Giancarlo Tomezzoli – Anatole Klyosov

DNA GENEALOGY AND LINGUISTICS. A NEW MIGRATION / LINGUSTICTIC / SETTLEMENT PARADIGM FOR ANCIENT EUROPE

Povzetek

DNA RODOSLOVJE IN JEZIKOSLOVJE NOV SELITVENI / JEZIKOVNI / NASELITVENI PRIMER ZA STARODAVNO EVROPO

Prispevek poskuša spojiti podatke sodobnega rodoslovja in DNA rodoslovja na način, da bi dobili združljiv selitveni / jezikovni / naselitveni primer (vzorec) (SJN) za opisovanje selitev in naselitev ljudstev in jezikov v Evropi po zadnji ledeni dobi. V SJN vzorcu so bili zaznani trije pomembni dejavniki:

- R1a haploskupina nosilcev, ki so navadno označeni kot Arijci, ki so 20.000 pred n. št. med svojimi selitvami iz osrednje Azije in Altaja prišli po južni poti v Evropo okoli leta 10.000 pred n. št., prinesli proto indoevropske (IE) in indoevropske jezike in se potem selili na vzhod iz Evrope na Ruske ravnice in Indijo kot legendarni Arijci. V prvi polovici tretjega tisočletja pred n. št. so se selili s svojim IE jezikom nazaj iz Ruske ravnice v srednjo, zahodno in južno Evropo in s seboj v Evropo vodili ljudstva, ki so se pozneje imenovala Kelti, Germani, Italiki, Grki, Iliri in Baltoslovenі.
- R1b haploskupina nosilcev, ki so navadno označeni kot Arbini in ki so od okoli 16.000 let pred n. št. med svojimi selitvami iz osrednje Azije v Evropo po severni poti prišli v Evropo med okoli 4.800 in 4.500 pred n. št., so prinesli ne- indoevropske jezike.
- E, F, G, J, I, K haploskupina nosilcev, za katere ostaneta selitvena pot in čas prihoda v Evropo 5.000 pred n. št. nejasna in ne govorijo IE jezikov. Domneva je, da je bil prihod Arijcev R1a v Evropo miroljuben, ne nazadnje ni znakov, da bi ti bili morda nosili gene nasilne do prvotnih prebivalcev. Vsekakor pa je prihod Arbinov (R1b) v Evropo zaznamoval skoraj popolno odstranitev skupin E, F, G, J, I, K iz Evrope.
- Glede na poglavitne sodobne jezikoslovne teorije je mogoče dognati:
- anatolska teorija je v splošnem primerljiva s SJN vzorcem;
- vaskonsko in afro-azijska teorija o prvotni prebivalstveni podlagi je delno združljiva s SJN vzorcem;
- kurganska teorija in paleolitska teorija nepretrgane poselitve se zdita nezdružljivi z zgodovino Evrope, ki temelji na SJN vzorcu.
- Razen tega so v letih od 1990 do 2000 očetje, utemeljitelji teorij in genetike prebivalstva, naredili napake v tem, kar imenujejo »gensko rodoslovje« ali »prebivalstvena genetika« in nekaterih vidikih izven afriških domnev, ki so bile dokazane z DNA rodoslovjem, teče tukaj tudi razprava.

Introduction

"Genetics studies" is a vague term applicable to studies either of the whole human genome or to the so-called autosomes, which include genes and SNPs (Single Nucleotide Polymorphisms) in chromosomes, besides Y chromosome. Y chromosome contains almost no genes. In fact, SNPs and STRs (Short Tandem Repeats), which form haplotypes of Y chromosome, are located on non-recombinant parts, so that they are not genes because these last belong to recombinant parts that recombine from mother's and father's portions of chromosomes. Thus, studies into SNPs and STRs of Y chromosome cannot be considered as genetic studies.

The earlier (1990-s – 2005-s) blood groups and short haplotypes (such as 5-6-marker haplotypes) studies of different human populations, were a brave attempt to enter a new and largely unknown field. Unfortunately, those studies very often "cut corners" and suffered improvisation, sometime having lack of any ground. Most of the principal "findings" were practically invented by "population geneticists" without any supportive data.

