

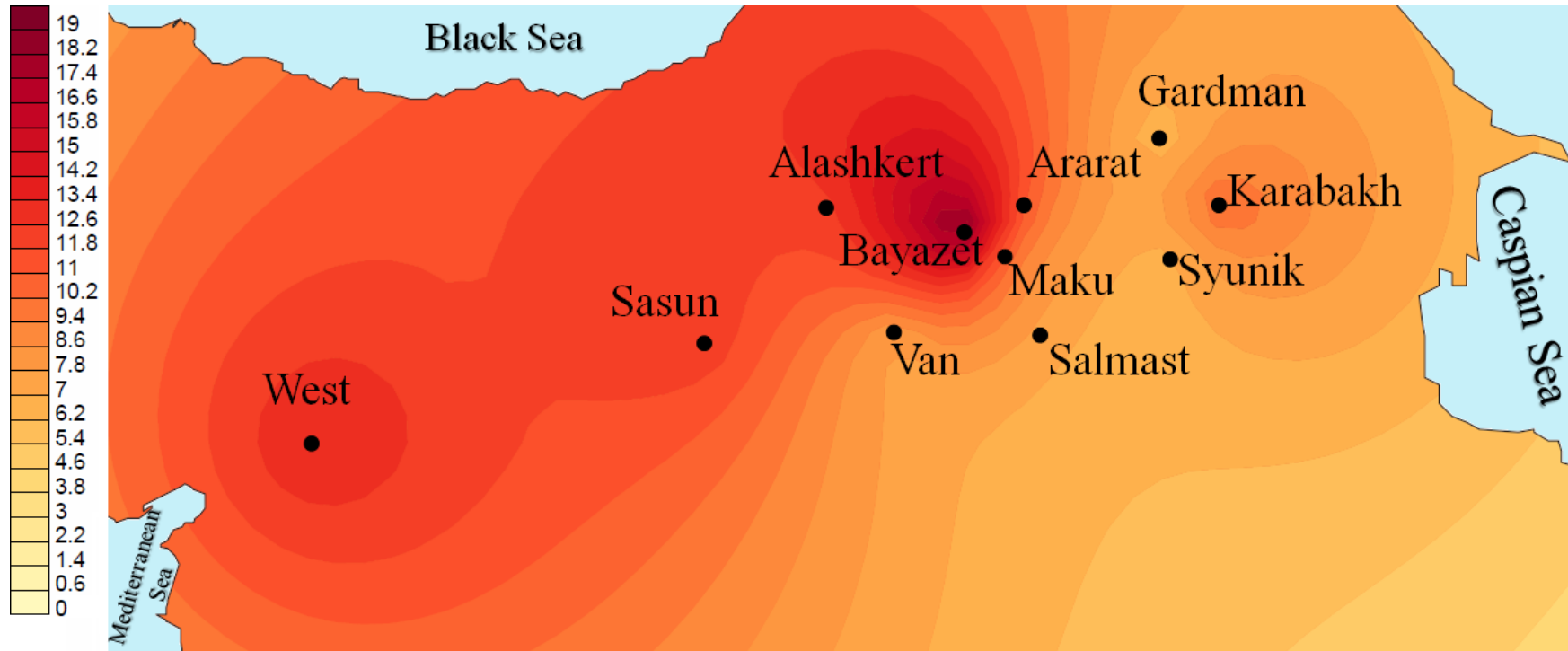
# HAPLOGROUPS DESCRIPTION

HAPLOGROUP	AGE OF ORIGIN	PLACE OF ORIGIN
		<b>NORTHEASTERN AFRICA</b>
		Bidirectional migrations between northeastern and eastern Africa (at least 2 episodes between 23.9-17.3 ky and 18.0-5.9 ky ago), trans-Mediterranean migrations directly from northern Africa to Europe (mainly in the last 13.0 ky), and flow from northeastern Africa to western Asia between 20.0 and 6.8 ky ago ( <a href="#">Cruciani et al., 2007</a> ).
<i>E1b1b1a1-M78</i>	~18.600 years ( <a href="#">Cruciani et al., 2007</a> )	
		<b>ARMENIAN HIGHLAND</b>
		Linked with post-ice-age expansions in Europe. Associated with the spread of agriculture, especially in the European Context ( <a href="#">Rootsi et al., 2012</a> )
<i>G-M201</i>	~23.000 years ( <a href="#">Hallast et al., 2015</a> )	
		<b>BALKAN</b>
		It is the only major clade of the Y phylogeny that is widespread over Europe but virtually absent elsewhere. Hg I could have played a central role in the process of human recolonization of Europe from isolated refuge areas after the Last Glacial Maximum ( <a href="#">Rootsi et al., 2004</a> )
<i>I-M170</i>	~20.600 years ( <a href="#">Hallast et al., 2015</a> )	
		<b>NEAR EAST</b>
		It was spread by two temporally distinct migratory episodes, the most recent one probably associated with the diffusion of Arab people who, mainly from the 7th century A.D., expanded to northern Africa. The first migration, probably in Neolithic times, brought J-M267 to Ethiopia and Europe. The lineage shows its highest frequencies in the Middle East, North Africa, and Ethiopia ( <a href="#">Semino et al., 2004</a> )
<i>J1-M267</i>	~24.000 years ( <a href="#">Semino et al., 2004</a> )	
		<b>NEAR EAST</b>
		Associated with the spread of agriculture, especially in the European Context ( <a href="#">Semino et al., 2004</a> )
<i>J2-M172</i>	~18.500 years ( <a href="#">Semino et al., 2004</a> )	
		<b>NEAR EAST</b>
		Spread to Europe with the Neolithic farmers from the Levant ( <a href="#">Myres et al., 2011</a> )
<i>R1b1a2-M269</i>	~11.000 years ( <a href="#">Myres et al., 2011</a> )	
		<b>INDUS VALLEY</b>
		Have high frequency in South Asia and Eastern Europe. Consistent with its wide geographic spread, the coalescent time estimates correlate with the timing of the recession of the Last Glacial Maximum and predate the upper bound of the age estimate of the Indo-European language tree ( <a href="#">Underhill et al., 2010</a> )
<i>R1a1a-M198</i>	~15.000 years ( <a href="#">Underhill et al., 2010</a> )	
		<b>NEAR EAST</b>
		This rare and informative haplogroup has a complex history of dispersal within the Near East and from the Near East to Europe and sub-Saharan Africa. The presence of different subclades of T chromosomes in Europe may be explained by both the spread of Neolithic farmers and the later
<i>T-M184</i>	~30.000 years ( <a href="#">Mendez et al., 2011</a> )	

