

# **Missing Links in Paternal Haplogroup J1-M267. Filling in the J1-M267 Phylogenetic Gap. Two Mesolithic Clades of Human Y chromosome haplogroup J1-M267: J1-FGC6064 and J1-ZS6599.**

Preprint - 25th/September/2021

Version 1.0

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## **Abstract:**

Y chromosome haplogroup J1-M267 has been investigated by many authors in several recent articles and studies, but some important basal branches have not been included or are unknown in previous articles. We are going to investigate the Northern Middle Eastern phylogenetic structure, the spatial and ethnic locations of Human Y chromosome haplogroup J1>M267>FGC6064 and J1>M267>ZS6599 strategic branches for the dispersion of the J1 haplogroup. We study high-coverage whole Y chromosome sequences and results of genotyped specific samples of basal branches of haplogroup J1>M267. Here we are going to add, incorporate and investigate two important phylogenetic basal branches for the entire phylogenetic organization, location, demographic history, development and geography of J1-M267 haplogroup: J1> M267> Z2215> Z2217> L620> FGC6064 and J1> M267> Z2215> Z2217> L620> PF4816> ZS6599. The genotyped samples showed deeply rooted nodes and genetic bifurcations probably related to the existence of an ancient Mesolithic and Neolithic population with an ancient and rich J1-L620 basal diversity of this haplogroup in a mating complex in Northern Middle East and Iran since 15000 years before present (ybp).

**Keywords:** Y Chromosome. Demographic history. Haplogroup Y-DNA J1-M267. Phylogenetic tree. J1-FGC6064 and J1-ZS6599.

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## Introduction

The structure of some crucial basal J1 branches has been previously unknown in recent Y-DNA J1 articles. “Haplogroup J1-M267 probably evolved in the region encompassing northeastern Syria, southeastern Turkey, and northwestern Iran<sup>2</sup>” (Sahakyan et al. 2021) but this process has not been more detailed or categorized in function of some missing strategic J1 branches. Ancestry related to ancient Iranians in all Middle Easterners was potentially introduced via Y chromosome haplogroup J1<sup>3</sup> (Almarri et al. 2021). It's not possible to understand the complete evolution of derived J1 branches in West Asia, Northern Africa and Europe without a complete Mesolithic phylogenetic tree. We are going to reveal and discuss some new Y-DNA J1 tree nodes related to the following branches: J1> M267> Z2215> Z2217> L620> FGC6064 and J1> M267> Z2215> Z2217> L620> PF4816> ZS6599.

Data and SNPs are also available at the ISOGG YBrowse database (International Society of Genetic Genealogy human Y-chromosome Browser<sup>4</sup> and YFull J1 Project and YFull tree<sup>5</sup>):

Y-DNA J1-L620 was formed around 18300 ybp with a block of SNPs going to around 14900 ybp with two new posterior divisions: J1-L620>FGC6064 and J1-L620>PF4816. J1-L620>FGC6064 is almost immediately subdivided in J1-L620>FGC6064>FGC6020 and J1-L620>FGC6064>ZS7134 formed circa 14000 ybp. FGC6020 is divided in FGC6018 and ZS4118 formed around 8000 ybp. ZS7134 is divided in Y177646 and Y48949 formed around 13000 ybp. J-PF4816 also formed 14900 ybp is almost immediately subdivided in J1-L620>PF4816>ZS6599 and J1-L620>PF4816>L136 formed circa 13900 ybp. J1-L620>PF4816>ZS6599 is subdivided in

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<sup>2</sup> Sahakyan, H., Margaryan, A., Saag, L. et al. Origin and diffusion of human Y chromosome haplogroup J1-M267. *Sci Rep* 11, 6659 (2021).  
<https://doi.org/10.1038/s41598-021-85883-2>

<sup>3</sup> Almarri et al., 2021, The genomic history of the Middle East. *Cell* 184, 4612–4625 September 2, 2021 <sup>a</sup> 2021 The Author(s). Published by Elsevier Inc.  
<https://doi.org/10.1016/j.cell.2021.07.013>

<sup>4</sup> ISOGG YBrowse database (International Society of Genetic Genealogy human Y-chromosome Browser, [ybrowse.org/gb2/gbrowse/chrY](http://ybrowse.org/gb2/gbrowse/chrY))

<sup>5</sup> <https://www.yfull.com/tree/J1/> YFull YTree v9.04.00 (September 2021).

J1-L620>PF4816>ZS6599>ZS6638 and another branch formed around 12900 ybp. They are mainly located in Iranian, Armenian and Kurdish areas or in close areas like the Persian Gulf and only a few clusters are in more distant places, so they represented or were part of a very ancient Iranian-like population in those regions with bushy and diverse J1-L620 branches. Another characteristic of both branches is the dimension of the frontier, they are J1 frontier branches in relation to languages, ethnicities and religions for a long time.