Human "population genetics" commonly aims at finding some correlations between genotype and phenotype. A typical task of population geneticists was to determine how haplogroups and subclades are spread among the actual populations. They recorded percentages of various genetic features among different populations, normally without differentiating haplogroups or haplotypes, and tried to find correlations between those features. For example, they found that, Bashkirs and American Indians occupy different spots in those correlations, based on some selected average indications, without considering some alleles or their combinations. This has nothing to do with DNA genealogy.

DNA genealogy investigates the "molecular history" or evolution of DNA by studying the features of the Y chromosomes (in males) or mtDNA (in females, and one generation down in males). Haplotypes of Y chromosome are a very precise tool, for example, by 111-marker haplotypes it resolves DNA-lineages down to 4-generation increments. mtDNA is much cruder tool, and its resolution often goes not below of thousands of years. DNA genealogy is thus also a historical science in which time plays an important role, which allows tracing migrations and evolution of populations.

In an attempt of understanding the settlement of ancient populations speaking different languages in Europe after the last Ice Age period we were faced with the results of several main linguistic theories which are described in a huge number of publications. Those publications define the aspects of their respective own theory, expose their theory supporting arguments, discuss the inter-relationships with other theories, and often contest, contradict, or reject some or many of aspects of the other theories concerning the ancient settlement of Europe. In this paper we summarize said main linguistic theories with the aim to outline groundless and erroneous linguistic hypotheses and concepts in the light of DNA genealogy. Overall, we aim at establishing a consistent and reasonable migration/linguistic/settlement (MLS) paradigm for ancient Europe from the Palaeolithic up to about the Bronze Age on the basis of the DNA genealogy.

Ancient migrations to, from, and within Europe as revealed by DNA Genealogy

The α-haplogroup of the Y-chromosome (cf. Fig. 1), which is present in almost all males living today (except archaic African lineages A0, A00, etc., not shown in Fig. 1), arose around 160,000 ybp (Klyosov and Rozhanskii [1]) in a location currently unknown. Essentially, the alpha-haplogroup was a haplogroup produced by a survived common ancestor of the "anatomically modern man" as it is known today. We can only conjecture where that common ancestor might have lived; it seems that he could live in a vast triangle from Central Europe and the Isles to the West, through the Russian Plain to the East, to Levant (or the Middle East) to the South (Klyosov and Rozhanskii [2]). This huge area is defined by the most ancient skeletal fragments of the "anatomically modern homo" (AMH) found in Europe dated by 45-43,000 ybp (Benazzi et al. [3]; Higham et al. [4]), and in the Russian Plains (Eastern Europe) dated between 40,000 and 29,000 ybp (by skeletal fragments), and between 45,000-42,000 ybp (by optically stimulated luminescence dating of settlements rests) (Prat et al. [5]; Anikovich et al. [6]).

The haplogroup tree of Fig. 1 shows the chronological positions of haplogroups of the most recent common ancestors (TMRCAs) of *H. sapiens* (Klyosov and Rozhanskii [1]). To prepare this tree, 7,415 haplotypes from 46 subclades of 17 major haplogroups were analysed.