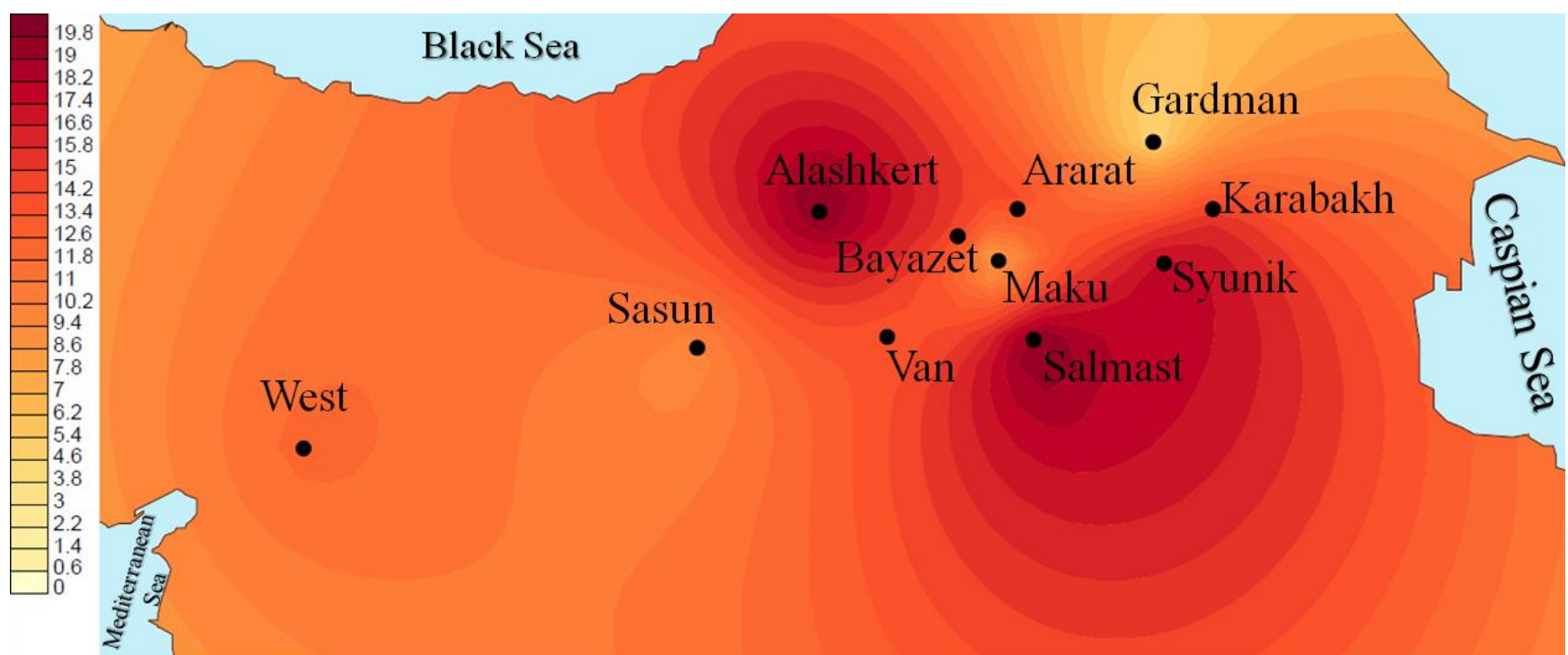
dispersal of Jews from the Near

The Armenian paternal genetic pool displays immense diversity of lineages, indicating a big number of founding fathers of the population.