## Results

We have a database of Y-DNA J1 results from the following Projects: FTDNA J1-M365 Project, now part of the J1-FGC6064 clade, YFULL J1 Project and other public Projects like FTDNA J-M267. We also investigated STR Projects like Y-STR Haplotype Reference Database (YHRD) and former Projects like The Sorenson Molecular Genealogy Foundation (SMGF) and other pioneer articles. We observed the presence of J1>M267>FGC6064>M365 in the Gilaki and Mazandarani populations of the South Caspian region of Iran, and a distribution in Iranian populations<sup>6</sup>.

The next-generation high-coverage investigation of more than 30 samples of J1-FGC6064 and J1-ZS6599, downstream of J1-L620, revealed the importance of both branches as significant and strategic intermediaries and links in the chain to reconstruct the spatial trail and the development of other downstream J1-L136 branches, like J1-P58 and J1-ZS4393, other branches that spreaded to the South in the Levant, Arabia and Northeast Africa, while the studied J1-FGC6064 and J1-ZS6599 are mostly present in the North and Northwest Zagros, in Northern Iran, Southern Caspian Sea, Eastern Anatolia, Northwest Iraq or in the Northern Persian Gulf with almost no occurrences in the Eastern Mediterranean regions or in Central or Western Arabia, in a clear spatial phylogenetic frontier of difference, what is an indicative of the origin of the most basal J1-L620 branches before the division of

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<sup>6</sup> STR analysis and modals in “Western European J1-M365 position in the J1 haplogroup Y chromosome phylogenetic tree”. Ricardo Costa de Oliveira. Universidade Federal do Paraná. Version January 2014.

Southern J1-P58 expansion in the Bronze Age. In linguistic terms J1-FGC6064 and J1-ZS6599 are usually more related to Indo-European languages than to Afro-Asiatic ones, so we can observe the prevalence of Iranian and not Semitic languages in the same phylogenetic division and spatial frontier.

The first reference associated with a J1-FGC6064 downstream branch was M365, a Y-chromosome single-nucleotide polymorphism (SNP). M365 was previously classified as J1b by the International Society of Genetic Genealogy (ISOGG - 2008) and in Karafet et al, New Binary Polymorphisms Reshape and Increase Resolution of the Human Y-Chromosomal Haplogroup Tree<sup>7</sup> (Karafet, 2008). M365 was first reported in a 2004 article (Cinnioglu, 2004)<sup>8</sup>. M365 was found in Eastern Anatolia (Semino et al. 2004), observed J-M365 in two Turks and one Georgian<sup>9</sup>.

M365 is recurrent in several other haplogroups and even J1 branches as we can observe in some articles and FTDNA projects.

In 2009 Sérgio Tofanelli et al. wrote an article about “J1-M267 Y lineage marks climate-driven pre-historical human displacements” and they found recurrent types of M365 former J1b in some Qatari samples<sup>10</sup>. The same mistake or confusion was made in Al-Zahery et al. “In search of the genetic footprints of Sumerians: a survey of Y-chromosome and mtDNA variation in the Marsh Arabs of Iraq” when they associated M365

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<sup>7</sup> Karafet TM, Mendez FL, Meilerman MB, Underhill PA, Zegura SL, Hammer MF. New binary polymorphisms reshape and increase resolution of the human Y chromosomal haplogroup tree. *Genome Res.* 2008 May;18(5):830-8. doi: 10.1101/gr.7172008. Epub 2008 Apr 2. PMID: 18385274; PMCID: PMC2336805.

<sup>8</sup> *Hum Genet* (2004) 114 : 127–148 DOI 10.1007/s00439-003-1031-4 Excavating Y-chromosome haplotype strata in Anatolia Cengiz Cinnioglu · Roy King · Toomas Kivisild · Ersi Kalfoglu · Sevil Atasoy · Gianpiero L. Cavalleri · Anita S. Lillie · Charles C. Roseman · Alice A. Lin · Kristina Prince · Peter J. Oefner · Peidong Shen · Ornella Semino · L. Luca Cavalli-Sforza · Peter A. Underhill

<sup>9</sup> *Am J Hum Genet.* 2004 May; 74(5): 1023–1034. Published online 2004 April 6. Origin, Diffusion, and Differentiation of Y-Chromosome Haplogroups E and J: Inferences on the Neolithization of Europe and Later Migratory Events in the Mediterranean Area.

