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GENETIC AFFINITY OF ASSYRIANS LIVING IN ARMENIA TO DIFFERENT ETHNIC GROUPS OF THE NEAR EAST AND SOUTH CAUCASUS

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Genetic structure of the Assyrian population was studied using 12 SNP and 6 microsatellite (STR) markers on Y chromosome and the results were compared with other ethnic groups of the Near East region analyzed by the same set of markers. The results reveal that Assyrians are genetically quite distant from Arabs, who also speak Semitic language, and are closer to other populations of the Near East and the South Caucasus. Two main lineages based on Y-chromosomal data were observed within the population which possibly reflects two distinct sources genetically contributed to the origin of Assyrians.

Assyrians – Near East – Y chromosome – single nucleotide polymorphism – microsatellite

Ասորիների գենետիկական կառուցվածքն ուսումնասիրվել է ըստ Y քրոմոսոմի վրա գտնվող 12 SNP և 6 (STR) միկրոսատելիտային մարկերների, և արդյունքները համեմատվել են Մերձավոր Արևելքի այլ էթնիկական խմբերի հետ, որոնք հետազոտվել են ըստ նույն մարկերների: Արդյունքները ցույց են տալիս, որ ասորիները գենետիկորեն բավականին հեռու են արաբներից, ովքեր նույնպես խոսում են սեմիթական լեզվով, և ավելի մոտ են Մերձավոր Արևելքի և Անդրկովկասի այլ պոպուլյացիաներին: Ասորիների մոտ նկատվել է երկու հիմնական տոհմագծեր ըստ Y քրոմոսոմային տվյալների, ինչը հավանաբար վկայում է ասորիների երկակի ծագման մասին:

Ասորիներ - Մերձավոր Արևելք - Y քրոմոսոմ - եզակի նուկլեոտիդային պոլիմորֆիզմ - միկրոսատելիտ

Генетическая структура ассирийской популяции исследована на основе 12 SNP и 6 микросателлитных (STR) маркеров Y хромосомы. Полученные результаты сопоставлены с соответствующими параметрами для различных этнических групп региона Ближнего Востока, изученных с использованием того же набора генетических признаков. Выявлено, что ассирийцы генетически далеки от арабов, также говорящих на семитском языке, и ближе к другим популяциям Ближнего Востока и Южного Кавказа. Наличие двух наиболее часто встречающихся родословных в патрилинеальном генофонде, возможно, свидетельствует об участии двух различных источниковых популяций в генетической истории ассирийцев.

Ассирийцы – Ближний Восток – Y хромосома – единичный нуклеотидный полиморфизм – микросателлит

Assyrians, one of the mighty powers of antiquity, prospered around the area of Fertile Crescent in 3rd-1st millennia BC. Since their downfall around 7th century BC, Assyrians have lived under rules of different peoples (Rogers, 1901). During many centuries they have also spread all over the world and founded numerous Assyrian Diaspora communities in different countries. Although the bulk of Assyrians currently lives in the region of their origin, in nowadays Iraq, Syria, Iran, Turkey and Lebanon, large communities exist in North America, Europe, Australia, Russia and Caucasus.

In Armenia, Assyrians constitute the third largest ethnic minority after Yezidis and Russians. According to different sources, about 3,500-6,000 Assyrians currently live in the country, mainly in three villages: Verin Dvin, Dimitrov and Arzni. Assyrians and Armenians had contacts since ancient times, from the period of Kingdom of Urartu. Nevertheless, current Assyrian communities in Armenia are mainly the descendants of Assyrians who moved to Armenia after Russian-Persian war in the beginning of 19th century from northern part of Persia. A second wave of migration to Armenia occurred in the beginning of 20th century from South-Eastern Turkey after Assyrian Genocide. Although nowadays Armenian-Assyrian marriages are not rare, just a few generations ago Assyrians were strictly isolated and were not mixing with other ethnic groups (Asatryan, Arakelova, 2002).