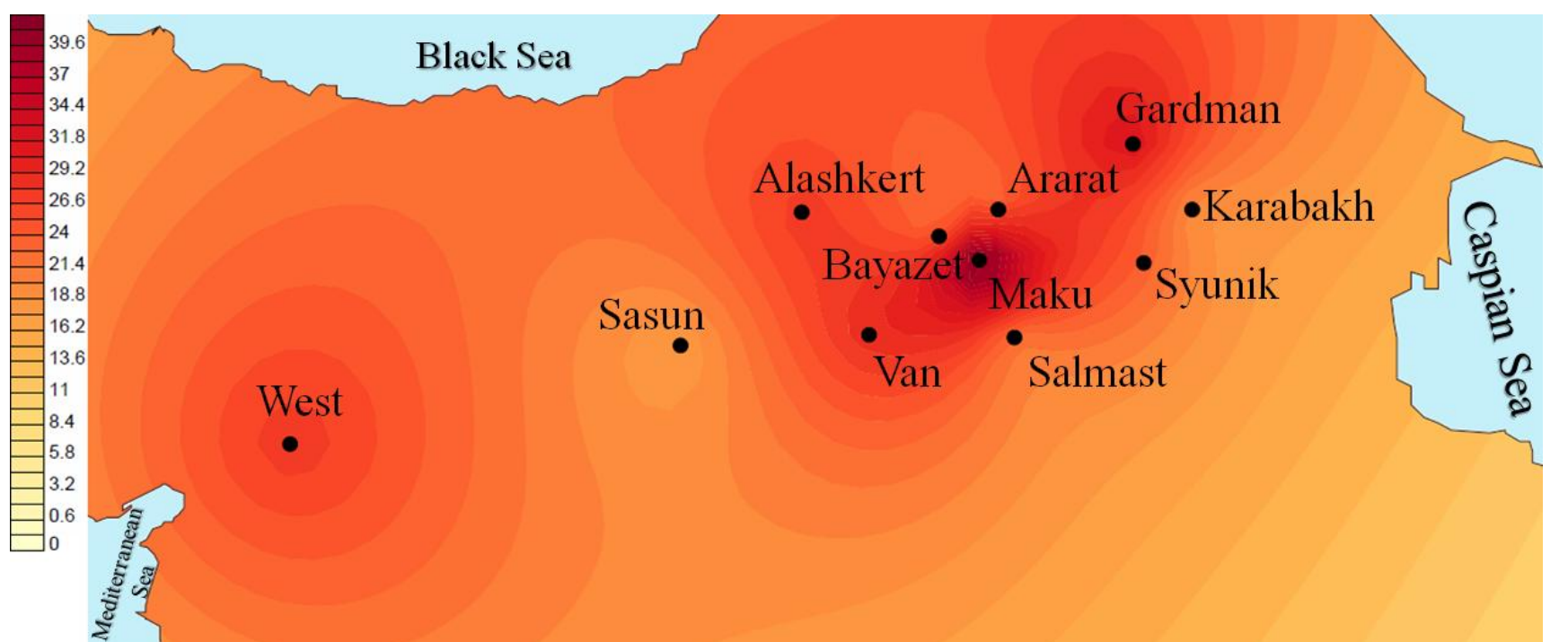
## GEOGRAPHIC DISTRIBUTION (%) OF MAIN PATERNAL LINEAGES



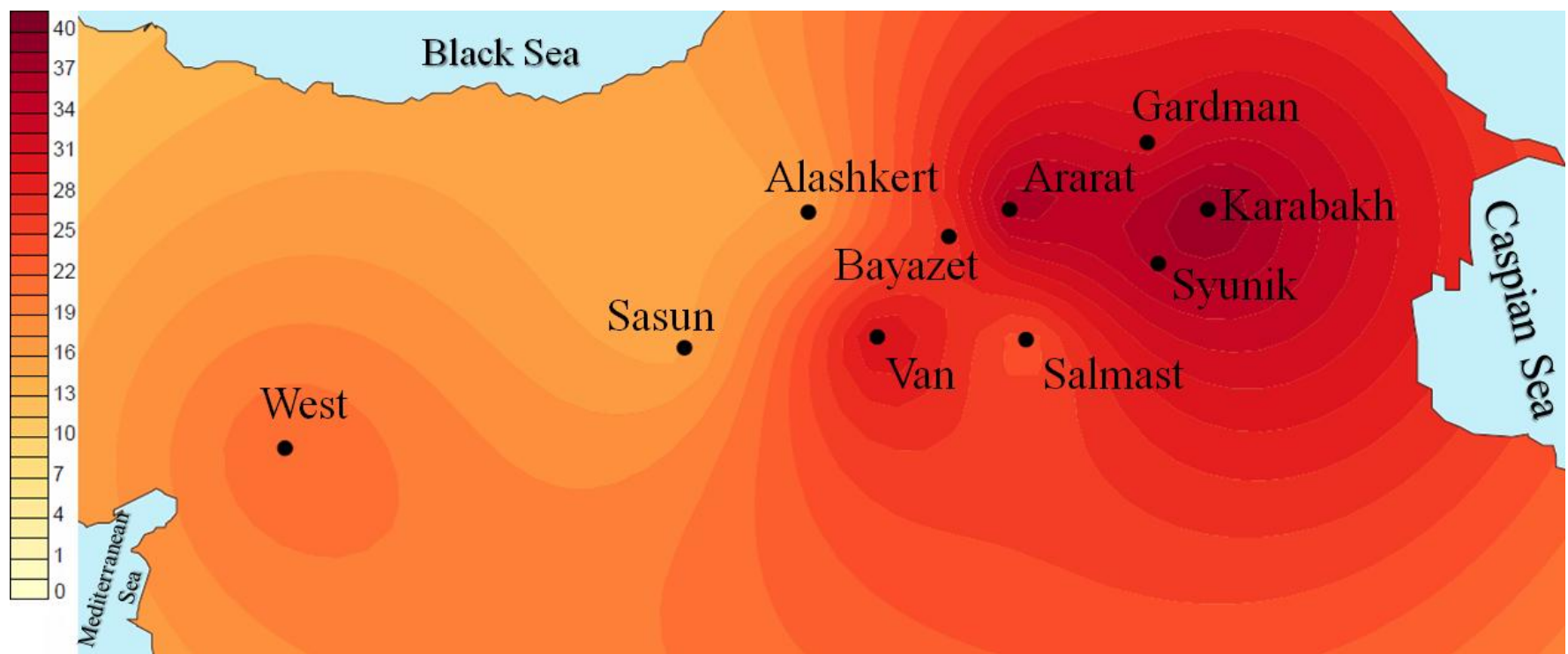
HAPLOGROUP G-M201



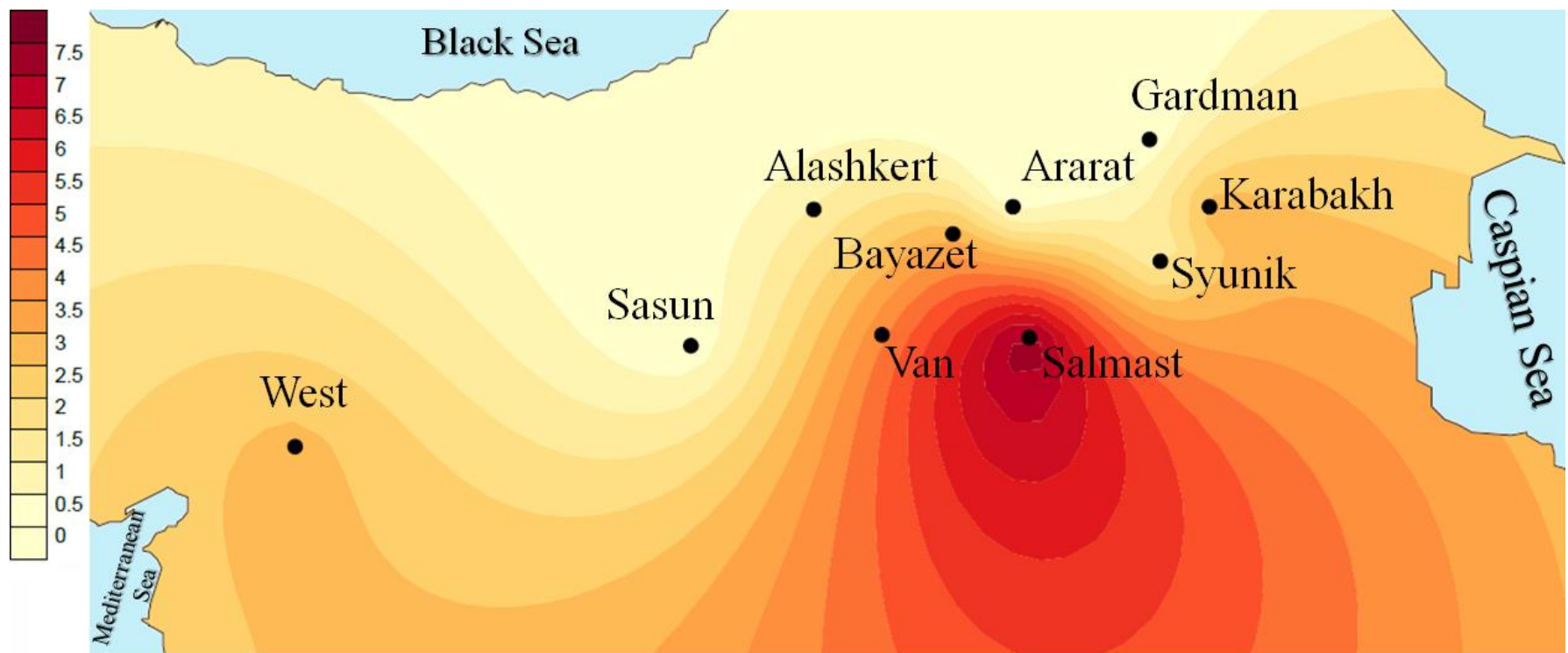