<sup>10</sup> Tofanelli S, Ferri G, Bulayeva K, et al. J1-M267 Y lineage marks climate-driven pre-historical human displacements. *Eur J Hum Genet.* 2009;17(11):1520-1524. doi:10.1038/ejhg.2009.58.

downstream of PAGE08/P58<sup>11</sup>. Only next generation high coverage could correctly fix and solve the insertion of M365 in different J1 branches and chain block the correct trail of J1 SNPs.

One Brazilian Portuguese was the first to discover FGC6064 branch with 188 new SNPs, from FGC5987 to FGC6175 <sup>12</sup>. Now we know the first discovered M365 is in the block of SNPs J-FGC6018 BY33232 BY82032 FGC5989 FGC5991 FGC5997 FGC6000 FGC6002 FGC6004 FGC6007 FGC6009 FGC6010 FGC6011 FGC6013 FGC6014 FGC6017 FGC6019 FGC6023 FGC6033 FGC6038 FGC6042 FGC6060 FGC6061 FGC6065 FGC6067 FGC6071 FGC6073 FGC6079 FGC6081 FGC6087 FGC6088 FGC6092 FGC6106 FGC6119 FGC6120 FGC6121 FGC6123 FGC6124 FGC6133 FGC6137 FGC6140 FGC6143 FGC6146 FGC6149 FGC6151 FGC6158 FGC6164 FGC6165 FGC6172 FGC6173 FGC8029 FT423860 FT423861 FT423896 FT423897 FT423898 Y19466.

As a member of a small J1 clade that reached the end of Atlantic Eurasia in Portugal we know a lot about the dynamics of frontiers. A Portuguese cluster was also found with several nodes in Northern Portugal during the Christian Reconquista matching a Northern Iranian, last known ancestor shared with a sample from Mazandaran-Iran, with a common ancestor around 2400 ybp and branching in Northern Portugal around 1500 ybp in YFull tree.

The shared Portuguese-Iranian SNPs - J-FGC6024 BY33225 BY46007 FGC5990 FGC5992 FGC6025 FGC6032 FGC6039 FGC6040 FGC6041 FGC6047 FGC6056 FGC6066 FGC6075 FGC6077 FGC6094 FGC6097 FGC6107 FGC6109 FGC6128 FGC6132 FGC6134 FGC6139 FGC6147 FGC6157 FGC6166 FGC6171 FGC83651 FGC83652 Y19467 Y19468

The Portuguese lineage SNPs FGC6035 AM00043 BY40153 BY40154 FGC6026 FGC6083 FGC6085 FGC6095 FGC6111 FGC6168 FGC6175

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<sup>11</sup> Al-Zahery, N., Pala, M., Battaglia, V. *et al.* In search of the genetic footprints of Sumerians: a survey of Y-chromosome and mtDNA variation in the Marsh Arabs of Iraq. *BMC Evol Biol* 11, 288 (2011). <https://doi.org/10.1186/1471-2148-11-288>

<sup>12</sup> Western European J1-M365 position in the J1 haplogroup Y chromosome phylogenetic tree. Ricardo Costa de Oliveira. Universidade Federal do Paraná. Version January 2014. The social and religious origin of the individual is Catholic, Old Christian - Cristão Velho, in Colonial Brazil from the Minho, Portugal.

Licinio Manco et al. The Eastern side of the Westernmost Europeans: Insights from subclades within Y-chromosome haplogroup J-M304. *American Journal of Human Biology*. Vol. 30 ISSN: 1042-0533 Ed.: Willey-Blackwell

FGC8031. FTDNA J1-M365 has the first Portuguese, Azorean SNP from Ilha do Pico, BY82400, under FGC6035.

In West Asians J1-FGC6064 we have Iranians from Mazandaran, one Kurd from Erbil-Iraq, another Kakai from Kirkuk-Iraq, both from ancient Iranian speaking communities in Iraq, we have Armenians samples from Armenia and one ethnic Armenian from New Julfa, Isfahan - Iran, so the clade is interesting to track ancient Indo-European and Iranian speaking populations in the Bronze Age and Iron Age in ancient lineages present in the region. A new Armenian Bronze Age branch of the lineage. He may have belonged to the Trialeti-Vanadzor [Kirovakan] culture or the Urmia ware and before to the Trialetian Mesolithic and Caspian Mesolithic culture from that region. He could also be another testimony mark of the separation of Armenian and Iranian branches/languages in time and space in the same ancient ancestral lineage. A link between the CHG/Iran continuum. The Armenian and the English now are classified in FTDNA as J-ZS11946 and they are sharing the new SNPs: BY84695 FT123093 FT123108 FT123331 FT123693 FT123694 FTB30774 FTB30795 Y286544 Y73555 ZS11939 ZS11943 ZS11944 ZS11947 ZS11954 ZS11955 ZS11961 ZS11969 ZS11970 ZS11971 ZS11975 ZS11976. In YFull<sup>13</sup>. We can observe one fact, the creation of new phylogenetic nodes in the core and extremely competitive areas of Eastern Anatolia and NW Iran is extremely difficult because it's an ancient populous area with an established settled population with a good continuity since the Mesolithic and no substantial changes happened because the proportions of haplogroups in the Bronze Age and Iron Ages are more or less the same since the Early Bronze Age. People could move from the Northern Caspian Sea to Mongolia and Portugal changing everything in the way but in the Southern Caspian Sea the continuity has been extremely fixed, with few alterations. I keep the idea that J1-FGC 6064 is more bushy in ancient Iranian populations from NW Iran and the Southern Caspian Sea, what we will be able to visualize when we get more local Iranian high-coverage samples in a good quantity. The only Iranian population that reached the Western Atlantic shores in a significant movement with Alanic warriors, named kings and