There are very few genetic studies comparing Assyrians with other ethnic groups of the region. A recent study by Lashgary et al. (2011) showed certain relatedness of Assyrians to Armenians and some other populations from Iran according to Y-chromosomal single nucleotide polymorphism (SNP) markers. However, a comprehensive study of Assyrian population comparing them with a broad range of populations is necessary to identify the position of Assyrians on the genetic landscape of the Middle East and their ancient relationships with neighboring populations. Additionally, such a detailed study is important to assess the role of recent migratory events and contacts with other ethnic groups in shaping the genetic structure of different Diaspora communities of Assyrians. Since the Assyrians speak a Semitic language it is interesting to test if they are genetically closely related to other Semitic-speaking populations of the South-West Asia.

In this paper we studied the genetic diversity of Assyrians according to Y-chromosomal SNP and microsatellite markers and compared them to other populations of the Near East and South Caucasus.

Mouth swabs from 106 self-identified Assyrian adult males who gave their informed consent were anonymously collected in three villages in Armenia where Assyrians mainly reside: Arzni, Dimitrov and Verin Dvin.

Materials and methods. DNA was extracted by standard phenol-chloroform method. All samples were genotyped for 12 binary Y chromosome polymorphisms: 92R7, M9, M13, M20, sY81, SRY+465, SRY4064, SRY10831, Tat, M17, Alu insert – YAP, and p12f2 (Rosser et al., 2000; Weale et al., 2001) and and screened for six microsatellite (short tandem repeat, STR) markers: DYS19, DYS388, DYS390, DYS391, DYS392, and DYS393 (Thomas et al., 1999). Haplogroups (hg) were defined by SNP markers according to the Y Chromosome Consortium nomenclature (2002). Microsatellite repeat numbers were assigned according to nomenclature of Kayser et al. (1997).

Pairwise genetic distances (FST and RST) based on SNP and microsatellite markers were estimated from analysis of molecular variance (AMOVA) ΦST values using Arlequin program (Excoffier et al., 2005). Principal Coordinates Analysis was conducted on similarity matrices based on RST values. Signature haplotype analysis (high frequency modal haplotypes and modal clusters (Thomas et al., 1998; 2002; Wilson et al., 2001) was performed manually.

Comparative data sets were taken from different sources: Turkey (n=523 representing 10 different geographic regions) from Cinnioglu et al. (2004), Sephardi Jews (n=78), Bedouins (n=32), Kurds (n=95), Palestinian Arabs (n=143), Kurdish Jews (n=99), Ashkenazi Jews (n=79) from Nebel et al., (2001). Samples representing four different Armenian subpopulations were collected in Armenia and Diaspora: Syunik region (n=296), Karabakh region (n=216) and Historic

Western Armenia (n=400) (partly published in Weale et al. (2001)). Syrians (n=72) were taken from Weale et al., (2001). The rest of comparative data sets are unpublished so far - Azeri (n=99), Farsi (n=96), Yezidis (n=202), Hamshen (n=82) and Yemenis (n=93). All samples were typed for the same Y chromosomal markers.

Results and Discussion. The results of Y chromosome typing have revealed 6 SNP haplogroups and 37 different microsatellite haplotypes in Assyrians. The most frequently encountered haplogroup (41.51%) is P*(xR1a), followed by haplogroup J (37.74%). Haplogroup K*(xL,N3,O2b,P) is also relatively common in Assyrians (15.09%). The frequency of haplogroup P*(xR1a) is one of the highest in the region of the Middle East and is very close to Syunik (40.2%) and Karabakh (43.06%) (Tab. 1).

