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MATRILINEAL GENETIC STRUCTURE OF ARMENIANS OF ARTSAXH

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The Armenians living in Artsakh, a landlocked region in the South Caucasus, are characterized by strong and distinct national identity. The genetic legacy of this geographic group is of particular scientific interest due to its reproductive isolation during many centuries. However, there is no comprehensive study of matrilineal genetic variation of the Artsakh population so far. Here, we have analyzed the high resolution mitochondrial DNA typing data of 44 unrelated males from Artsakh and compared it with those of other neighboring Armenian and non-Armenian populations. The results indicate that matrilinear gene pool of the Artsakh population predominantly comprises the European lineages, while only weak traces of Central Asian genetic influence were detected. In addition, along with other Armenian geographic groups, the Armenians of Artsakh has close genetic affinity to the Near Eastern populations.

Artsakh Armenians – mtDNA – population genetics

Արցախում, Հարավային Կովկասի լեռնային շրջանում, բնակվող հայերը, բնութագրվում են հստակ արտահայտված ազգային ինքնությամբ: Տվյալ աշխարհագրական խմբի գենետիկական կառուցվածքի ուսումնասիրությունը բազմադարյան մեկուսացման պատճառով առաջացնում է մեծ գիտական հետաքրքրություն: Սակայն, մինչ օրս ամբողջությամբ ուսումնասիրված չէ տվյալ պոպուլյացիայի մայրագծային գենետիկական բազմազանությունը: Այստեղ մենք վերլուծել ենք Արցախում բնակվող 44 հայրական գծով ոչ ազգակից տղամարդկանց միտոքոնդրիումային ԴՆԹ-ի գենատիպավորման արդյունքները և համեմատել դրանք հայկական և տարածաշրջանի այլ պոպուլյացիաների համապատասխան տվյալների հետ: Ստացված արդյունքների համաձայն Արցախի պոպուլյացիայի մայրագծային գենոֆոնդի գերակշռող մասը բաղկացած է եվրոպական հապլոխմբերից, դրա հետ մեկտեղ Կենտրոնասիական գենետիկական հետքերը գրեթե բացակայում են: Բացի այդ, հայերի այլ աշխարհագրական խմբերի հետ մեկտեղ, Արցախի պոպուլյացիան ունի գենետիկական ակնհայտ նմանություն մերձավորարևելյան եթնիկական խմբերի հետ:

Արցախի հայերը – միտոքոնդրիումային ԴՆԹ – պոպուլյացիոն գենետիկա

Армяне Арцаха, горного региона на Южном Кавказе, характеризуются выраженной национальной идентичностью. Многовековая изоляция данной географической группы вызывает пристальный научный интерес к изучению ее популяционной структуры. Однако до настоящего времени отсутствуют достаточно полные сведения о матрилинейной составляющей ее генофонда. Мы проанализировали результаты высокоразрешающего генотипирования митохондриальной ДНК у 44 не родственных по отцовской линии мужчин, жителей Арцаха, и сравнили их с соответствующими данными по остальным географическим группам армян и других популяций региона. Полученные результаты выявили, что большая часть матрилинейного генофонда популяции Арцаха представлена европейскими гаплогруппами, в то время как центральноазиатские родословные практически отсутствуют в

нем. Кроме того, наряду с другими географическими группами армян, карабахская популяция характеризуется выраженным генетическим сходством с этническими группами Ближнего Востока.

Армяне Арцаха – митохондриальная ДНК – популяционная генетика

The origin of the population of Artsakh is among primary issues in the Armenian studies and remains the subject of intensive debates for scholars of various disciplines. According to the historical records, Artsakh was a part of the Greater Armenia and played an important role in its administrative and cultural life [1, 2]. The region has its specific background and peculiarities, being separated from the entire Armenia since the beginning of V century AD with the preservation of unique ethno-national identity of the population.

The paucity of unequivocal linguistic, historical and archaeological data necessitates the use of more sensitive and objective approaches to reconstruct the history of this population. With the recent rapid development of molecular techniques, genetic studies have been extensively applied to shed light on the genetic roots of Armenians from Artsakh. Here, we have analyzed high resolution mitochondrial data and compared the output with comparative datasets of other Armenian and neighboring populations from the region.

Materials and methods. DNA samples from 44 unrelated individuals, whose ancestors inhabited Artsakh region at least on the grandmother level, were collected and further typed for mtDNA HVSI region. Additionally, for the analysis we used unpublished data of Armenians representing different regions within the Armenian Highland: Salmast (n=200), central (n=85) and western parts of the plateau (n=44). Our Armenian samples were compared with those of other ethnic groups – Libyans (n=30), Tunisians (n=160), Syrians (n=230), Lebanese (n=970), Palestinians (n=120) [3], Ashkenazi-Jews (n=583) [4], Chechens (n=176), Ingushs (n=103), Dargins (n=110) [17], Georgians (n=104) [12, 15], Turks (n=104) [13, 15], Iranians (n=181) [6], Austrians (n=187), Germans (n=527), Scottish (n=891) [11], Mongols (n=47), Buryats (n=295) [5].