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<sup>13</sup> <https://www.yfull.com/tree/J-FGC6031/>

demographic impact were the Alans in the fall of the Roman Empire, so somehow they jumped from the Caspian Sea to Roman Gallaecia, Lusitania and Northern Portugal<sup>14</sup>, where we can find several Medieval nodes of this Iranian branch during the Portuguese Christian Reconquista and the Portuguese seaborne Empire.

In the next downstream node and branch of J1-L620>PF4816>ZS6599 we can find in YFull and FTDNA trees individuals from Armenia, Kuwait, Russia Turkey, Oman, Yemen and from distant places like China, Spain, Lybia. Individuals from this branch can also be found in the Baloch population of Pakistan J1a2 > ZS6591<sup>15</sup>.

New samples and clusters from those two clades J1-FGC6064 and J1-ZS6599 (and others) can help to build a molecular clock of the growth, separation and distribution of some specific Iranian languages from the region.

## Discussion

Small basal branches can change the phylogenetic tree just like the original case of Y-DNA A00<sup>16</sup> (Mendez et al. 2013) or they can reveal

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<sup>14</sup> HYDATIUS (c. 400 - c. 469 A.D.). Chronicon · Fasti · Christian Latin · The Latin Library · The Classics Page.XVII. Subversis memorata plagarum grassatione Hispaniae provinciis, barbari ad pacem ineundam, Domino miserante conversi, sorte ad inhabitandum sibi provinciarum dividunt regiones. Gallaeciam Wandali occupant et Suevi, sitam in extremitate Oceani maris occidua. Alani Lusitaniam et Carthaginiensem provincias, et Wandali cognomine Silingi Baeticam sortiuntur. Hispani per civitates et castella residui a plagis, barbarorum per provincias dominantium se subjiciunt servituti. <http://thelatinlibrary.com/hydatius.html>

<sup>15</sup> Forensic features and genetic legacy of the Baloch population of Pakistan and the Hazara population across Durand-line revealed by Y chromosomal STRs. Atif Adnan et al. <https://doi.org/10.1101/2020.11.21.392456> 2020. <https://www.biorxiv.org/content/10.1101/2020.11.21.392456v1.supplementary-material>

<sup>16</sup> Fernando L. Mendez, Thomas Krahn, Bonnie Schrack, Astrid-Maria Krahn, Krishna R. Veeramah, August E. Woerner, Forka Leypey Mathew Fomine, Neil Bradman, Mark G. Thomas, Tatiana M. Karafet, Michael F. Hammer An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree The American Journal of Human Genetics, Volume 92, Issue 4, 4 April 2013, Pages 637.

paths of expansion just like Y-DNA H2 in Neolithic Europe<sup>17</sup> (Rohrlach et al. 2021) .

The ancient Iranian population who bred and born Iranian J1-L620 on the land. L620>FGC6064 and L620>PF4816>ZS6599 are in good part basal Indo-European or Iranian with Bronze Age and Iron Age nodes, branches and diverse samples. The Iranian and Indo-European frontier separating Semitic and Afro-Asiatic spaces perpassing and close to the Zagros Mountain range in the vicinity of the modern Iraq/Iran border.

Iran is completely undersampled in terms of high-coverage Y-DNA and ancient DNA (we would need a study about the capillarity of at least 5000 samples to have a critical mass and a notion of the Y-DNA structures found there in different regions), the only information we have is related to the perception of the bushy phylogenetic ancient nodes in the tree of some haplogroups like J1 and they reveal a large Mesolithic/Neolithic/Bronze Age population that persisted and survived in the core area of that genetic cauldron. Another feature is the mobile 360° expansion to all directions. Iranian ancestry with J1 and J2 derived branches expanded to the South (Arabia) and Southwest (Levant), we know the expansion to the West (Anatolia/Mediterranean), to the East (Central Asia and Indian Subcontinent), to the North (Steppe), we can find the Iranian/Caucasian autosomal component in all directions with substantive impact transforming all demographies in the Bronze Age.

