

О «МАССОВОЙ МИГРАЦИИ ИЗ СТЕПИ» В ЕВРОПУ БРОНЗОВОГО ВЕКА

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АВТОРСКОЕ РЕЗЮМЕ

Более полувека назад археолог Мария Гимбутас выдвинула так называемую «курганную теорию», одним из основных положений которой было то, что прото-индоевропейские языки распространились в Западную Европу из причерноморских и прикаспийских степей примерно 3000 лет до н.э., когда тысячи конных наездников вторглись на запад, уничтожили коренное население и принесли оставшимся индоевропейские языки. Обычно принимается, что исходным регионом вторжения была ямная культура, или древняя культурно-историческая общность (3300-2600 лет до н.э.). Эта концепция была поддержана несколько лет назад геномными исследованиями (Haak, Lazaridis, Patterson 2015: 207-215), где упор был сделан на ямную культуру, в которой на многих костных остатках было продемонстрировано, что все они содержат гаплогруппу R1b, ту самую, которая доминирует среди современного мужского населения Западной Европы. Поскольку позже было определено, что основным субкладом/снипом в ямной культуре был R1b-Z2103, то можно ожидать, что этот субклад (с нижестоящими снипами) окажется преобладающим для мужского населения Центральной и Западной Европы. Нами показано, что это не так. Здесь мы представляем данные из наиболее известных баз данных FTDNA и YFull, содержащих более 15 тысяч образцов европейских ДНК, которые показывают, что R1b-Z2103 и нижестоящие снипы (которые образовались за последние тысячелетия, и обычно связываются археологами и палеогенетиками со «степными культурами») почти полностью отсутствуют в Европе. Их доля обычно составляет для всех регионов Западной и Центральной Европы единицы процентов, и чаще доли процентов. Представленные нами данные показывают, что древние носители субклада R1b-Z2103 продвинулись из ямной культурно-исторической общности и сопряженных «степных культур» не на запад, но на юг, на Кавказ и далее в Анатолию и регионы Ближнего Востока. Например, носители снипа Z2103, которые сейчас живут в Армении и Турции, далеко превосходят по численности тех, кто в совокупности живут в Центральной и Западной Европе.

КЛЮЧЕВЫЕ СЛОВА: Мария Гимбутас, бронзовый век, курганная теория, археология, ДНК-генеалогия.

