგუფია, რომელმაც შეითვისა ალანური ენა ჯერ კიდევ შუა საუკუნეებში. არაა გამორიცხული, რომ ადრე ისინი ერთ-ერთ კავკასიურ ენაზეც მეტყველებდნენ, რაზეც მიგვანიშნებს პოპულაციების გენეტიკური ანალიზის შედეგები.

XX ს. 90-იან წლებში კლასიკური გენეტიკური მარკერებით (მრატის ცილები, სისხლის ჯგუფები, ერთროციტული ენზიმები) ჩრდილოეთ და სამხრეთ ოსეთში მცხოვრებ ძირძველ მოსახლეობაზე ჩატარებული გამოკვლევებით დამტკიცდა, რომ ისინი არსებითად განსხვავდებიან აღნიშნული მარკერების მიხედვით. ჩრდილოელი ოსები, სამხრეთ კავკასიაში მცხოვრებ ოსებთან შედარებით, გენეტიკურად დიდ მსგავსებას ამჟღავნებენ ჩრდილოეთ კავკასიის ეთნიკურ ტომებთან, სამხრეთელი ოსები კი, გენეტიკურად ნათესაურ თვისობას ამჟღავნებენ სამხრეთკავკასიელი ეთნიკური ტომების მიმართ, მათ შორის ქართველებთან

კლასიკური გენეტიკური მარკერების გამოყენებით დამტკიცდა, რომ კავკასიელების მსგავსად, ჩრდილოელი ოსები მაღალ თვისობას ავლენენ რუსული ეთნიკური ტომების მიმართაც.

ამ პრობლემით მრავალი მეცნიერი დაინტერესდა და თანამედროვე გენეტიკური მარკერების გამოყენებით (მიტოქონდრიული დნმ-ის ჰიპერვარიანტული თანმიმდევრობა – HVI, Y ქრომოსომის ბიალელური მარკერი, Y ქრომოსომის მოკლე ტანდემის განმეორება – STR) დაიწყო ფუნდამენტური კვლევები. მეცნიერებმა მიზნად დაისახეს დაედგინათ, თუ რა სახის გენეტიკური მსგავსება არსებობს ჩრდილოელ და სამხრეთელ ოსებსა და მათ მეზობელ და სამხრეთკავკასიელ ჯგუფებს შორის. როგორც ცნობილია, ჩრდილო ოსეთში წარმოდგენილია ოსების 5 ეთნიკური ჯგუფი (ალაგირი, დიგორა, არდონი, ზამანკული, ზულკა), სამხრეთ კავკასიაში კი – ოსების ერთი ეთნიკური ჯგუფი. ისინი ენობრივად იზოლირებული არიან კავკასიურ ენებზე

მეტყველი პოპულაციებისაგან. ოსების ორივე ნაწილი გენეტიკურად განსხვავდებიან მიტოქონდრიული დნმ-ისა და Y ქრომოსომის მიხედვით. თუ მიტოქონდრიული დნმ გარკვეულწილად მათ მსგავს წარმომავლობაზე მიგვანიშნებს, Y ქრომოსომის მიხედვით, ჩრდილოელი ოსები, გენეტიკური ნათესაობის მიხედვით გაცილებით ახლოს არიან ჩრდილოკავკასიურ პოპულაციებთან, ვიდრე სამხრეთელ ოსებთან. სამხრეთელი ოსები კი პირიქით, გამოირჩევიან მაღალი თვისობით სამხრეთკავკასიურ პოპულაციებთან. ამგვარად, კლასიკური გენეტიკური ტექნოლოგიების გამოყენებით დადგენილი იქნა, რომ არ არსებობს ბიოლოგიური მტკიცებულება ჩრდილოელი და სამხრეთელი ოსების გენეტიკური მსგავსების შესახებ. როგორც ჩანს, წარსულში გეოგრაფიულად მეზობელ ჩრდილო და სამხრეთ კავკასიელებში გენების დინამიკა ისე წარიმართა, რომ კავკასიაში პრაქტიკულად ჩამოყალიბდა გენეტიკურად გაუცხოებული ჩრდილოელი და სამხრეთელი ოსური პოპულაციები. საგულისხმოა ისიც, რომ უახლესი მონაცემებით, ოსებსა და ირანელებს შორის აზოტოვან ფუძეთა შეწყველების მაჩვენებელი საკმაოდ დაბალია, თუმცა ეს საკმარისი აღმოჩნდა ოსების ირანული წარმომავლობის დასამტკიცებლად. არის მოსაზრება, რომ ოსების მსგავსება კავკასიელებთან განპირობებულია ოსების მიგრაციის შედეგად გენეტიკური ტრანსლოკაციებით კავკასიურ ეთნიკურ ტომებსა და ოსებს შორის, რაზეც მიგვანიშნებს მათ შორის Y ქრომოსომის მსგავსება.

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