Table 1. The distribution of the most frequent Y chromosomal haplogroups in Assyrians and comparative data sets

Population	Haplogroup				
	P*(xR1a)	BR*(xDE,JR)	E*(xE3a)	K*(xL,N3,O2b,P)	J
Ashkenazi Jews (n=79)	0.1139	0.0633	0.2278	0.0380	0.4304
Assyrians (n=106)	0.4151	0.0094	0.0283	0.1509	0.3774
Azeris (n=99)	0.1111	0.2323	0.0808	0.0303	0.3939
Bedouins (n=32)	-	0.0625	0.1875	-	0.6563
Central Turkey (n=90)	0.2000	0.1889	0.0889	0.0556	0.3444
East-South Turkey (n=43)	0.2093	0.1860	0.0930	0.0698	0.3256
East Turkey (n=82)	0.1951	0.0976	0.1463	0.0244	0.3902
Farsi (n=96)	0.1771	0.0625	0.0729	0.0521	0.5000
Istanbul (n=78)	0.1410	0.2179	0.1410	0.0513	0.2821
Hamshen (n=82)	0.0854	0.4390	0.0488	0.0122	0.3171
Karabakh (n=216)	0.4306	0.1157	0.0278	0.0509	0.3056
Kurdish Jews (n=99)	0.2020	0.0606	0.1212	0.1919	0.3737
Kurds (n=95)	0.1684	0.1684	0.0737	0.0421	0.4000
North-East Turkey (n=83)	0.1566	0.1928	0.0843	0.1084	0.2892
North Turkey (n=29)	0.3448	0.2414	0.0345	0.0345	0.3448
North-West Turkey (n=55)	0.1636	0.1818	0.1636	-	0.4364
Palestinian Arabs (n=143)	0.0839	0.0629	0.2028	0.0699	0.5524
Sephardi Jews (n=78)	0.2949	0.1154	0.1923	0.0769	0.2821
South Turkey (n=33)	0.2121	0.1212	0.1212	0.0606	0.3939
Syrians (n=72)	0.0972	0.0417	0.2083	0.0417	0.5417
Syunik (n=296)	0.4020	0.0912	0.0405	0.0405	0.3716
Western Armenia (n=400)	0.2425	0.2100	0.0325	0.0725	0.3725
West Turkey (n=30)	0.2333	0.2667	0.0667	0.1000	0.1667
Yemenis (n=93)	0.0323	0.1935	0.0645	-	0.6022
Yezidis (n=202)	0.2822	0.0495	0.1584	0.0644	0.4158

In contrast, the haplogroup is much less common in Arabs who are also Semitic-speaking as Assyrians (0% in Bedouins, 8.39% in Palestinian Arabs, 9.72% in Syrians, 3.23% in Yemenis). The frequency of haplogroup J in Assyrians is comparable to that in the populations of Southwest Asia, being widespread in the region. When comparing the genetic distances based on Y chromosomal haplogroups (FST), the same pattern is observed: Assyrians are very close to Syunik and Karabakh, i.e. to Eastern Armenians, and are quite far from all Arabic groups.

In order to make inferences about ancient genetic contacts and directions of migrations we have compared the frequencies of modal (the most frequently encountered) STR haplotypes in Assyrians and comparative data sets (Tab. 2). The results show that Assyrians bear two modal lineages: 14-12-24-10-13-13 belonging to hg P*(xR1a) and encountered in 11.32%, 14-13-23-10-11-12 belonging to hg J, also in 11.32%. The former haplotype is one-step neighbor to so-called “Atlantic Modal Haplotype” (AMH, Wilson et al., 2001); another one-step mutation neighbor, 14-12-24-11-13-12 has the highest frequency in Karabakh and Syunik (Weale et al., 2001). The frequency of Atlantic Modal Cluster (AMC, AMH and all one-step mutation neighbors combined) is 13.21% in Assyrians, 13.89% in Karabakh and 16.89% in Syunik. This may indicate that the Assyrian gene pool carries rather distinct signal of pre-Neolithic migration to western and northern Europe (Wilson et al., 2001, Weale et al., 2001) and the first modal haplotype if typing more markers presumably belongs to the lineage R1b (Myres 2011, Balaresque 2010). The second modal haplotype may represent another constituent part of the Assyrian gene pool, the indigenous one. The spread of haplogroup J is reflecting spatial dispersal of first farmers (Quintana-Murci et al., 2001).

Table 2. The most frequently encountered Y chromosomal microsatellite haplotypes in some of the populations studied. AJ, Ashkenazi Jews; Asr, Assyrians; Aze, Azeris; CT, Central Turkey; ET, East Turkey; Far, Farsi; Kar, Karabakh; NET, North-East Turkey; Syr, Syrians; Wst, Western Armenia; Yzd, Yezidis.