ON «MASSIVE MIGRATION FROM THE STEPPE» TO THE BRONZE AGE EUROPE

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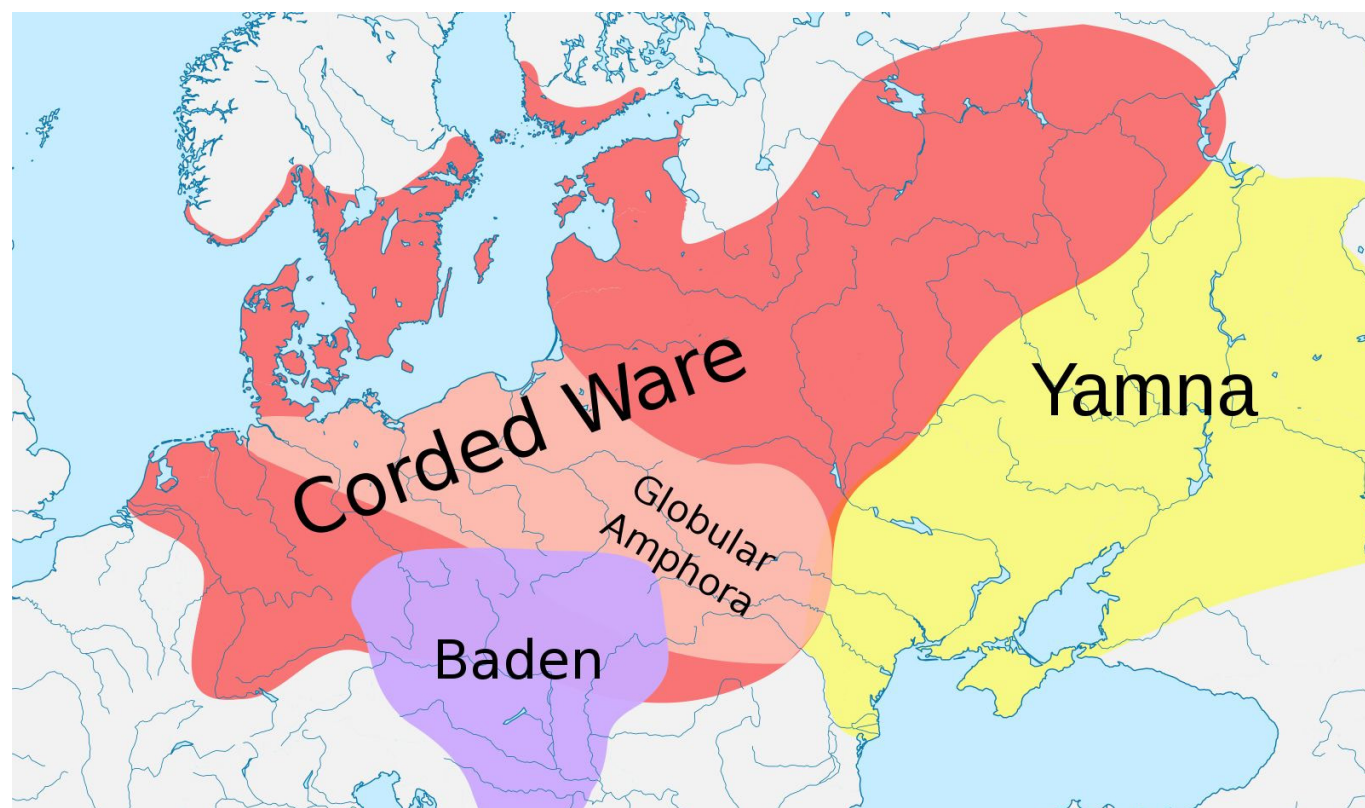
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ABSTRACT

Decades ago, Marija Gimbutas had advanced the so-called Kurgan hypothesis, a core of which was a suggestion that Proto-Indo-European (PIE) spread from the Pontic-Caspian steppe around 3000 BCE, when thousands of horsemen have swept into Bronze Age Europe. It is commonly accepted by those who support the hypothesis which is also referred to as the Kurgan theory that PIE herders have spread mainly from Yamnaya archaeological horizon. This concept has been promoted recently by genome studies (Haak, Lazaridis, Patterson 2015: 207-215) that allegedly showed mass migration from Yamnaya to Europe. As a result, as commonly proposed, the Yamnaya contributed to at least half of central Europeans' genetic ancestry. Since the principal Y-chromosomal haplogroup identified in Yamnaya was R1b with the only «deep» subclade/SNP Z2103, one could expect that Z2103 along with its downstream subclades is the predominant subclade in Central and Western Europe. Here we present data from major databases (FTDNA and YFull) amounting to more than 15 thousand entries from Europe, which show that R1b-Z2103 and its downstream subclades, representing present-day descendants from Yamnaya (and associated archaeological «steppe cultures») are almost absent in Europe; present in singular percent or, more often, in fractions of a percent. We also present data that R1b-Z2103 bearers moved from Bronze Age Yamnaya and associated steppe cultures not to the West, but to the South,

to the Caucasus, Anatolia, and Middle East regions. For example, Z2103 descendants who live in Armenia or Turkey exceed in numbers in said databases all Z2103 descendants living in Central and Western Europe combined.

KEYWORDS: Marija Gimbutas, Bronze Age, Kurgan hypothesis, Archaeology, DNA Genealogy.