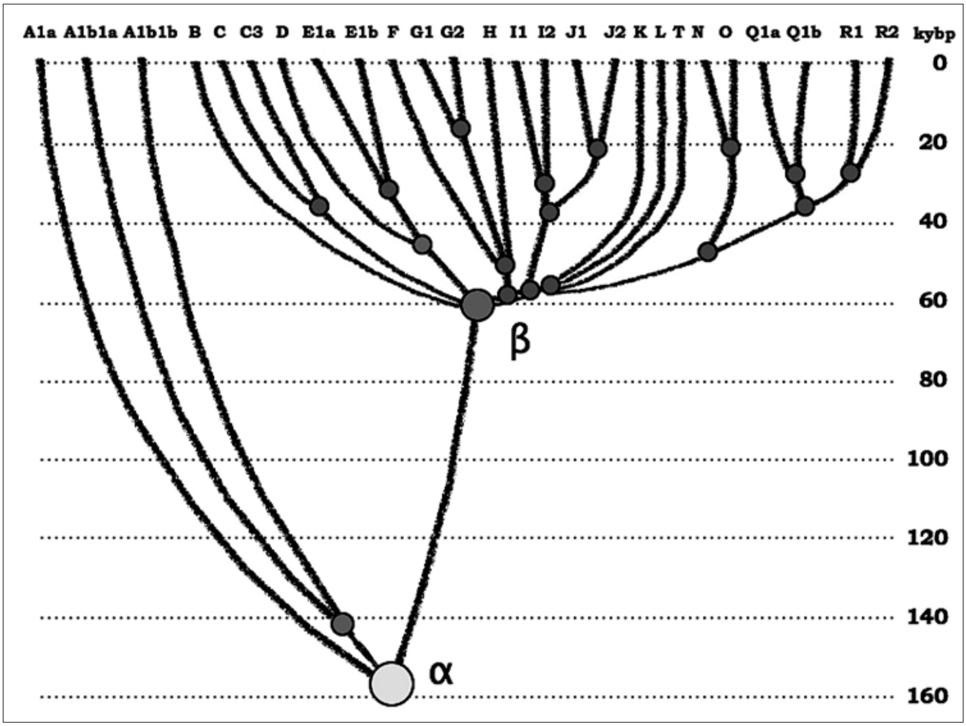

Fig. 1: Haplogroup tree of the H. sapiens Y-chromosome derived from haplotypes and subclades (Klyosov and Rozhanskii [1]) .

The timescale on the vertical axis shows thousands of years from the common ancestors of the haplogroups and subclades. The tree shows a chronological position of the α-haplogroup, which is ancestral to both the African and non-African haplogroups, and the β-haplogroup, which is equivalent to haplogroup BT in the current classification. The left branch haplogroup A represents the African haplogroups, and they arose 160,000 – 140,000 ybp. Non-African β-haplogroup and its descendants arose ~ 64,000 ybp. Haplogroups F through T represent Europoeids (Caucasoids) who arose ~ 58,000 ybp (Klyosov and Rozhanskii [1]).

The most ancient Middle East skeletal fragments allegedly belonging to AMH reveals some pronounced archaic features, and it is questionable whether they do belong to AMH (Bednarik [7], [8]). The most ancient African skeletal remnants undisputedly resembling the AMH are dated by only 34,000 ybp; the older bones, dated by 200-160,000 ybp and more recent, possess some pronounced archaic features, and can be assigned to the AMH or *H. sapiens* with significant reservations (Klyosov and Rozhanskii [1], [2]). Some of them might belong to bearers of a recently discovered haplogroup A0, which arose some 200,000-260,000 years ybp, or even earlier. This might be the only truly "African haplogroup" by its origin and is very distant, mutation-wise, hence, time-wise, from other haplogroup A haplotypes.

Around 140,000 ybp, a common ancestor of the African lineages A - in fact, there is a number of them, and the term haplogroup A essentially represents an umbrella over various A haplogroups, some of them quite distant from others - split from the α-haplogroup (ibid.) and allegedly migrated to Africa from an yet undisclosed location of said vast triangle. In Africa, the incoming bearers of haplogroup A and later haplogroups B, E and bearers of haplogroup R1b, etc., have mixed with bearers of the African haplogroup A0 or rather, with bearers of a number of A0 haplogroups, and that explain why black African populations have developed a wide variety of haplogroups and, hence, a great genetic diversity. Thus, this genetic diversity is a result of mixing of many different haplogroups-populations rather than a diversification of one ancient African haplogroup-population.

The non-African lineage of the β-haplogroup, first represented by the initial haplogroup BT, has a common ancestor who lived 64,000±6,000 ybp (cf. Figs. 1 and 2), and who descended from the α-haplogroup. The huge time-gap, almost 100,000 years, between the chronological positions of the α- and β-haplogroup apparently results from a population bottleneck around 64,000 ybp, which might point at a catastrophic event, such as the eruption of the Indonesian Toba volcano around 70,000 ybp. The Toba eruption and/or other consequent catastrophic events largely disrupted the environment and almost terminated the non-African population. The fact that no skeletal remnants having β-haplogroup itself and/or its more ancient ancestors have been found could be due to various causes, not last that they might be buried under volcanic ash.

The ß- or BT haplogroup in the current classification, has successively, step-wise, produced all other descending twenty haplogroups of the Y chromosome from B through T (cf. Fig. 2). Two of them, R1a and R1b embrace respectively about 50% of the East European and 60% of the West/Central European actual populations, respectively. Other European populations belong to haplogroups primarily of I1, I2, E1b, J1, J2, N1c, G2, Q, and a few more minor haplogroups, commonly of a fraction of per cent in the populations.