We associate the growth and ramifications of J1-FGC6064 and J1-ZS6599 with the Bølling–Allerød warming (14500-12500 ybp) in Northern Middle-East because they were successful clades branching in the Mesolithic period where not all haplogroups survived in extremely competitive and populous core areas related later to the first Neolithisation in Western Iran and Eastern Anatolia. FGC6064 and ZS6599 are the transition between J1 most basal Northern branches and the Southern J1-L136 with J1-P56 and J1-P58 expansion, something happened just before the biggest expansion, probably an accumulation

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<sup>17</sup> Rohrlach, A.B., Papac, L., Childebayeva, A. *et al.* Using Y-chromosome capture enrichment to resolve haplogroup H2 shows new evidence for a two-path Neolithic expansion to Western Europe. *Sci Rep* 11, 15005 (2021). <https://doi.org/10.1038/s41598-021-94491-z>.



of new technologies, new social, economic, cultural, technological and political organizations.

The depth of some J1-FGC6064 branches like J-Y177646 in two Armenians formed 13400 ybp and TMRCA 13400 ybp is showing early splits found in Eastern Anatolia and Armenia.

### Archaeological Basal and Indo-European J1. Ancient DNA

One individual found in Satsurbliia Cave, Western Georgia - J1-Y6313-FT33726-FT34521 (13130-13380 ybp)<sup>18</sup>

There are two ancient archaeological J1 from the North: I0211 - Karelia Man - Age Estimate: 6850-5000 BCE - Yuzhny Oleni Ostrov, Northern Russia<sup>19</sup> and Popovo2 - Age Estimate: 5500-5000 BCE - Lake Lacha, Northern Russia<sup>20</sup>. No known branches.

J1 sample found in Early Bronze Age, Afanasievo culture, Mongolia. 3.1 (Afanasievo Mongolia) - J1-Z2215-Z2217- CTS1026-Y136727 - (CTS1026>pre-Y136727/3107-2917 BC).

I6221 - Mongolia\_Chalcolithic\_1\_Afanasievo - Bayankhongor aimag, Erdenetsogt sum, Shatar chuluu kurgan 2 mtDNA U5a1+@16192<sup>21</sup> / SHT002 - SHT002.A0101 SHT002.A0101 M U5a1 J1a (J-CTS5368)<sup>22</sup> - "The Early Bronze Age Afanasievo culture in the Altai-Sayan region is genetically indistinguishable from Yamnaya, confirming an eastward

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<sup>18</sup> Jones, E., Gonzalez-Forbes, G., Connell, S. *et al.* Upper Palaeolithic genomes reveal deep roots of modern Eurasians. *Nat Commun* 6, 8912 (2015). <https://doi.org/10.1038/ncomms9912>

<sup>19</sup> Genome-wide patterns of selection in 230 ancient Eurasians" Iain Mathieson - Nature - 2015)

<sup>20</sup> The genetic prehistory of the Baltic Sea region - Alissa Mittnik - Nature - 2018.

<sup>21</sup> The Genomic Formation of Human Populations in East Asia Wang et al. bioRxiv 2020. Wang, CC., Yeh, HY., Popov, A.N. *et al.* Genomic insights into the formation of human populations in East Asia. *Nature* 591, 413–419 (2021). <https://doi.org/10.1038/s41586-021-03336-2>

<sup>22</sup> A dynamic 6,000-year genetic history of Eurasia's Eastern Steppe - Choongwon Jeong et al. bioRxiv 2020. Choongwon Jeong, Ke Wang, et al. A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe, *Cell*, Volume 183, Issue 4, 2020, Pages 890-904. e29, ISSN 0092-8674, <https://doi.org/10.1016/j.cell.2020.10.015>.

expansion across the steppe"<sup>23</sup>, so the J1 individual found in Afanasievo represented a mainstream part and component of Yamnaya-Afanasievo's stock, probably associated with the Iranian/Caucasus Ancestry (Iran-CHG).

J1 sample found in Yamnaya-Like Khvalynsk Y-DNA<sup>24</sup>.