Decades ago, Marija Gimbutas had advanced the so-called Kurgan hypothesis (Gimbutas 1963: 815-836; 1973: 163-214; 1979: 113-137), a core of which was a suggestion that Proto-Indo-European (PIE) spread from the Pontic-Caspian steppe around 3000 BCE, when thousands of horsemen have swept into Bronze Age Europe. It is commonly accepted by those who support the hypothesis, also referred to as the Kurgan theory, that PIE herders spread mainly from Yamnaya archaeological horizon and brought Indo-European (IE) languages to Europe. Alternative views on the origin of IE languages, such as Anatolian hypothesis (Renfrew 1987; 2000), suggest that they originated in Anatolia in the Stone Age and moved to Europe with the spread of farming. There are similar in-kind views such as the Balkan hypothesis, among others; however, the Kurgan theory as associated with Yamnaya culture has been promoted recently by genome studies (Haak, Lazaridis, Patterson 2015: 207-215) which allegedly shown mass migration from Yamnaya to Europe. As a result, it is commonly stated that the Yamnaya contributed to at least half of the central Europeans' genetic ancestry. An impact of the Haak's paper (Haak, Lazaridis, Patterson 2015: 207-215) was quite significant; by October, 2022 it has collected 1680 citations in the literature¹.

Let us examine basics for reality of that "mass migration" from Yamnaya to Europe. As it was reported in the same paper (Haak, Lazaridis, Patterson 2015: 207-215), and

confirmed in several other papers (Allentoft, Sikora, Sjögren 2015: 167-172; Mathieson, Lazaridis, Rohland et al. 2015: 499-503), the principal Y-chromosomal haplogroup identified in Yamnaya, was predominantly haplogroup R1b (11 out of 12 ancient samples, with an exception of a single haplogroup I2a in Kalmykia), with the only "deep" subclade/SNPs R1b-Z2103 (equivalent to R1b-Z2105 and R1b-CTS1078) in four samples out of seven samples in Yamnaya-Samara, and in one sample out of five samples in Yamnaya-Kalmykia. The remaining seven samples of R1b haplogroup were typed only for "shallow" SNPs, such as R1b-M269, which is not informative in this context (it was formed around 13300 years before present², while Yamnaya culture is dated between 5300 and 4600 years before present, ybp). For a comparison, subclade R1b-Z2103 arose around 5900 ybp³, not too long before Yamnaya itself. Hence, it may be indicative for migrations of Yamnaya people. Also, R1b-Z2103 was found in the neighboring Poltavka archaeological culture as two out of three ancient samples (Mathieson, Lazaridis, Rohland et al. 2015: 499-503), and the remaining sample was again R1b-M269.

Based on what is said above, we can employ R1b-Z2103 as a marker which would have followed Yamnaya (and Poltavka) people wherever they moved. Based on the Kurgan theory along with its support by Haak's paper

1 Electronic resource: https://scholar.google.com/scholar?hl=en&as_sdt=40000007&q=Haak&btnG= (Date of access - 19.11.2021).

2 Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021).

3 Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021).

Country/region (entries)	R1b, percent of all haplogroups	R1b-P312, percent of R1b entries	R1b-U106, percent of R1b entries	R1b-Z2103, percent of R1b entries
France (2546)	68	n/a	n/a	0.35
France (228)	59	n/a	n/a	0
Belgium (318)	66	48	12	0.47
Netherlands (523)	47	30	17	0.40
Benelux (392)	63	37	38	1.2
Iberia (2567)	54	n/a	n/a	0.07
British Isles (2232)	70	n/a	n/a	0
British Isles (4854)	67	n/a	n/a	0

Table 1. Data from the FTDNA European projects, available in open access in the format FTDNA <country>. n/a – data are not reported in the database

Country/region	R1b	R1b-P312	R1b-U106	R1b-Z2103
France	189	158	23	8
Belgium	35	26	8	1
Netherlands	63	30	32	1
Germany	246	119	92	18
Poland	104	37	41	17
Spain	158	144	10	4
Portugal	195	177	13	5
England	379	245	122	12
Ireland	466	432	29	5
Scotland	373	318	54	1
Wales	36	34	2	0

Table 2. Data from YFull, number of entries.

Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021);
Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021)

(Haak, Lazaridis, Patterson 2015: 207-215), we would have expected to discover R1b-Z2103 in great amounts in Central and Western Europe. Remarkably, it is not so. Not even close. It turned out that the predominant R1b subclade in Europe is R1b-P312 that was not detected in Yamnaya, and was spread all over Europe by Bell Beakers.

