Institute of Molecular Biology
NAS, Armenia

CHECKING THE HYPOTHESIS OF A BALKAN ORIGIN OF THE ARMENIANS

Levon Yepiskoposyan,[1] Peter Hrechdakian,[2] Hovann Simonian[3]

[1]Institute of Molecular Biology, National Academy of Sciences, Yerevan, Armenia; [2]Armenian DNA Project at Family Tree DNA; [3]University of Southern California (USC), Los Angeles

Background

The origin of Armenians is a controversial subject for anthropologists, archaeologists, historians and linguists. Among several hypotheses on this point, one prevails. The ancient Greek historian Herodotus described the Armenians as Phrygian colonists because of their speech and the garments they wore: "The Armenians, who are Phrygian colonists, were armed in the Phrygian fashion. Both nations were under the command of Artochmes, who was married to one of the daughters of Darius" [Herodotus: History, VII, 73]. In the same time there are no convincing linguistic, archaeological and ethnographical evidences supporting this opinion. The recent advances in molecular genetics technique allow thoroughly assessing different aspects of human evolutionary history. Here, we tested the traditional Balkan version of the origin of Armenians based on the Y-chromosomal markers.

Material and methods

We used the results of high-resolution typing in 1226 DNA samples representing 11 Armenian geographic groups covering the whole area of the Armenian plateau and the database of the Armenian DNA project at Family Tree DNA comprising a general Armenian population (Table). As possible signals of Balkan influence the presence of the E1b1b1a1-M78 haplogroup with its major sub-branches (E1b1b1a1b-V13, E1b1b1a1a-V12 and E1b1b1a1c-V22) were considered (Fig. 1) in Greek [King et al., 2008] and Bulgarian [Karachanak et al., 2013] samples. The age of Y chromosomal lineages was calculated using 8 STR markers based on evolutionary mutation rates suggested by Zhivotovski et al. (2004) in populations with five or more samples. Haplogroup frequencies and STR allelic variances are shown as spatial gradient maps using the program Surfer v.9.0.343 (http://www.goldensoftware.com).

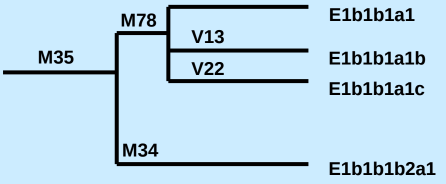

Figure 1. Phylogenetic tree of Y chromosomal lineage E1b1b1-M35

Results and discussion

The frequencies of the E1b1b1a1-M78 clade in Armenians are quite low in nine out of eleven geographic groups and in the general dataset, ranging from 0 to 2.9% (Table). The highest rate (7%) of the supposed Balkan lineages is observed in a sample representing the south-eastern part of the Armenian Highland (regions of Khoy and Salmas, currently north-west Iran). The mean age of the major sub-lineage (E1b1b1a1b-V13) of the this haplogroup in this region based on 8 STR markers is 14.6 ky (Fig. 2), and this value is much higher than that shown for the Greek and Bulgarian samples. The large temporal difference clearly evidences that the E1b1b1a1b-V13 haplogroup among south-eastern Armenians is more ancient and clearly was not introduced by back-migration from Balkan region. This lineage was most probably introduced to this region as a result of migrations from Africa to Europe via Near East [Cruciani et al, 2007]. In this context, it is also worth considering a possible coherence between temporal and spatial axes of cultural (e.g. linguistic, archaeological) and genetic traits, in this case implying the spread of Indo-European languages and the haplogroup E1b1b1a1-M78.

The other two highly encountered Y chromosomal lineages in Balkan region, haplogroups I2a (though here we consider the clade I-M170 which includes the I2c (L596) branch that seems to be native to West Asia and is found in Armenians) and R1a1a (Greece: 13.2% and 15.8%, respectively; Bulgaria: 26.6% and 17.5% respectively), are also detected at low frequencies in the Armenian subpopulations as indicated in the Table.

Populations	Haplogroups			Ref.
	E1-M78	I-M170	R1a-M198	
Alashkert (n=98)	1	3.1	4.1	Unpublished
Ararat valley (n=110)	0	2.7	0.9	Herrera et al., 2012
Bayazet (n=102)	2.9	3.9	2	Unpublished
Gardman (n=96)	0	8.3	5.2	Herrera et al., 2012
Hamshen (n=55)	0	5.5	1.8	Unpublished
Karabakh (n=105)	2.9	1.9	0	Unpublished
Salmast (n=200)	7	1.5	5.5	Unpublished
Sasun (n=104)	0	0	1	Herrera et al., 2012
Syunik (n=105)	1	1.9	3.8	Unpublished
Van (n=103)	3.9	1.9	0	Herrera et al., 2012
Western Armenia (n=148)	2.7	4.1	5.4	Unpublished
Greece (n=114)	27.2	13.2	15.8	King et al., 2008
Bulgaria (n=808)	19.6	26.6	17.5	Karachanak et al., 2013

Table. Most frequent Y chromosomal haplogroup frequencies (%) in the plausible source populations and different Armenian geographic groups.

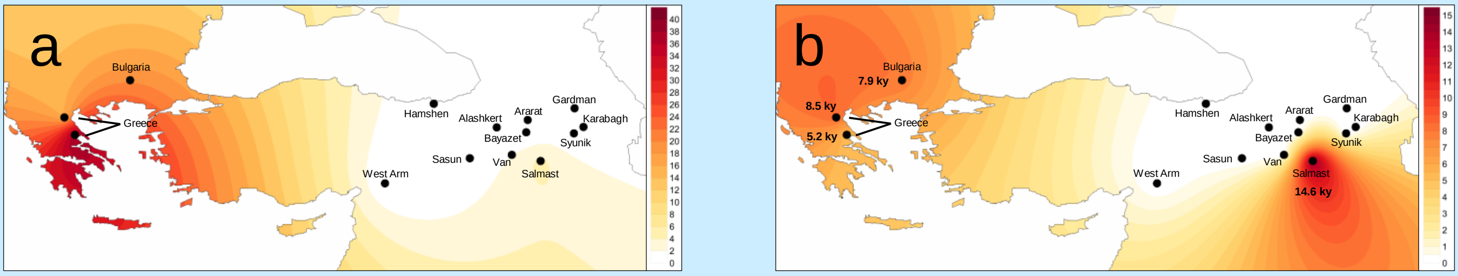

Figure 2. Geographic distribution of Y-chromosomal haplogroup E1b1b1a1-M78 frequencies (a) and age (ky) of its major sublineage E1b1b1a1b-V13 (b).

Conclusion

The distribution pattern of Y chromosome lineages in modern Armenian gene pool does not indicate the presence of any significant signals of Balkan genetic influence. Thus our results provide strong basis to state that the patrilineal genetic structure of the Armenians does not support the broadly accepted historical assumption of their Balkan origin.

European Human Genetics Conference
June 8-11, 2013, Paris, France

References

Cruciani et al: *MolBiolEvol* 2007, 24: 1300–1311.
Herrera et al: *Eur J Hum Genet* 2012, 20: 313–320.
Karachanak et al: *PLoSOne* 2013, 8: e56779.
King et al: *Ann Hum Genet* 2008, 72: 205–214.
Zhivotovsky et al: *Am J Hum Genet* 2004, 74: 54–61.