J1 samples were found in Central Asia, The formation of human populations in South and Central Asia<sup>25</sup>:

I1784; 2201-2031 BC; Gonur; Turkmenistan; BMAC;  
J1-L620>PF4816>ZS6599>ZS4428>ZS6592

I12481; 3500-2800 BC; Geoksyur; Turkmenistan; Geoksyur\_EN;  
J1-L620>PF4816>ZS6599>ZS4428>ZS6592

I8504; 3092-2925 BC; Geoksyur; Turkmenistan; Geoksyur\_EN;  
J1-L620>PF4816>ZS6599>ZS4428>ZS6592

Gonur Tomb 2380 sample 17 (I1784): Date of 2201-2031 calBCE (3720±30 BP, Poz-83485). "Genetically male. Nicknamed the 'Tomb of the Warrior,' this was skeletally a male, 40 to 50 years old at the time of his death, flexed supine and oriented north-northwest. The neck of the man was broken, and this was the probable cause of his death. He was buried in a shaft grave on the southeast edge of the large cemetery. This very rich grave was accompanied by one bronze knife, one silver plate, one bronze vessel (diameter 16 cm and height 12 cm), one bronze mace head in the form of a horse head, one bronze mace head with four spikes, one bronze semi-cylindrical artifact near the head, one bronze leaf-shaped arrowhead near the pelvis, and one bronze plate with perforations wrapped in linen cloth near the right shin"<sup>26</sup>.

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<sup>23</sup> Allentoft, M., Sikora, M., Sjögren, KG. *et al.* Population genomics of Bronze Age Eurasia. *Nature* 522, 167–172 (2015). <https://doi.org/10.1038/nature14507>

<sup>24</sup> Dispersals and Diversification Linguistic and Archaeological Perspectives on the Early Stages of Indo-European - Ancient DNA, Mating Networks, and the Anatolian Split. By: David W. Anthony. Brill. 2019. ISBN-10: 9004414509

<sup>25</sup> Narasimhan VM, Patterson N, Moorjani P, et al. The formation of human populations in South and Central Asia. *Science*. 2019;365(6457):eaat7487. doi:10.1126/science.aat7487

<sup>26</sup> Supplementary Materials for The formation of human populations in South and Central Asia. [science.sciencemag.org/content/365/6457/aat7487/suppl/DC1](https://science.sciencemag.org/content/365/6457/aat7487/suppl/DC1)

They were related to Iranian populations<sup>27</sup>. “In discussions about possible candidates for founding the BMAC, we often come across Indo-Iranians or Aryans. For example, Sarianidi himself was convinced that they were the ones who founded Gonur”<sup>28</sup>.

J1 samples found with the Sarmatians and Alans. J1 samples identified as Sarmatians (years 200-300 AD): A80303 - J1 (Y-DNA), H1c21 (mtDNA) and A80304 - J1 (Y-DNA), K1a3 (mtDNA)<sup>29</sup>.

J1 individuals found in “Ancient DNA analysis of Early Medieval Alan populations of the North Caucasus”<sup>30</sup>. When we observe the detailed plot of this investigation we observe the Alans were matching positions with Caucasian, Iranian and Armenian individuals.

The same J1 lineage from Gonur and Geoksyur found in Eastern Kazakhstan. MMR001.A0101 Mayemer-II mound 1 7th-5th c. BCE Mayemer-II\_600\_BCE MMR001.A0101 Mayemer-II mound 1 Steppe\_Central\_Nomad\_IA Mayemer-II\_600\_BCE MMR001.out Kazakhstan -600 C4a1a4a J-M304 J1> M267> CTS12238> Z2217> L620> PF4832> ZS6599> ZS6602> ZS6592. Early Saka period Mayemer, on the left bank of the Naryn River, in the Katonkaragai district of East Kazakhstan region<sup>31</sup>.

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<sup>27</sup> Victor Sarianidi, *Margiana and Protozoroastrism* (Athens: Kapon edition, 1998) and idem, *Necropolis of Gonur* (Athens: Kapon edition, 2007).

<sup>28</sup> What Language Was Spoken by the People of the Bactria-Margiana Archaeological Complex? In: "At the Shores of the Sky" Author: Alexander Lubotsky Type: Chapter Pages: 5–11 DOI: [https://doi.org/10.1163/9789004438200\\_003](https://doi.org/10.1163/9789004438200_003)

<sup>29</sup> Афанасьев Г.Е., Вень Ш., Тун С., Ван Л., Вэй Л., Добровольская М.В., Коробов Д.С., Решетова И.К., Ли Х.. Хазарские конфедераты в бассейне Дона // *Естественнонаучные методы исследования и парадигма современной археологии*. М. 2015. С.146-153.

<sup>30</sup> Murat Dzhaubermezov et al. 27th Annual Meeting of the European Association of Archaeologists (EAA), which will be held in Kiel, Germany from 8 to 11 September 2021. Abstracts.