HAPLOGROUP J1-M267



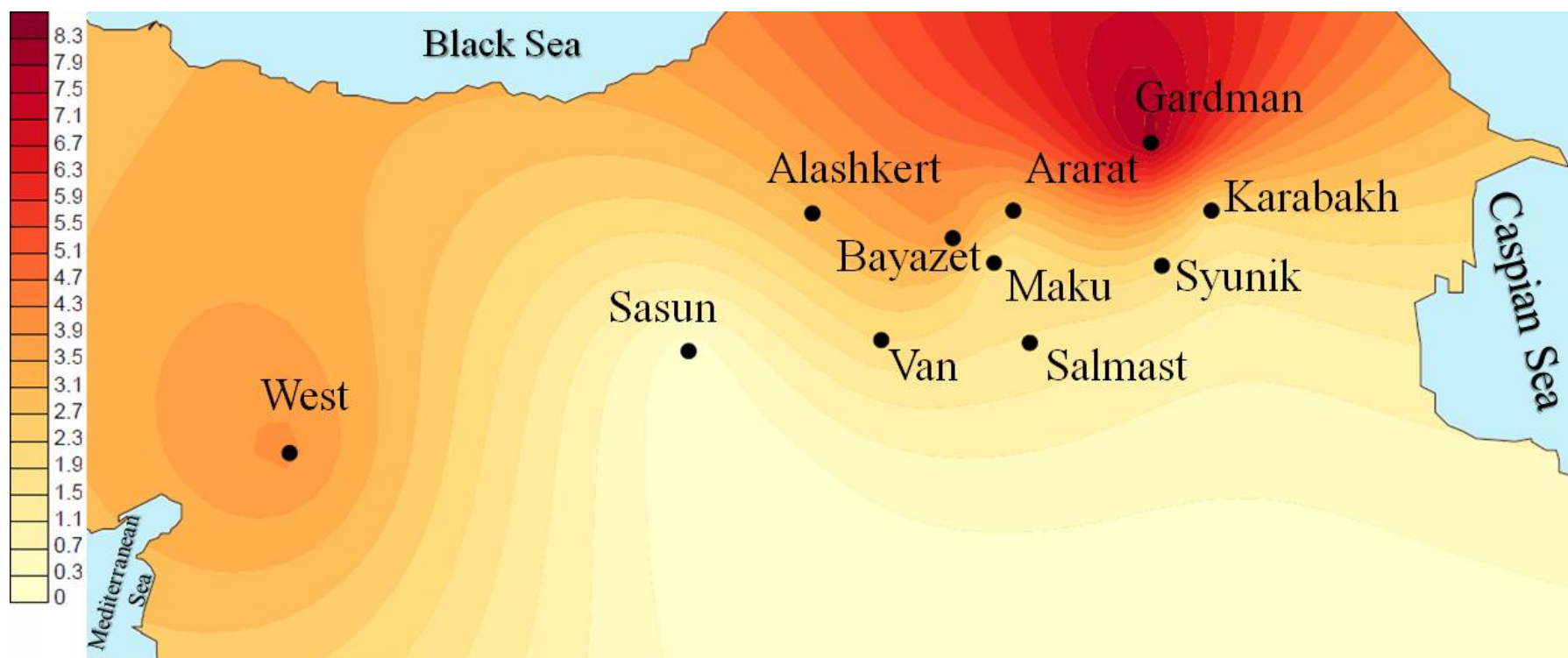
HAPLOGROUP J2-M172



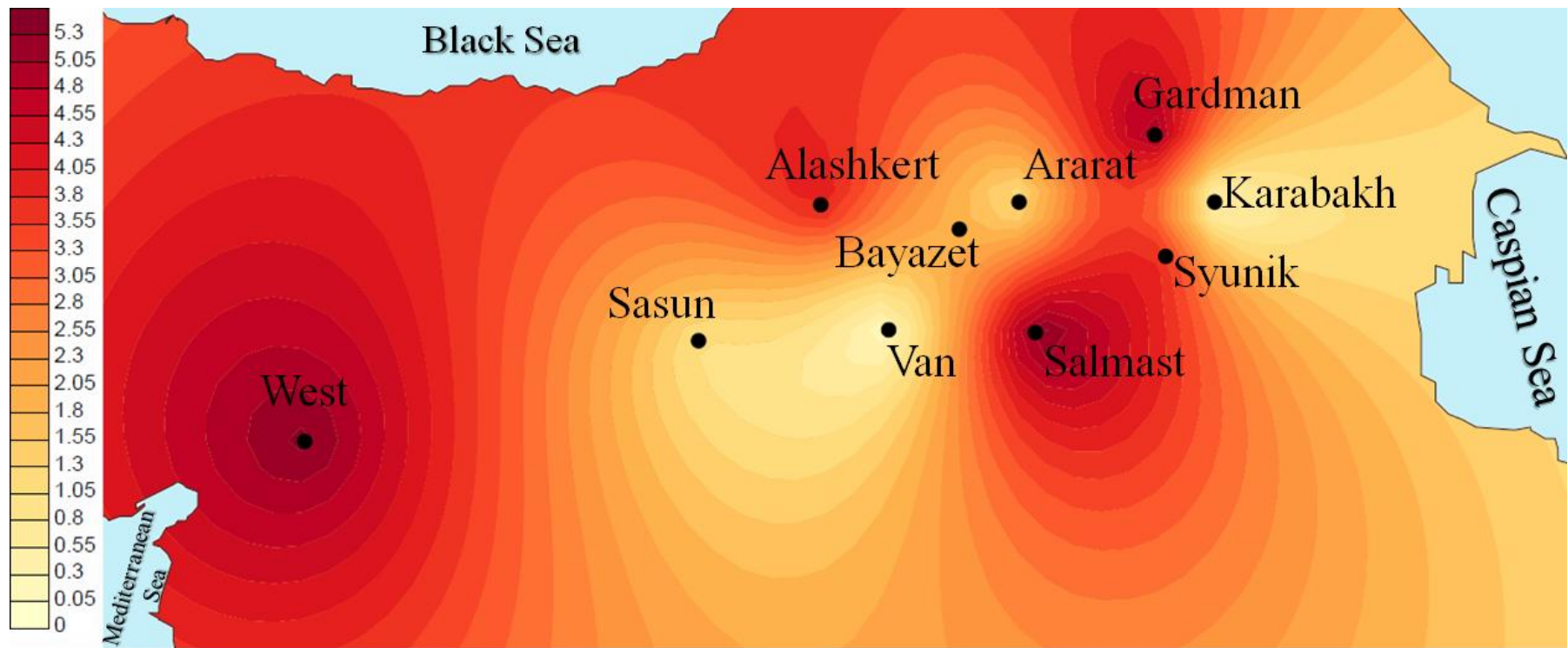
HAPLOGROUP R1b1a2-M269



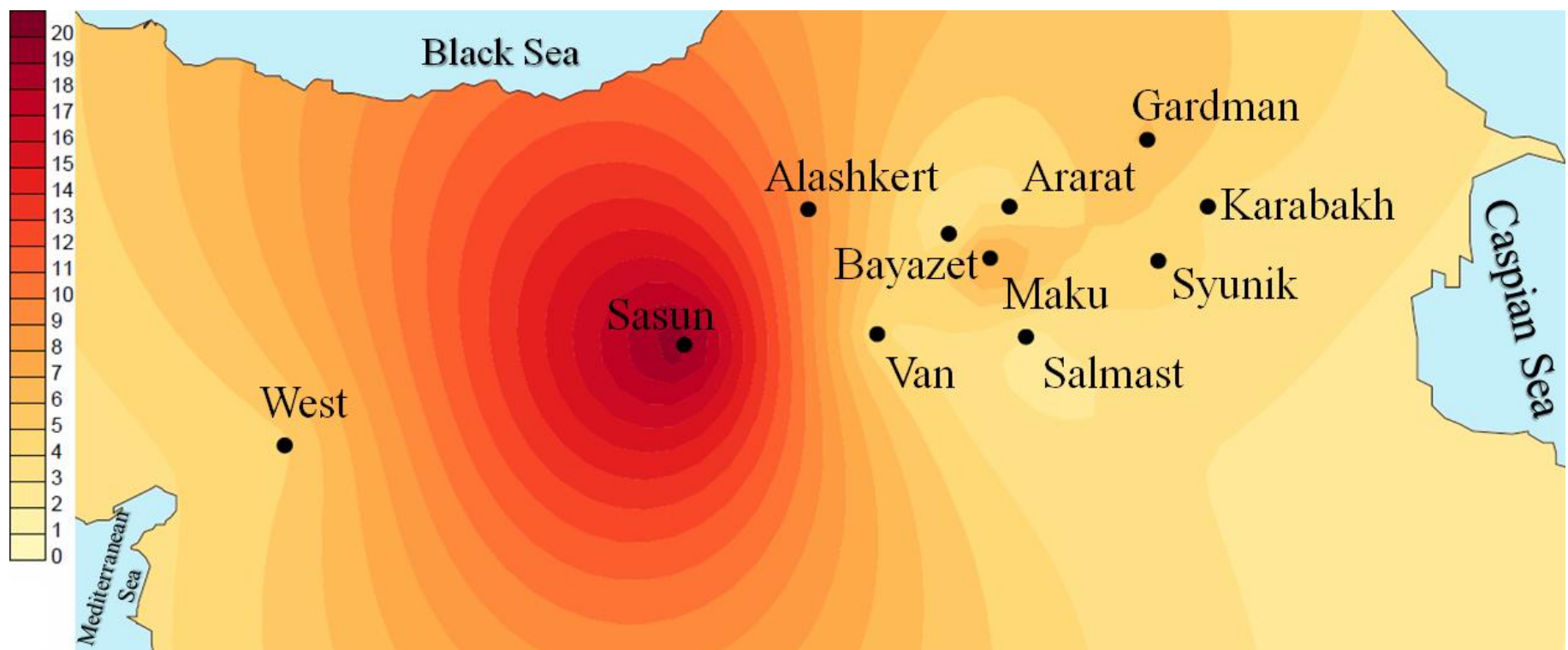
HAPLOGROUP E1b1b1a1-M78