A0 P305, **V148, V166, V239**

- **A0a V152**
  - **A0a1** P114
- **A0b L896, L1000**

α-haplogroup L985, L1003, V161, V168, V171

- **AT** P108, **V221**
  - **A** M31, P82, V4, V14, V25
  - **B (β-haplogroup) L413,** M42, **M91, V29, V31**
    - **B** M60, M181, M247
    - **CT** M168, M294
      - **DE** M1/YAP, M145, P144, P183
        - **D** M174
        - **E** L339, L856, M40, M96, P171, P176
      - **CF** P143
        - **C** M130, M216, P184, P260
        - **F** M89, M235, P158, P316
          - **G** L116, L154, L520, M201, P257, U2
          - **H** M69, M370
          - **IJK** L15, M522
            - **IJ** M429, P130
              - **I** L41, M170, M258, U179
              - **J** 12f2.1, L134, M304, P209
            - **K** M9, P128, P132
              - **LT** L298, L811
                - **L** L855, L863, M11, M20, M185
                - **T** L206, L445,M184, M193, M272
              - **K (xLT)** M526
                - **M** P256
                - **NO** M214, P188, P195
                  - **N** M231
                  - **O** M175, P186, P196
                - **P** L138, L268, **L781,** M45,P207, P295,**V231**
                  - **Q** M242
                  - **R** M207, P224, P285,
                    - **R1** M173, M306
                      - **R1a** L62, M420
                      - **R1b** M343
                - **S** M230, P202, P204

Fig. 2: The haplogroups overall tree – archaic African lineage A0, α-haplogroup and β- or BT haplogroup.

DNA genealogy considers each haplogroup of Y chromosome as representing an individual main tribe. Each haplogroup (cf. Fig. 2) has a series of SNPs, i.e. practically irreversible mutations, which in turn form a haplogroup or subclade (these terms are used interchangeably, depending of a context) tree. Each haplogroup tree contains as primary entry the SNP which defines the haplogroup. Many of the haplogroups contain a number of SNPs (cf. Fig. 2), which have appeared at different times. Downstream haplogroups or subclades (cf. Fig. 2) define sub-tribes, or clans, i.e. derived populations, each of which is marked with a characteristic SNP.

R1a is the tribe, conventionally indicated as the Aryans, which embraces about 50% of the current population of Eastern Europe. The main reason of such a name is that this haplogroup/SNP has marked the DNA of the legendary Aryans who arrived to India around 3500 ybp, and currently up to 72% of the upper Indian castes bear R1a haplogroup (Sharma et al. [9]).

- **R1a** L62, M420
  - **R1a1** L122/M448, M459
    - **R1a1a** M17, M198
      - **R1a1a1** M417 (Old European branch)
        - **R1a1a1a** Z645, Z647
          - **R1a1a1b1** Z283 (Eurasian branch)
            - **R1a1a1b1a Z282 (Young Eurasian branch)**
              - **R1a1a1b1a1** M458 (European branch)
              - **R1a1a1b1a2** Z280 (Central Eurasian branch)
              - **R1a1a1b1a3** Z284 (Scandinavian branch)
          - **R1a1a1b2** Z93 (South Eastern branch)
            - **R1a1a1b2a Z94 (Young South Eastern branch)**
              - **R1a1a1b2a1** L342.2 (Aryan branch)
                - **R1a1a1b2a1a** L657 (Young Aryan branch)

Fig. 3: Haplogroup/subclade tree of R1a in an abbreviated version, see ISOGG, 2013 (http://www.isogg.org/tree/).

Haplogroup R1a-L62 (cf. Fig. 3) arose apparently in Central Asia and maybe in the Altai region (South Siberia) around 20,000 ybp (Klyosov and Rozhanskii [1]). Its subclade M17 is observed in North China, with a common ancestor of about the same time. Both L62 and M17 migrated from Central Asia across Tibet, Hindustan, Iranian Plateau, and Anatolia around between 12,000 and 10,000 ybp. Their downstream subclade M417 crossed Asia Minor and entered the Balkans between 10,000 and 9,000 ybp, spread all over Europe to the Isles between 9,000 and 5,000 ybp, formed around 5,700 ybp the recently discovered Z645 branch, the Eurasian branch Z283 and its South-Eastern branch Z93 with its downstream Aryan branch Z342.2 around 4,900 ybp, and the Central Eurasian branch Z280 around 4,900 ybp (Rozhanskii and Klyosov [10]). The Central Eurasian branch R1a-Z280 presently embraces about half of the East European males, and the Aryan branch R1a-L342.2 is currently observed in Russians, Ukrainians, in southern populations in Asia such as Kyrgyz, Kazakh, Tajik people, also in Iran, India, in the Middle East, and along the ancient migration route from the Russian Plain to the Middle East, particularly in Armenia and Turkey. The R1a haplotypes excavated in Andronovo archaeological culture sites several thousand kilometres east of the Ural Mountains, with datings between 3,800-and 3,400 ybp (Kayser et al. [11]) very likely belong to L657 subclade (Klyosov [12]).