[https://submissions.e-a-a.org/ea2021/repository/preview.php?Abstract=2378&fbclid=IwAR0LNz291yQMhj41CoEIbtLbsAhQHBP0kQmX67XZGhfB-JByf4ol\\_vJmM2M](https://submissions.e-a-a.org/ea2021/repository/preview.php?Abstract=2378&fbclid=IwAR0LNz291yQMhj41CoEIbtLbsAhQHBP0kQmX67XZGhfB-JByf4ol_vJmM2M)

<sup>31</sup> Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians - Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians - *Science Advances* 26 Mar 2021: Vol. 7, no. 13, eabe4414 DOI: 10.1126/sciadv.abe4414

One Y-DNA J1 from Iron Age Scythian Kazakhstan. MJ-52; 798-546 BC; Aksu-Ayulu; Kazakhstan; Scythian\_IA; J1a-L620 (xL136,P58)<sup>32</sup>. So another basal J1-L620.

One J1-L620 individual found in Tell Kurdu. KRD003; 5706-5622 BC; Tell Kurdu, Turkey; Tell Kurdu\_EC/Halaf\_related; J1-L620 (xPF4816,FGC6031,Y48949). Tell Kurdu 6739 ± 23 cal BCE 5661-5630 cal BCE 5706-5622<sup>33</sup>. So one more basal J1-L620.

## Nodology and Cladistics

We observed the node density in longer branches, the most ancient and basal Northern Middle Eastern (Anatolian, Armenian, Iranian, Caucasian), J1 branches, compared to derived and recent branches of the J1 tree, like Southern (Arabic, Levantine, African) types of J1-P58, where there are more recent nodes and thus branches are typically shorter.

Selected J1 basal branches structured around 10000ybp - 8000BC and still found in living individuals (via YFull YTree v9.04.00) and some of the archaeological discoveries.

1 - J1-Y6313 - formed 18300 ybp.

1.1 - J1-Y6313-FT33726 - formed 16100 ybp.

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<sup>32</sup> Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance Mari Jarve et al. [https://www.cell.com/current-biology...822\(19\)30712-2](https://www.cell.com/current-biology...822(19)30712-2) Jarve et al., 2019, Current Biology 29, 2430–2441 July 22, 2019 <sup>a</sup> 2019 Elsevier Ltd. <https://doi.org/10.1016/j.cub.2019.06.019> MJ-52 UT-4-17 Scy\_Kaz Eastern Scythian Tooth, M3 Tooth, M3 Shetsky District, Karagandinsk Region, Kazakhstan 48.7493583 N, 73.6997028 E Aksu-Ayuly-4 Mound 3 2800-2400 BP 2535 ± 30 2748-2496 BP Steppe, eastern part of the Kazakh Upland. The mound (2.2 x 3.2 m, height 0.15 m) was partially destroyed. The rectangular grave pit (0.8 x 1.95 m, depth 0.8 m) with sloping walls was oriented from NW to SE. A male skeleton lay extended on its back on the bottom of the pit, head oriented to the NW. 1998.

<sup>33</sup> Skourtanioti E, Erdal YS, Frangipane M, Balossi Restelli F, Yener KA, Pinnock F, Matthiae P, Özbal R, Schoop UD, Guliyev F, Akhundov T, Lyonnet B, Hammer EL, Nugent SE, Burri M, Neumann GU, Penske S, Ingman T, Akar M, Shafiq R, Palumbi G, Eisenmann S, D'Andrea M, Rohrlach AB, Warinner C, Jeong C, Stockhammer PW, Haak W, Krause J. Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus. Cell. 2020 May 28;181(5):1158-1175.e28. doi: 10.1016/j.cell.2020.04.044. PMID: 32470401.

1.1.1- J1-Y6313-FT33726-FT265222 - formed 16100 ybp.

1.1.2- J1-Y6313-FT33726-FT34521 - formed 16100 ybp.

1.1.2 (Satsurbliia) - J1-Y6313-FT33726-FT34521 (13130-13380 ybp).

1.2 - J1-Y6313-Y6304 - formed 16100 ybp.

1.2.1- J1-Y6313-Y6304-F2306 - formed 11500 ybp.

1.2.2- J1-Y6313-Y6304-Y19093 - formed 11500 ybp.

2 - J1-Z2215 - formed 18300 ybp.

2.1 - J1-Z2215-Y29696 - formed 18300 ybp.

2.1.1 - J1-Z2215-Y29696-PF7261 - formed 12600 ybp.

2.1.1.1- J1-Z2215-Y29696-PF7261-ZS3290 - formed 11600 ybp.

2.1.1.2- J1-Z2215-Y29696-PF7261-PH128 - formed 11600 ybp.

3-J1-Z2215-Z2217-CTS1026- formed 18300 ybp.

3.1-J1-Z2215-Z2217-CTS1026-Y136727 - formed 17400 ybp.

3.1 (Afanasiovo Mongolia) - J1-Z2215-Z2217- CTS1026-Y136727 - (CTS1026>pre-Y136727/3107-2917 BC).

