

Haplogroup R1a, Its Subclades and Branches in Europe During the Last 9,000 Years

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ABSTRACT

This study identifies and describes 38 branches of the haplogroup R1a STR haplotypes which currently exist in Europe or which migrated from Europe to areas in the east, south, and southeast between 6000 and 4500 years before the present (ybp). The study is based on 2471 haplotypes which have been tested for either 67- or 111-markers; it essentially creates a unified robust system, which assembles dozens of R1a-SNPs and thousands of STRs and assigned haplotypes to branches, some of which do not have SNP assignments as yet. The assembled system consists of base (deduced ancestral) haplotypes, one for each STR branch and for each SNP-assigned subclade, each with its characteristic (ancestral) set of alleles, arranged in the chronological space from ~ 9000 ybp to 1300 ybp. We found that the most ancient R1a subclades (R1a1-M198- and R1a1a-M198+/M417-) bearers of which currently live in Europe (the present day haplotypes are scattered between England and the Balkans) appeared in Europe at least 7300 ybp, and possibly 9000 ybp. R1a' s three principal downstream subclades, L664 (North-Western branch), Z93 (South-Eastern branch), and Z283 (Eurasian branch), split from their common European ancestor at about the same time, around 7000 - 6000 ybp. L664 apparently stayed in North-Western Europe; its lineage recovered and began expanding ~ 4575 ybp. The Z93 subclade began to expand during the Aryan migrations, on the Aryan's journey to India and the Middle East in the 3rd-2nd millennia BC. The Z283 subclade split ~ 5500 ybp into three branches. One of them, Z280 (the Central Eurasian branch) moved east to the Russian Plain in 4800 - 4600 ybp, and formed at least 16 sub-branches there and in the course of the later westward repopulation of Europe in the 1st millennium BC – 1st millennium CE. Some of the older branches, like the Russian Plain branch, largely stayed in the present Russia-Ukraine-Belarus-Poland-Baltic countries region, and were described by early historians as the Scythians, Antes, Veneti, and a multitude of different proto-Slavic tribes (though many of them belonged to haplogroups other than R1a, primarily I1 and I2). Those R1a branches which are " older" than 3000 years, such as the Russian Plain branch (4600 ybp), the Western Eurasian (4300 ybp), and the Balto-Carpathian (4300 ybp), did not move en mass to Europe but stayed behind at the Russian Plain. In the middle of 1st millennium CE, the time of the collapse of the Roman Empire, multiple migrations of R1a were taking place eastward and westward; these migrations gradually formed the current landscape of R1a in Europe. All 38 branches and their datings are listed in the Appendix of this paper; current distribution maps are shown in the body of the paper.

KEYWORDS

Y Chromosome; Mutations; Haplotypes; Haplogroups; TMRCA; STR; SNP; R1a1

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References

- [1] Abu-Amero, K. K., Hellani, A., Gonzalez, A. M., Larruga, J. M., Cabrera, V. M., & Underhill, P. A. (2009). Saudi Arabian Y-chromosome diversity and its relationship with nearby regions. *BMC Genetics*, 10, 59. doi:10.1186/1471-2156-10-59
- [2] Balanovsky, O., Rootsi, S., Pshenichnov, A., Kivisild, T., Churnosov, M., Evseeva, I., Pocheshkhova, E. et al. (2008). Two sources of the Russian patrilineal heritage in their Eurasian context. *American*