It seems that only two latest subclades on the tree (Fig. 3), L342.2 and L657, can be considered as descendants of the actual Aryans, which match history, archaeology, and languages of the steppe people, who rode chariots and, in the middle of the 2nd millennium BC, arrived to India ("Indo-Aryans"), Iran ("Avesta Aryans"), and Mesopotamia ("Mitanni Aryans") (Klyosov and Rozhanskii [2]).

R1b is the tribe, conventionally indicated as the Arbins, which includes about 60% of the current population of Western and Central Europe.

• • **R1b** M343
• • • **R1b1** M415
• • • • • **R1b1a1** M73
• • • • • **R1b1a2** M269
• • • • • • **R1b1a2a** L23
• • • • • • • **R1b1a2a1** Z2105
• • • • • • • • **R1b1a2a1a** L51
• • • • • • • • • **R1b1a2a1a1** L11
• • • • • • • • • • **R1b1a2a1a1a** U106
• • • • • • • • • • • • • **R1b1a2a1a1a3b1** U198
• • • • • • • • • • **R1b1a2a1a1b** P312
• • • • • • • • • • • **R1b1a2a1a1b2** U152
• • • • • • • • • • • **R1b1a2a1a1b3** L21
• • • • • • • • • • • • • • • **R1b1a2a1a1b3a1a1** M222

Fig. 4: Haplogroup/subclade tree of R1b in an abbreviated version, see ISOGG, 2013

Haplogroup R1b-M343 (cf. Fig. 4) arose apparently in Central Asia and maybe in the Altai region (South Siberia) around 16,000 ybp (Klyosov [12]). Its subclade M73 is observed in Siberia and Middle Asia, M269 in Bashkortostan near South Ural, L23 and its downstream Z2105 on the Russian Plain, in the Caucasus and Mesopotamia between 6,200 and 5,500 ybp. L51 and L11 on the migration route between the Middle East and the Pyrenees between 5,500 and 5,000 ybp. U106 and P312 arose in Iberia around 4,800 ybp and apparently became the initial population of the Bell Beaker culture of the continental Europe. L21 arose apparently in South of France about 4,000 ybp and moved to the Isles. M222 currently constitutes near 25% of the Irish population, with a common ancestor who lived between 2,000 and 1,400 ybp (Klyosov [12]).

Besides R1a bearers, in Europe since ~ 9,000 ybp, and R1b bearers, in Europe since ~ 4800 ybp, ancient Europe was inhabited by bearers of other haplogroups, among them E1b, G2a, F, I1, I2, J2, K. Their migration routes and dates of arrival to Europe remain obscure. Haplogroup E1b apparently moved to Europe from North Africa or from the Middle East, as well as haplogroup J2. Haplogroup G2a moved apparently from the Near Asia, probably from the Iranian Plateau. Haplogroup I1/I2 might have moved from the Russian Plain, westward, maybe even as the earlier haplogroups IJK (see Fig. 2), between 45,000 and 40,000 ybp. Haplogroups F and K in Europe remain undated.

An excavated E1b-V13 marked DNA from ancient bones was dated by 7,000 ybp (Lacan et al. [13]). Strikingly enough, present day bearers of E1b-V13 haplotypes all coalesce to a common ancestor who lived only 3,600 ybp. In other words, the contemporary V13 haplotypes reveals a gap between 7,000 and 3,600 ybp. The same gap pattern is observed with almost all haplotypes of the ancient Europe except R1b, which apparently played an important role in the settlement of ancient.