R1b-P312 is related to R1b-Z2103 through their common ancestor R1b-L23 as follows⁴:

R1b-M343 > L754 > L388 > P297 > M269 > L23 > (Z2103 + L51)

L51 > L52 > PF6538 > L151 > (P312 + U106)

Subclade L23 arose about 5900 ybp, and both Z2103 and L51 were formed within a short time after it⁵. Those calculations were made based on a quantity of SNPs formed between subclades, systematically reported by YFull group⁶.

As one can see, centuries prior Yamnaya bearers of Z2103 and L51 appear to have split, with Z2103 have establishing Yamnaya, and L51 elsewhere, through migration of yet unidentified. Bearers of L51 that were excavated in Poland, dated 4301-4411 ybp; their (subclade) descendants of L151 were found in Czechia dated 4850-4150 ybp, and of PF6538 were identified in burials in Poland⁷ dated 4409-4301 and 4429-4299. Those are likely descendants of Bell Beakers, though it has to be determined.

Thus, the question remains: where did bearers of R1b-Z2103 migrate from Yamnaya? It would appear, not to Central and Western Europe (Klyosov 2012: 87-105). Tables 1 and 2 show some data, taken from FTDNA and YFull data bases. Percentages as referred to as a fraction of present-day R1b bearers (FTDNA), numbers on the right referred to entries (YFull) where subclades were identified.

The last two sets are available in FTDNA Projects only as “British Isles DNA Project”⁸ that combines England, Ireland, Scotland, and Wales. Out of total 4854 entries (including the preceding 2232 results, published separately in the Project) there were 3235 R1b results, that is 67% of all, and among

4 Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021); Electronic resource: <https://isogg.org/tree/index.html> (Date of access - 19.11.2021).

5 Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021).

6 Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021).

7 Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021).

8 Electronic resource: <https://www.familytreedna.com/public/britishisles/default.aspx?section=yresults> (Date of access - 19.11.2021).

Country/region (entries)	R1b, percent of all haplogroups	R1b-P312, percent of R1b entries	R1b-U106, percent of R1b entries	R1b-Z2103, percent of R1b entries
Armenia (1338)	27	6	0	88
Turkey (325)	22	n/a	n/a	56

Table 3. Data from the FTDNA Armenian and Turkey projects.

Electronic resource: <https://www.familytreedna.com/public/ArmeniaDNAProject?iframe=yresults> (Date of access - 19.11.2021);

Electronic resource: <https://www.familytreedna.com/public/turkey?iframe=yresults> (Date of access - 19.11.2021)

Country/region	R1b	R1b-P312	R1b-U106	R1b-Z2103
Armenia	85	15	0	70
Turkey	73	11	4	57

Table 4. Data from YFull, number of entries

Electronic resource: <https://www.yfull.com/tree/R1b/> (Date of access - 19.11.2021);

Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021)

them there was not a single R1b-Z2103, “Yamnaya”-related entry.

As one can see, both present-day Central and Western Europe do not show any significant amounts of R1b-Z2103, “Yamnaya”, or “steppe”-related descendants. Their amount among total R1b bearers in Europe consists of a fraction or at best low per centages. This is inconsistent with a hypothesis that Yamnaya bearers moved to Bronze Age Europe and consequently, brought with them Indo-European languages, and are ancestors of most of European men. A suggestion spelled out in the Haak et al. paper (Haak, Lazaridis, Patterson 2015: 207-215) “R1a and R1b are the most common haplogroups in many European populations today, and our results suggest that they spread into Europe from the East after 3,000 BC” is principally incorrect (at least regarding R1b haplogroup), because the authors should have considered “branches”, or subclades, or SNPs of the haplogroups. We do not consider here migrations of R1a bearers in Bronze Age Europe (and Asia), it is a matter of separate studies.

Hence, the question arises: where the Yamnaya R1b-Z2103 people went, if not to Central and Western Europe? The answer becomes rather obvious, as soon as we look at present-day distributions of Z2103 (the most detailed pattern is provided by YFull, which publishes “deep” SNPs all around the world).