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- [3] Behar, D. M., Thomas, M. G., Skorecki, K., Hammer, M. F., Bulygina, E., Rosengarten, D., Jones, A. L. et al. (2003). Multiple origins of Ashkenazi Levites: Y chromosome evidence for both Near Eastern and European Ancestries. *American Journal of Human Genetics*, 73, 768-779. doi: 10.1086/378506
- [4] Childe, G. (1926). *The Aryans: A study of Indo-European origins*. Dorchester: Dorset Press.
- [5] Cinnioglu, C., King, R., Kivisild, T., Kalfoglu, E., Atasoy, S., Cavalleri, G. L., Lillie, A. S. et al. (2004). Excavating Y-chromosome haplotype strata in Anatolia. *Human Genetics*, 114, 127-148. doi: 10.1007/s00439-003-1031-4
- [6] Felsenstein, J. (2004). *PHYLIP (Phylogeny Inference Package)*. Version 3.6. Seattle: Department of Genome Sciences, University of Washington.
- [7] Gamkrelidze, T. V., & Ivanov, V. V. (1995). *Trends in linguistics 80: Indo-European and the Indo-Europeans*. Berlin: Mouton de Gruyter.
- [8] Gray, R. D., & Atkinson, Q. D. (2003). Language-tree divergence times support the Anatolian theory of Indo-European origin. *Nature*, 426, 435-439. doi: 10.1038/nature02029
- [9] Haak, W., Brandt, G., de Jong, H. N., Meyer, C., Ganslmeier, R., Heyd, V., Hawkesworth, C. et al. (2008). Ancient DNA strontium isotopes, and osteological analyses shed light on social and kinship organization of the Later Stone Age. *Proceedings of the National Academy of Sciences of the United States of America*, 105, 18226-18231. doi: 10.1073/pnas.0807592105
- [10] Kayser, M., Lao, O., Anslinger, K., Augustin, C., Bargel, G., Edelman, J., Elias, S. et al. (2005). Significant genetic differentiation between Poland and Germany follows present-day political borders, as revealed by Y-chromosome analysis. *Human Genetics*, 117, 428-443. doi: 10.1007/s00439-005-1333-9
- [11] Keyser, C., Bouakaze, C., Crubezy, E., Nikolaev, V. G., Montagnon, D., Reis, T., & Ludes, B. (2009). Ancient DNA provides new insight into the history of south Siberian Kurgan people. *Human Genetics*, 126, 395-410. doi: 10.1007/s00439-009-0683-0
- [12] Kharkov, V. N., Stepanov, V. A., Borinskaya, S. A., Kozhekbaeva, Zh. M., Gusar, V. A., Grechanina, E. Ya., Puzyrev, V. P. et al. (2004). Gene pool structure of Eastern Ukrainians as inferred from the Ychromosome haplogroups. *Russian Journal of Genetics*, 40, 326-331. doi: 10.1023/B:RUGE.0000021635.80528.2f
- [13] Kharkov, V. N., Stepanov, V. A., Feshchenko, S. P., Borinskaya, S. A., Yankovsky, N. K., & Puzyrev, V. P. (2005). Frequencies of Ychromosome binary haplogroups in Belarussians. *Russian Journal of Genetics*, 41, 928-931. doi: 10.1007/s11177-005-0182-x
- [14] Klyosov, A. A. (2009a). DNA Genealogy, mutation rates, and some historical evidences written in Y-chromosome. I. Basic principles and the method. *Journal of Genetic Genealogy*, 5, 186-216.
- [15] Klyosov, A. A. (2009b). DNA Genealogy, mutation rates, and some historical evidences written in Y-chromosome. II. Walking the map. *Journal of Genetic Genealogy*, 5, 217-256.
- [16] Klyosov, A. A. (2010a). DNA lineages and origin of the " Tenth's " , the North-Western European subfamily R1a1 with YS388 = 10. *Proceedings of the Russian Academy of DNA Genealogy*, 2, 983-1028.
- [17] Klyosov, A. A. (2010b). DNA lineages and origin of the Tenth's, the R1a1 subfamily with DYS388=10: The story in progress. *Proceedings of the Russian Academy of DNA Genealogy*, 3, 2205-2217.
- [18] Klyosov, A. A. (2011). Biological chemistry as a foundation of DNA genealogy: The emergence of " molecular history " . *Biokhimiya (English transl.)*, 76, 517-533.
- [19] Klyosov, A. A. (2012). An emerging pattern of L664 SNP mutation in the Tenth's (bearers of DYS388=10), North-Western branch of R1a1 haplotypes. *Proceedings of the Russian Academy of DNA Genealogy*, 5, 30-37.
- [20] Klyosov, A. A., & Rozhanskii, I. L. (2012). Haplogroup R1a as the Proto Indo-Europeans and the legendary Aryans as witnessed by the DNA of their current descendants. *Advances in Anthropology*, 2, 113. doi: 10.4236/aa.2012.21001
- [21] Li, C., Li, H., Cui, Y., Xie, C., Cai, D., Li, W., Mair, V. H. et al. (2010). Evidence that a West-East admixed population lived in the Tarim Basin as early as the early Bronze Age. *BMC Biology*, 8, 15.

- [22] Renfrew, C. (2000). 10,000 or 5000 year ago? Questions on time depth. In Renfrew, C., McMahon, & A., Trask, L. (Eds.), *Time depth in historical linguistics* (pp. 413-439). Cambridge: The McDonald Institute for Archaeological Research.
- [23] Rozhanskii, I. L., & Klyosov, A. A. (2011). Mutation rate constants in DNA genealogy (Y chromosome). *Advances in Anthropology*, 1, 2634. doi:10.4236/aa.2011.12005