It seems that the arrival of the Aryans (R1a) in Europe was peaceful; at least, there are no indications that it might have been genetically violent. However, the arrival of the Arbins (R1b) to Europe was marked by almost complete elimination of the autochthonous haplogroups from Europe; E1b-V13 has practically disappeared, and started to proliferate only around 3,600 ybp; G2a fled to the Asia Minor and to Mesopotamia and Caucasus; R1a fled to the Russian Plain; I1 has practically disappeared and started to proliferate only around 3,600 ybp; I2 fled to the Isles and to the Russian Plain, and started to proliferate in Eastern Europe only around 2,300 ybp. Only R1b itself has proliferate without any obstacles from about 4,200 ybp to the present time.

The above description forms a basis for consideration of movement of peoples and languages in Europe from about 9,000 to 2,000 ybp.

A view of DNA genealogy: Basic concepts on connections of haplogroups and languages

As it has been shown, DNA genealogy allows tracing migrations and evolution of ancient tribes or peoples, but, apparently, it does not allow specifically tracing languages. Neither haplogroups nor languages stay the same in the course of migrations: haplogroups can disappear by extermination of their bearers, epidemics, ecological catastrophes, in those cases also their corresponding languages typically disappear, otherwise languages can be adopted by different bearers. In some cases a victorious people can adopt the language of a won people, for example when the majority of the women come from the won people and continue to teach their language to children or in the case of a more advanced civilization of the won people or for other cultural or economic reasons. Even if the haplogroup stays and maintains itself in the course of long migrations. languages could evolve following the rules of glottochronology, natural dynamics of languages, linguistic contact and borrowing of words.

However, once identified certain haplogroups of a people with a language (or a conjectured language, based, for example, on the haplogroups and the language of their current descendants), it is possible to follow the routes of migrations of both the people and the language. We suggest that a language can migrate and evolve along with the migration and evolution of haplogroups even over a long time and large distances, bearing in mind that: (1) the connection haplogroups / languages has to be verified by any possible means: linguistic, genetic and archaeological, (2) the language evolve along time and distances, (3) languages can be adopted by bearers of different haplogroups in case of particular events.

In this context, we can trace a new migration/linguistic/settlement (MLS) paradigm for ancient Europe according to the DNA genealogy.

As already said, the haplogroup R1a arose in Central Asia around 20,000 ybp (Klyosov and Rozhanskii [1]), migrated westward from the Altai region or North China by the southern route, i.e. via Tibet and Hindustan, Iranian plateau and Anatolia (between 10,000 and 9,000 ybp) to the Balkans and spread over Europe, then moved East to the Russian Plain to India (among other possible directions of R1a migrations). Thus, the proto-Indo-Europeans (PIE) language supposed existing in Anatolia between 10,000 and 9,000 ybp (Gray and Atkinson [14]; Bouckaert et al. [15]) could have been formed during the long migration from Altai to Anatolia. Then, it migrated together with the R1a haplogroup, in the Balkans where initiated to split into branches around 6,000 ybp which arrived around 4,800 ybp in the Russian Plain as Indo-Europeans (IE) languages. DNA genealogy has firmly confirmed that haplogroup R1a arrived to India as the legendary Aryans around 3,500 ybp, since even today up to 72% of the Indian upper castes are R1a bearers (Sharma et al. [9]). Therefore, it is allowed to conclude that it was indeed R1a haplogroup which carried the PIE language from about 20,000 to 10,000 ybp, and IE languages at least from about 10,000 to 3,500 ybp. Besides, the fact that the Russian Plain continue to speak IE languages, that up to 63% of Russians of today are bearers of R1a haplogroup, and that there are marked similarities between Slavic languages and Sanskrit permits to conclude that migrations of R1a haplogroup were indeed accompanied by PIE and IE languages.

As already said, the haplogroup R1b arose in Central Asia around 16,000 ybp (Klyosov [12]), and migrated westward by the northern route, i.e. via Northern Kazakhstan, Southern Ural, Middle Volga, then it went south over the Caucasus and probably along the eastern side of the Caspian Sea and Eastern Iran around 6500-6000 ybp. Then, it moved to the Middle East, the Tigris and Euphrates basin, apparently establishing the Sumer civilization between 5,500 and 5,000 ybp, and by several routes moved to Europe between 4,800 and 4,500 ybp (Klyosov [12]). Further, said northern route split to a first route which brought Arbins through Northern Africa to the Pyrenees and then as Bell Beakers culture around between 4,800 and 4,500 ybp to Northern Europe; a second route which brought Arbins to Europe through the Mediterranean islands and the Apennines, and yet a third route which brought Arbins around 4500 ybp to Europe through the Pontic steppes.