R1b-Z2103 migrated South of Yamnaya, to the Caucasus, and further to Anatolia and neighboring regions. The available data⁹ include 74 countries, of which Europe, as it was shown above, reveals insignificant amounts of “Yamnaya” subclade. In that regard, the most represented present-day countries are Armenia and Turkey, where 70 and 57 of R1b-Z2103 entries were identified¹⁰, respectively, compared to singular (typically) numbers for European countries (see above), or to Russia (26 entries), Ukraine (17), and some countries in the Caucasus, such as Chechen Republic (9), Georgia (7), etc. It may be noticed that several regions to South of Armenia and Turkey also reveals

R1b-Z2103 entries¹¹, such as Saudi Arabia (31), Kuwait (20), Iraq (11), UAE (7), Bahrein (5), Lebanon (4), Qatar (3), Yemen (3), Syria (3), etc.

Those observations are additionally reinforced by calculations of the TMRCA (Time to the Most Recent Common Ancestors) employing series of the present-day haplotypes (Klyosov 2009: 719-724; 2018; Klyosov, Kilin 2016: 51-71) of Z2103 subclade, which for Russia yields 4580±500 ybp (37 marker haplotypes) and 5010±660 ybp (less accurate calculations employing 12 marker haplotypes); for Armenia 4730±480 ybp (67 marker haplotypes), 4670±475 ybp (37 marker) and 5050±580 ybp (12 marker). All TMRCA values are compatible with archaeological dates for Yamnaya horizon (5300-4600 ybp). A combined series of present-day R1b-Z2103 haplotypes from Kuwait, Bahrein, UAE, Saudi Arabia, Yemen, Iraq, Syria, Jordan, Lebanon, and Palestine (69 haplotypes total in the 37-marker format) yields the TMRCA value of 4480±470 ybp, also withing error margin of dates for Yamnaya horizon. A combined dataset of present-day Z2103 haplotypes from France, Belgium, Netherlands, Spain, Italy (32 haplotypes total in the 37-marker format) yields the TMRCA value of 3970±440 ybp, close to the Yamnaya dates, albeit slightly less. However, rather scarce representation of R1b-Z2103 results in Europe compared to those in the South of Asia provides a serious argument against the major migration of Yamnaya settlers to Europe. This is also illustrated with results of ancient DNA samples. Of more than one thousand ancient DNA samples excavated in Europe, only few of them belong to R1b-Z2103 and its downstream subclades – two were found in Italy (Posth, Zaro, Spyrou 2021)¹², one in Bohemia (Papac, Ernee, Dobeš 2021; Patterson, Isakov, Booth 2022: 588-594), one in Czech Hallstatt (Patterson, Isakov, Booth 2022: 588-594), two in Serbia (Patterson, Isakov, Booth 2022: 588-594)¹³, one in France (Patterson, Isakov, Booth 2022: 588-594), one in the Netherlands (Patterson, Isakov, Booth 2022: 588-594), one in Hungary (Patterson, Isakov, Booth 2022: 588-594). Some

⁹ Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021).

¹⁰ Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021).

¹¹ Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021).

¹² Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021).

¹³ Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021).

of them are archaeologically dated rather recently, such as in Italy 650-850 ybp and 1740 ybp, in Poland 1400±390 BCE, in Czech 800-550 BCE, in Hungary 296 BCE, in West of Poland 170 BCE. Many more ancient R1b-Z2103 were found to the East – in Yamnaya and Afanasievo archaeological cultures, in the Altay and Xinjiang, in Iran, Kazakhstan, among Scythians and Sarmatians (Mathieson, Lazaridis, Rohland 2015: 499-503; Unterländer, Palstra, Lazaridis 2017)¹⁴, and, as it was shown above, mainly in the Caucasus, Anatolia, in the Middle East. This pattern is not compatible with the concept of “massive migration from the steppe” to Europe.

¹⁴ Electronic resource: <https://www.yfull.com/tree/R-Z2103/> (Date of access - 19.11.2021).

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