HAPLOGROUP I-M170



HAPLOGROUP R1a1a-M198

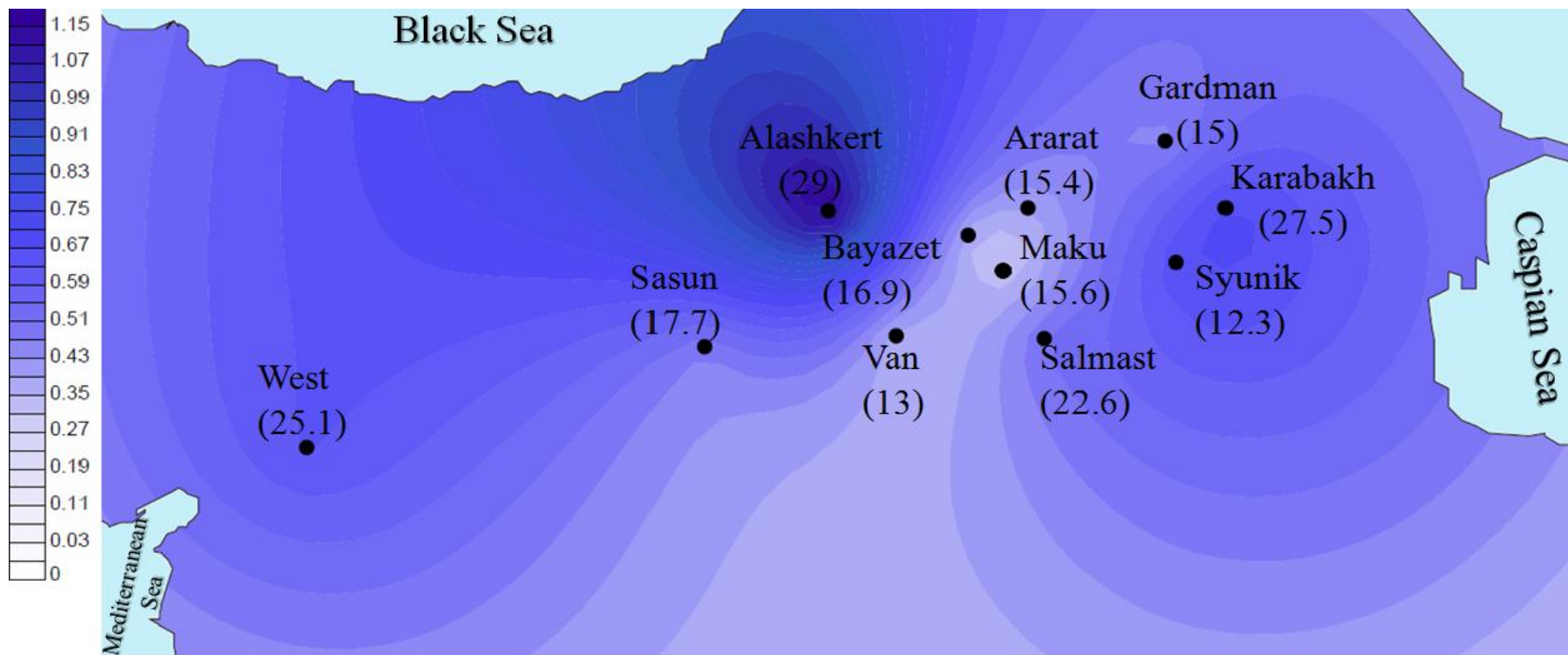


HAPLOGROUP T-M184

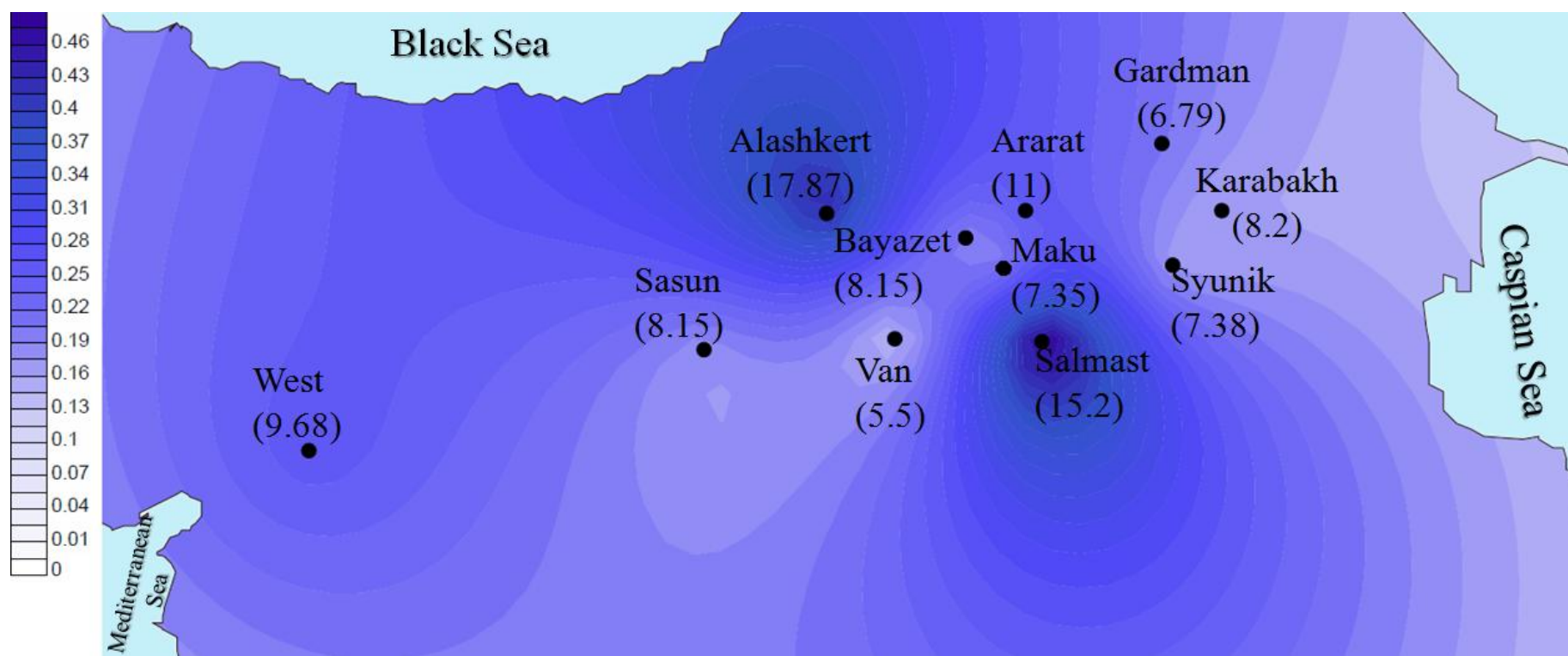
The Armenian paternal gene pool displays immense diversity of lineages, indicating a large number of founding fathers for the population. The vast majority of Armenian Y chromosomes belong to the lineages originated and expanded during or following the Neolithic.

Given that the Last Glacial Maximum event in the Armenian plateau occurred a few millennia before the Neolithic era, there population of the Highland was achieved mainly by the arrival of farmers from the Fertile Crescent.