3.2- J1-Z2215-Z2217-CTS1026-Z1828 - formed 17400 ybp.

4 - J1-Z2215-Z2217-L620-FGC6064 - formed 14900 ybp.

4.1 - J1-Z2215-Z2217-L620-FGC6064-FGC6031 - formed 14900 ybp.

4.2 - J1-Z2215-Z2217-L620-FGC6064-Y59693 - formed 14900 ybp.

4.2.1 - J1-Z2215-Z2217-L620-FGC6064-Y59693-Y48949 - formed 13400 ybp.

4.2.2 - J1-Z2215-Z2217-L620-FGC6064-Y59693-Y177646 - formed 13400 ybp.

5 - J1-Z2215-Z2217-L620- PF4816 - formed 14900 ybp.

5.1 -J1-Z2215-Z2217-L620- PF4816-ZS6599- formed 13900 ybp.

5.1.1- J1-Z2215-Z2217-L620- PF4816-ZS6599-ZS6638 - formed 12900 ybp.

5.1.1.1-J1-Z2215-Z2217-L620- PF4816-ZS6599-ZS6638-Y169874 - formed 12900 ybp.

5.1.1.1.1-J1-Z2215-Z2217-L620- PF4816-ZS6599- ZS6638- Y169874- FT33771 - formed 10700 ybp.

5.1.1.1.2-J1-Z2215-Z2217-L620- PF4816-ZS6599-ZS6638-Y169874-ZS6592 - formed 10700 ybp.

5.1.1.1.2 (Gonur, Turkmenistan)-J1- Z2215-Z2217-L620- PF4816-ZS6599-ZS6638- Y169874-ZS6592. BMAC Gonur Tomb of the Warrior(2201-2031 calBCE) and Geoksyur.

6 - J1-Z2215-Z2217-L620- PF4816-L136 - formed 13900 ybp, TMRCA 11400 ybp.

6.1 - J1-Z2215-Z2217-L620- PF4816-L136-ZS4393 - formed 11400 ybp.

6.1.1- J1-Z2215-Z2217-L620- PF4816-L136-ZS4393-ZS4416 - formed 11100 ybp.

6.1.2 - J1-Z2215-Z2217-L620- PF4816-L136-ZS4393-P56 - formed 11100 ybp.

6.2 - J1-Z2215-Z2217-L620- PF4816-L136-P58 - formed 11400 ybp

6.2.1 - J1-Z2215-Z2217-L620- PF4816-L136-P58-ZS12519 - formed 9100 ybp.

6.2.2 - J1-Z2215-Z2217-L620- PF4816-L136-P58-CTS9721- formed 9100 ybp.

We have more than 30 J1 basal nodes before J1-L136 and a big diversity of nodes in J1-FGC6064 and J1-ZS6599, more than 10 nodes, so they were and are important intermediaries in the complete J1 history.

We need the complete investigation of J1 history and we need to understand the social, demographic, linguistic and genealogical structures. Of course J1-FGC6064 and J1-ZS6599 are essential links in the J1-L620 formation and expansion because they are related to the same origin, location and dissemination of posterior J1-L620 branches. They were not Western Anatolians or Levantine Natufians but they were related to the expansion of Neolithic Iranian farmers and pastoralists in terms of ancient somatic variants. Living lineages have and had different genetic admixtures, ethnicities, languages, polities, religions, frontiers and conflicts and they were completely different since then.

The last minor branch in J1 downstream of J-P58 is J-ZS12473 with only four individuals in FTDNA database, what is another element in the Early Bronze Age dispersion of the J1 phylogenetic structure, because J1-P58-CTS9721 is a relatively recent and derived branch in relation to the ancient and most basal J1 branches, but J1-P58 had for some reasons a very big Southern expansion in the Levant and in Arabia. We can observe that J1-Z2215-Z2217-L620-FGC6064, the 4th node and J1-Z2215-Z2217-L620-PF4816-ZS6599 in the 5th nodes are Northern Middle Eastern or Iranian oriented and they were a testimony of the

previous location of J1-L620 before the Southerner expansion towards the Levant and Arabia associated only then with Semitic languages, while FGC6064 and ZS6599 also were part of the ancient Iranian and Indo-European languages running along the Zagros Mountains to the North and East.

## Conclusion

So we can observe evidences in the available results of several modern and archaeological Y-DNA J1 samples and branches related to ancient Iranian populations around the Northern Middle Eastern regions, the Iranian Plateau and the Caspian Sea adjacencies, since the Mesolithic and more studies and investigations are needed in order to deepen these findings and researches. The phylogeny demonstrates a rich diversity of J1a samples distributed throughout the Middle East, Anatolia, Caucasus, whereas Armenian and Iranian Indo-European branches represent an early split within J1a.

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