Haplogroup	Haplotype	Population AJ (n=79)	 Asr (n=106)	 Aze (n=99)	 CT (n=90)	 ET (n=82)	 Far (n=96)	 Kar (n=216)	 NET (n=83)
J	14 13 23 10 11 12	–	**0,1132**	0,0202	0,0111	0,0122	0,0104	0,0093	0,0482
J	14 15 23 10 11 12	0,0253	–	0,0505	0,0111	0,0610	0,0938	0,0741	0,0241
J	14 16 23 10 11 12	**0,1139**	–	0,0303	0,0444	0,0244	–	0,0139	0,0241
J	14 17 23 11 11 12	–	–	0,0101	0,0111	0,0122	–	0,0139	0,0120
P*(xR1 a)	14 12 24 10 13 13	–	**0,1132**	–	–	–	–	–	–
P*(xR1 a)	14 12 24 10 14 12	0,0253	0,0283	–	0,0222	–	–	0,0231	0,0120
P*(xR1 a)	14 12 24 11 13 12	0,0127	0,0094	0,0202	0,0333	0,0854	0,0104	**0,1111**	–

In order to obtain the visual representation of genetic relatedness of the populations studied we calculated genetic distances (RST) based on STR markers and performed Principal Coordinate Analysis. The resulting plot is shown on Fig. 1. The pattern constructed displays several important features worth mentioning. Firstly, Assyrians are close to Syunik and Karabakh which represent the Eastern "genetic province" of Historical Armenia. Secondly, Semitic-speaking four Arabic populations (Bedouins, Palestinian Arabs, Syrians and Yemenis) form a rather distinct cluster of comparative data sets which is genetically distant from Assyrians. In this particular case we can argue that linguistic affiliation does not correlate with genetic relatedness. One of the possible explanations of this difference is language replacement that took place several millennia ago.

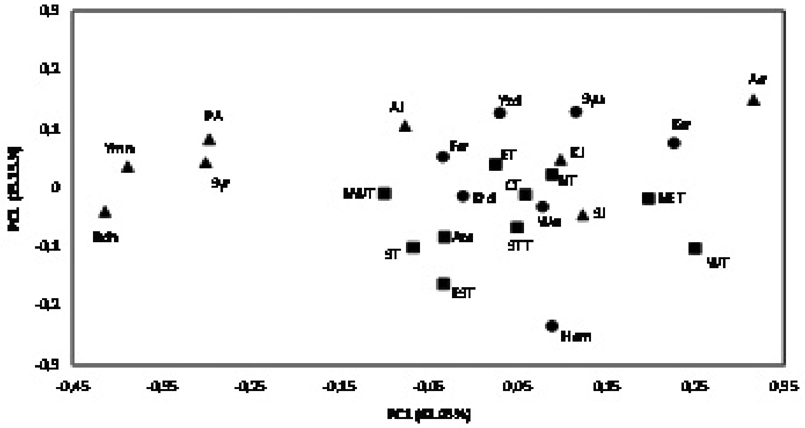

Fig.1. Principal coordinates plots (first two axes) based on Rst values calculated from microsatellite data. PC1 first axis, PC2 second axis. Numbers in brackets: percentage of total variation explained by each axis. Semitic-speaking (Afro-Asiatic) populations are depicted in triangles, Indo-European-speaking – in circles; Turkic-speaking (Altaic) – in squares. AJ, Ashkenazi Jews; Asr, Assyrians; Aze, Azeris; Bdn, Bedouins; CT, Central Turkey; EST; East-South Turkey; ET, East Turkey; Far, Farsi; Ham, Hamshen; Kar, Karabakh; Krd, Kurds; KJ, Kurdish Jews; NET, North-East Turkey; NT, North Turkey; NWT, North-West Turkey; PA, Palestinian Arabs; SJ, Sephardi Jews; ST, South Turkey; STT, Istanbul; Syr, Syrians; Syu, Syunik; Wst, Western Armenia; WT, West Turkey; Ymn, Yemenis; Yzd, Yezidis.