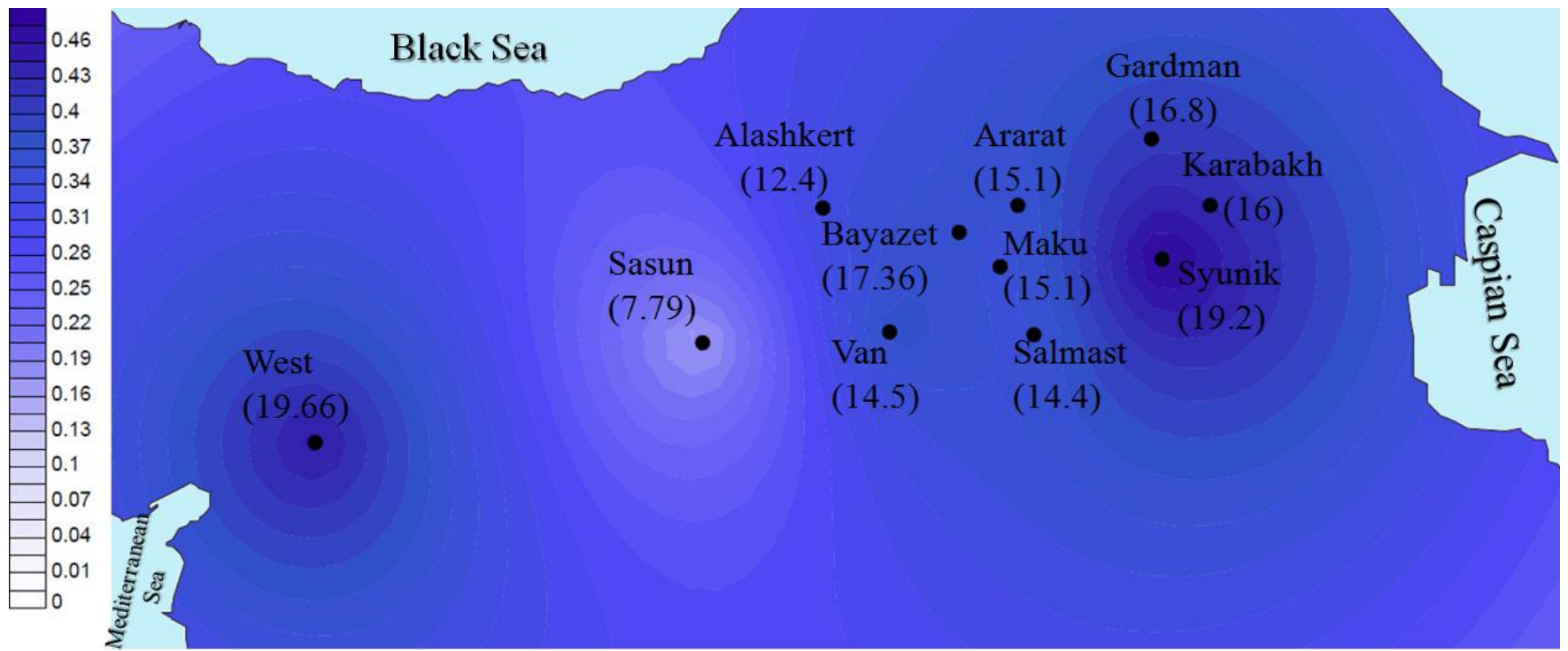
## ESTIMATED AGES (KILOYEARS) OF OCCURRENCE OF MAIN PATERNAL LINEAGES



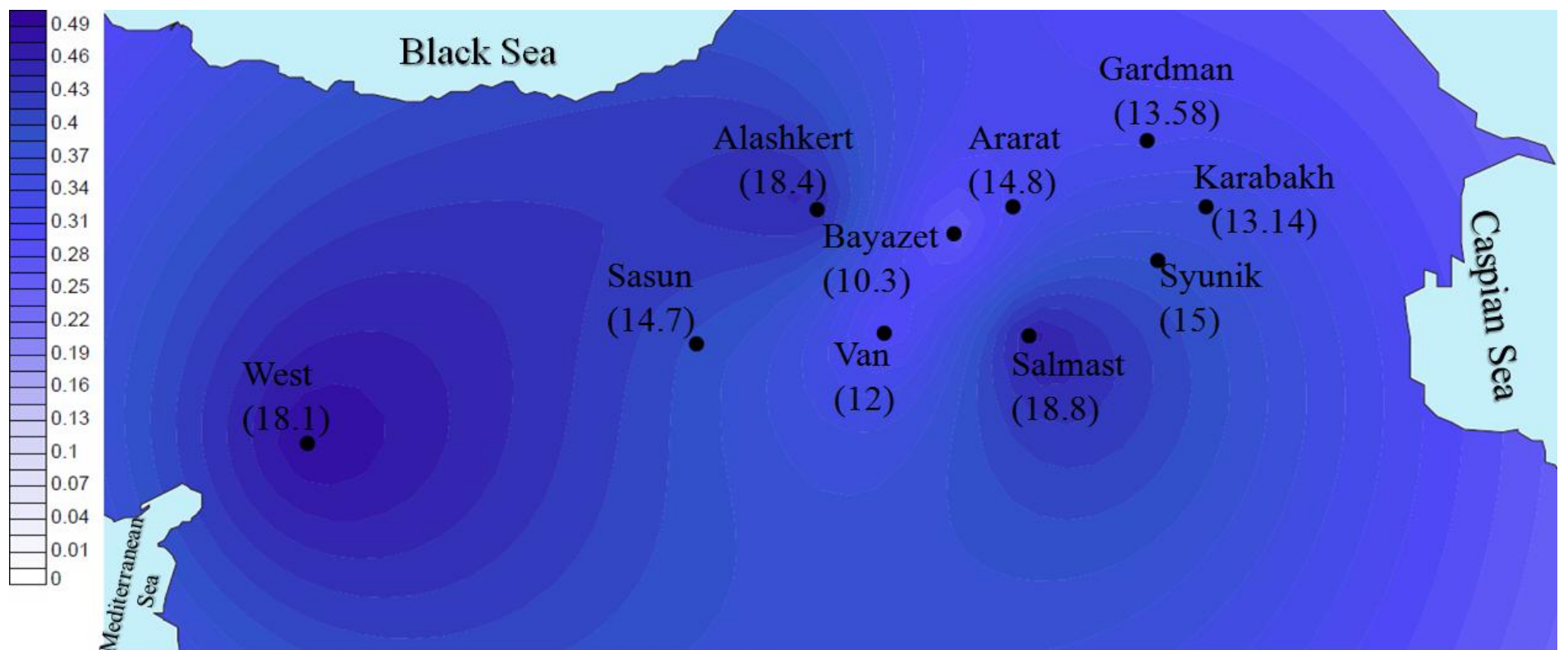
HAPLOGROUP G-M201



HAPLOGROUP J1-M267



HAPLOGROUP J2-M172



HAPLOGROUP R1b1a2-M269

## LACK OF EXTERNAL GENETIC TRACES IN THE ARMENIAN GENE POOL



## GEOGRAPHIC DISTRIBUTION (%) OF Y-CHROMOSOMAL HAPLOGROUPS OF CENTRAL ASIAN ORIGIN

No appreciable traces of genetic influence or distant input to the Armenian gene pool have been found despite frequent foreign invasions (*Hovhannisyan et al., 2014; Hellenthal et al., 2014*).

Of the primary reasons that have impeded genetic contact of Armenians with foreigners, the highland geography, early adoption of Christianity, and the formation of a strong ethnic and cultural identity can be considered the most likely.

Moreover, not only has there been insignificant admixture into the Armenian population within the last millennium, but recent evidence specifically points to a lack of genetic contribution from external sources within the last 3000 years (*Hellenthal et al., 2014*).