F_{ST} genetic distances based on mtDNA haplogroup frequency data were assessed using Arlequin v.3.5 package [8]. Principal Coordinate Analysis (PCA) was performed on similarity matrices calculated as one minus genetic distance using Genstat software [16]. To assess the summary statistics and gene diversity parameters of the samples, we have converted mtDNA haplotypes obtained by RFLP into mtDNA HVRI sequences from 16024-16400 b.p. positions by Haplosearch [10]. The mtDNA HVRI sequences were aligned with rCRS by multiple sequence alignment tool MUSCLE [7] and further were used to calculate basic parameters of genetic diversity of studied populations using the DnaSP v.5 software package [12].

Results and Discussion. The analysis of mitochondrial haplogroup distribution (fig.1) demonstrates the prevalence of the H, U, T and J lineages, together accounting for 69% of the sampled group. According to the geographic distribution, these lineages are considered as the European ones since these are found at very high proportions in the West European ethnic groups. Specifically, haplogroup H, which supposed to be originated in West Asia ca. 20-25 kya [9], is a modal matrilineal lineage in all Armenian populations. Notable, Central and Eastern Asian haplogroups, namely the lineages A, B, C, D, F, G, M and N, are not common in all Armenian populations and their aggregate frequency encompasses less than 6%.

In the Armenian samples from Artsakh, 38 different haplotypes, 58 segregating sites with total number of 58 mutations were observed. Highly negative value of Tajima's D parameter indicates the probable recent population expansion or the presence of purifying selection of some variable sites in the Armenian population. On the contrast to the Y chromosomal data [14], the gene diversity pattern in the population of Artsakh is among the highest ones in the region, indicating the absence of reproductive isolation for women.

Haplogroups	Population			
	CA (n=85)	Artsakh (n=44)	Salmast (n=200)	WA (n=44)
A	-	-	-	-
B	-	-	-	-
C	-	-	0.010	-
D	-	-	0.010	-
F	-	-	-	-
G	-	-	-	-
H	0.212	0.227	0.295	0.205
HV	0.082	0.068	0.075	0.114
I	0.024	-	0.010	0.045
J	0.106	0.114	0.150	0.159
K	0.059	0.091	0.045	0.023
L	0.012	-	-	-
M	0.012	-	-	-
N	0.047	0.023	0.030	0.114
R	0.047	-	0.010	0.023
T	0.165	0.182	0.110	0.136
U	0.200	0.205	0.165	0.159
V	-	-	0.005	-
W	-	0.068	0.050	0.023
X	0.035	0.023	0.035	-

Fig.1. mtDNA haplogroup composition of the Armenian populations studied.
(WA – Western Armenia, CA – Central Armenia).

To visualize genetic affinity between the populations studied, we have performed principal coordinate analysis based on the values of F_{ST} genetic distance (fig. 2). The results reveal strong regional clustering with the separation of African, East Asian, European and Middle Eastern/Caucasus clusters. Within the PCA plot, Armenians are appeared to be close to the populations from the Levant, indicating the genetic proximity of these groups.

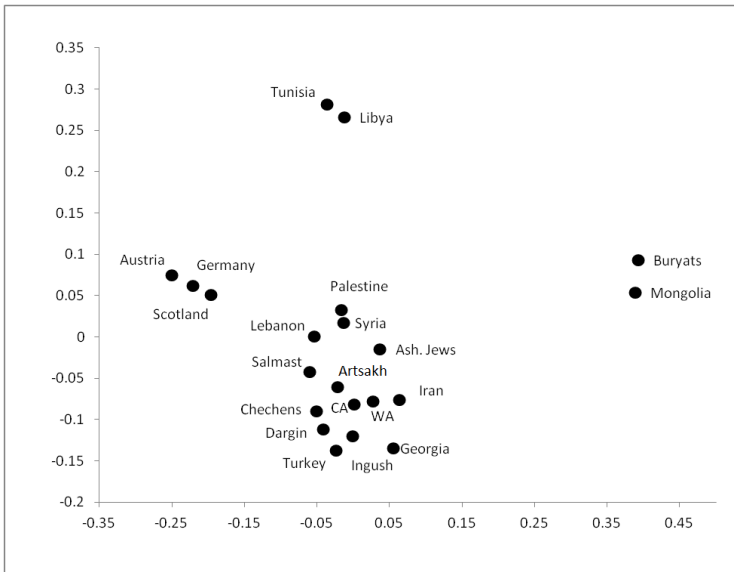


Fig.2. Principal coordinates plots (first two axes) based on F_{ST} values calculated from mtDNA haplogroup frequency data.

On the whole, matrilinear genetic structure of the population of Artsakh is characterized with high genetic diversity pattern. Studies based on both uniparentally transmitted genetic markers demonstrate close affinity of all Armenian and Near Eastern

populations. Further studies with sufficiently large sample sizes from the Artsakh region and using genome-wide data should provide further insights into the genetic peculiarities of the population.

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