Concluding, we can make preliminary suggestion about the dual origin of Assyrians living in Armenia. On one hand, the high frequency of Atlantic Modal Haplotype belonging to R1b lineage rather strongly demonstrates that the ancient Assyrians had significant genetic contacts with the peoples who migrated to North-West Europe, where the vast majority of Y-chromosomal lineages belong to R1b haplogroup (Wilson et al., 2001; Myres et al., 2011). On the other hand, the presence of haplogroup J strongly supports the idea about the Near Eastern origin of Assyrian population. New, higher resolution typing, including more SNPs and STRs, will allow clarifying the hypothesis discussed.

REFERENCES

1. *Asatryan G., Arakelova V.* The ethnic minorities in Armenia. Yerevan Press, Yerevan, Armenia, 2002.
2. *Balaresque P., Bowden G.R., Adams S.M., et al.* A Predominantly Neolithic Origin for European Paternal Lineages. PLoS Biology, *8*, 1, e1000285, 2010.
3. *Cinnioğlu C., King R., Kivisild T., et al.* Excavating Y-chromosome haplotype strata in Anatolia. Hum. Genet., *114*, 127-148, 2004.
4. *Excoffier L., Laval G., Schneider S.* Arlequin ver. 3.0: An integrated software package for population genetics data analysis. Evolutionary Bioinformatics Online, *1*, 47-50, 2005.
5. *Lashgary Z., Khodadadi A., Singh Y., et al.* Y chromosome diversity among the Iranian religious groups: a reservoir of genetic variation. Ann. Hum. Biol., *38*, 3, 364-371, 2011.
6. *Myres N.M., Rootsi S., Lin A.A., et al.* A major Y-chromosome haplogroup R1b Holocene era founder effect in Central and Western Europe. Eur. J. Hum. Genet., *19*, 95–101, 2011.
7. *Nebel A., Filon D., Brinkmann B., et al.* The Y Chromosome Pool of Jews as Part of the Genetic Landscape of the Middle East. Am. J. Hum. Genet., *69*, 1095–1112, 2001.
8. *Quintana-Murci L., Krausz C., Zerjal T., et al.* Y-chromosome lineages trace diffusion of people and languages in Southwestern Asia. Am. J. Hum. Genet., *68*, 537-542, 2001.
9. *Rogers R. W.* A History of Babylonia and Assyria. Volume 2. Eaton & Mains, New York, NY, USA, 1901.
10. *Rosser Z.H., Zerjal T., Hurles M.E., et al.* Y-chromosomal diversity in Europe is clinal and influenced primarily by geography, rather than by language. Am J Hum Genet, *67*, 1526-1543, 2000.
11. *Thomas M.G., Parfitt T., Weiss D.A., et al.* Y chromosomes traveling south: the Cohen Modal Haplotype and the origin of the Lemba - the "Black Jews of Southern Africa". Am. J. Hum. Genet., 66, 674-686, 2000.
12. *Thomas M.G., Skorecki K., Ben-Ami H., et al.* A genetic date for the origin of Old Testament Priests. Nature, 394, 138-140, 1998.
13. *Thomas M.G., Weale M.E., Jones A.L., et al.* Founding mothers of Jewish communities: geographically separated Jewish groups were independently founded by very few female ancestors. Am. J. Hum. Genet., 70, 6, 1411-1420, 2002.
14. *Weale M.E., Yepiskoposyan L., Jager R.F., et al.* Armenian Y chromosome haplotypes reveal strong regional structure within a single ethno-national group. Hum. Genet., 109, 659-674, 2001.
15. *Wilson J.F., Weiss D.A., Richards M., et al.* Genetic evidence for different male and female roles during cultural transitions in the British Isles. Proc. Natl. Acad. Sci. USA, 98, 9, 5078-5083, 2001.
16. Y Chromosome Consortium A nomenclature system for the tree of human Y-chromosomal binary haplogroups. Gen. Res., 12, 339-348, 2002.

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