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## Y CHROMOSOME DIVERSITY IN NOR JUGHA ARMENIANS: COMPARISON OF TWO DATA SETS

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Population genetic structure of Armenians living in Iran and in Diasporal community of London was comparatively studied based on 12 UEP and 6 STR Y chromosome markers. The results of the study have shown that genetically the two groups significantly differ from each other. This indicates that the dataset of Iranian Armenians collected outside Iran, due to historical and geographic peculiarities of population dispersal, is substantially biased and does not adequately represent the original community established in Iran since the beginning of 17<sup>th</sup> century AD.

*Iranian Armenians – Nor Jugha – Y chromosome – single nucleotide polymorphism (SNP) – microsatellites*

Ներկա աշխատանքում հետազոտվել է Իրանում և Լոնդոնում բնակվող հայերի գենետիկական կառուցվածքը, ըստ Y քրոմոսոմի 12 UEP և 6 STR մարկերների: Ստացված արդյունքները ցույց են տալիս, որ գենետիկական տեսակետից դիտարկվող խմբերը հավաստիորեն տարբերվում են միմյանցից: Դա վկայում է, որ Իրանի սահմաններից դուրս բնակվող պարսկահայերի ընտրանին, գաղթերի պատմական և աշխարհագրական առանձնահատկությունների պատճառով, գենետիկական կառուցվածքով զգալիորեն շեղված է և համապատասխանորեն չի արտացոլում երկրի հայկական համայնքը, որը հիմնվել է մ.թ. 17-րդ դարի սկզբում:

*Պարսկահայեր – Նոր Ջուղա – Y քրոմոսոմ – եզակի նուկլեոտիդային պոլիմորֆիզմ (SNP) – միկրոսատելիտներ*

На основе исследования 12 UEP и 6 STR маркеров Y хромосомы проведено сравнительное изучение популяционно-генетической структуры иранских армян и диаспоральной группы их соотечественников, проживающих в Лондоне. Полученные результаты указывают, что наблюдаемые популяции в генетическом отношении достоверно отличаются друг от друга. Это свидетельствует о том, что выборка иранских армян, проживающих за пределами Ирана, в силу исторических и географических особенностей их миграций, является существенно смещенной по своей генетической структуре и не отражает в полной мере исходную популяцию, появившуюся в стране в начале 17 века н.э.

*Иранские армяне – Нор Джуга – Y хромосома – полиморфизм единичных нуклеотидов (SNP) – микросателлиты*

Armenians have strong and distinct ethnic and cultural identity which unites them as an ethno-national group. Recent studies (Weale et al., 2001; Yepiskoposyan et al., 2001; Harutyunyan et al., 2009) revealed significant regional stratification (based on Y-chromosome diversity), on a level greater than that found in some comparisons between different ethno-national identities. Since early medieval time Armenians have dispersed to many regions of Middle East, western and central European countries thus starting a history of the Diaspora. The Armenian community of Nor Jugha (historically, the district of Esfahan) in Iran is one of the biggest Diaspora populations; it starts his history from the beginning of 17th century AD and represents a classical example of ethnic group genetically isolated from neighbouring populations due to state borders (from Turkey and Russia, then USSR) and religious differences (Christian vs. Muslim).

The principal aim of this report is to check if a sub-sample of the dataset taken from Diaspora communities of Nor Jugha Armenians (living beyond Iran) adequately describes Y-chromosome diversity in the Armenian population of Esfahan.

Mouth swabs from informed consenting self-identified Armenian males, unrelated at the paternal grandfather level, were collected in Iran (n=89) and in Armenia and UK (n=57). The samples were screened for 12 biallelic (UEP) markers and for 6 microsatellite markers (the set typed at the Centre for Genetic Anthropology, University College London). The details of genetic typing and the methods of subsequent statistical analysis of the data done by Arlequin package (Excoffier et al., 2005) are described earlier (Andonian et al., 2010).

The 12 SNP markers identified 7 haplogroups in Armenians from Esfahan and 5 haplogroups beyond Iran. The difference between the groups according to haplogroup structures is significant ( $P < 0.05$ ) while applying exact test for population differentiation (Nei, 1987). The modal (i.e. most frequently encountered) haplogroup in both groups is hg J (31.5% in Iran and 43.9% outside), followed by hg P\*(xR1a), BR\*(xDE, JR) and E\*(xE3a) (Table 1). The six microsatellite markers defined 72 haplotypes (51 in Iran, 38 outside Iran). The difference between the two data sets based on microsatellite and compound SNP+microsatellite haplotypes are also significant ( $P < 0.001$  in both cases).

The two sample sets share some frequently encountered haplotypes identified in more than 3% in one of the groups. The modal haplotype in Armenians from Esfahan (7.87 %) is not found outside Iran, while the modal haplotype outside Iran is also present at moderate rate in Iran (8.77 % and 3.37 %, respectively). If we compare modal clusters (as modal haplotypes and their one-step neighbors) between the two groups, we can state that both data sets share almost the same rate of modal cluster originally encountered outside Iran (19.1 % in Iran and 17.54 % outside Iran).

**Table 1.** Y chromosome haplogroup frequencies in two datasets of Iranian Armenians.

Haplogroup	Arm_IR (n=89)	IranAr (n=57)
P*(xR1a)	0.2584	0.3158
BR*(xDE, JR)	0.2022	0.0877
R1a1	0.0337	0.0175
J	0.3146	0.4386
E*(xE3a)	0.0787	0.1404
K*(xL, N3, O2b, P)	0.0337	-
L	0.0787	-

Genetic diversity values ( $h$ ) are quite similar ( $P > 0.05$ ) while comparing haplotypes (at microsatellite level only) or compound haplotypes (SNP+microsatellite level), though at haplogroup level (SNP only) the difference between corresponding  $h$  values is significant both by bootstrap and Bayesian methods (Thomas et al., 2002).

Thus, the results of the comparison between Nor Jugha Armenians living in Esfahan and outside Iran show that these two groups significantly differ from each other according to population genetic structure based on Y-chromosome diversity. It means that the dataset of Nor Jugha Armenians collected outside Iran, due to historical and geographic peculiarities of population dispersal, is substantially biased and does not adequately represent the original community established in Iran since the beginning of 17th century AD.

## REFERENCES

1. Andonian L., Harutyunyan A., Margaryan A., Khachatryan Z., Yepiskoposyan L. Iranian Armenians in the Armenian genetic landscape. *Electronic Journal of Natural Sciences*, 2, 15, 45-50, 2010.
2. 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.
3. Harutyunyan A., Khudoyan A., Yepiskoposyan L. Patrilocality and recent migrations have little impact on shaping patterns of genetic structure of the Armenian population. *Russian Journal of Genetics*, 45, 1125-1131, 2009.
4. Nei M., *Molecular Evolutionary Genetics*. Columbia University Press, New York, NY, USA, 1987.
5. Thomas M.G., Weale M.E., Jones A.L., Richards M., Smith A., Redhead N., Torroni A., Scozzari R., Gratrix F., Tarekegn A., Wilson J.F., Capelli C., Bradman N., Goldstein D.B., 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.
6. Weale M.E., Yepiskoposyan L., Jager R.F., Hovhannisyan N., Khudoyan A., Burbage-Hall O., Bradman N., Thomas M. Armenian Y chromosome haplotypes reveal strong regional structure within a single ethno-national group. *Hum. Genet.*, 109, 659-674, 2001.
7. Yepiskoposyan L.M., Oganesyan N.A., Khudoyan A.T. Variation in Short Tandem Repeats of human Y chromosome. *Genetika*, 37, 926-931, 2001.

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