In the first part of their migration, along the northern route, the Arbins crossed territories populated at least for the last two millennia, and very probably also earlier, by bearers of Turkic languages, such as, Chuvashs, Bashkirs, Tatars, and other. Therefore, it is allowed to conclude that the Arbins had carried languages which arguably were proto-Turkic, or Dene-Caucasian, or Sino-Tibetian; languages that we tentatively can call Arbins, or R1b, or NIE agglutinative languages. In the Caucasus, the Arbins left the northern Caucasian group of languages, together with a characteristic vigesimal, i.e. a base 20 counting system, the same vigesimal counting system that was brought by the Arbins two thousand years later to the Pyrenees. The Arbins brought their Arbin languages to Mesopotamia, to the Sumer state (Assyrians, the likely descendants of Sumers, today are largely R1b bearers, which is rather unusual for the Middle East - Klyosov [12]), then to Iberia, where the actual

Basques, who are 87-93% R1b bearers, also employ the same vigesimal counting system. Then the Arbins as Bell Beakers moved north to the continental Europe, and brought their agglutinative NIE languages, which apparently dominated in Europe between 4,500 and 3,500-3,000 ybp, and up to the first half of the 3rd millennium bp.

In the first half of the 3rd millennium bp many R1a peoples migrated with their IE languages from the Russian Plain to Central, Western and South Europe bringing in Europe peoples later called Celts (Hallstatt and La Tene cultures between 2,600 and 2,400 ybp), Germans, Italics, Greeks, Illyrians and Balto-Slavs. Part of the Arbin peoples adopted the IE languages, for the reason seen above, from the R1a peoples and introduced in exchange NIE loan words and grammatical structures. Another part of the Arbins, from which the Basques in the Pyrenees are probably descendants, as well as the Picts in Northern Scotland and the Etruscans in Tuscany, maintained their NIE languages into the 3rd millennium bp (Etruscans), up to the end of the 1st millennium AD (Picts) and up to now (Basques).

The main linguistic theories regarding the ancient European settlements

Let us move now to the main current linguistic theories on the European settlements, and compare their views with those of the MLS paradigm for ancient Europe. The main purpose of this is to outline misconceptions in said current linguistic theories.

The Vasconic and Afro-asiatic substratum theory: The linguistic view

The Vasconic and Afro-asiatic substratum theory by Vennemann [16], according to the synthesis by Baldi et al. [17], proposes that several millennia after the end of the last Ice Age, when the glaciers receded, around 10,000 ybp, NIE peoples initiated to settle Europe starting from its Southern portion. These peoples were responsible for many European toponyms, hydronyms as well as floral and faunal names some of which have survived up to our times. Krahe [18], [19] considered many of such toponyms and hydronyms as IE but Vennemann indicated that they contained NIE roots. Krahe (ibid.) argued that hydronyms from the Atlantic shore areas to the Baltic shore areas were imposed before the 3500 ybp, and preceded the formation of the IE Baltic, Celtic, Germanic, Illyrian, Venetic and Italic language groups. Because of their similarities Krahe (ibid.) concluded that said toponyms and hydronyms constituted a group descended from a common language system he named Old European (OE). This latter, in his opinion, constituted a language layer intermediate between the PIE and the IE Baltic, Celtic, Germanic, Illyrian, Venetic and Italic language groups.

Specifically, according to Vennemann [16], several structural characteristics of many toponyms, for example the name of the Bavarian town München (Munich) which contains the root *muno / muna* which in the Basque language means *hill, slope, riverbank,* and many hydronyms containing the roots *Ava, Ara, Ala, Sala* followed by a determinative or by a set of suffixes or a suffix sequence terminated by the vowel *a* indicated them as deriving from a NIE agglutinating language.

Schmid [20], [21] extended the OE concept of Krahe by including the Eastern Slavic languages. Vennemann named Vasconic the language family of the NIE populations that imposed said toponyms and hydronyms, and the Basque language would be the only surviving language of this family. Another argument in support of the Vasconic theory would be the persistence in modern languages of traces of the vigesimal, i.e. a base 20 counting system that would be a relic of the Vasconic culture.

Vennemann [16] observed also that on the Atlantic shore area of Europe there are toponyms that are neither Vasconic nor IEs. He named the languages responsible of these toponyms Semitidic, or Atlantic group of languages. These languages, related to the Mediterranean Hamito-Semitic languages, were spoken along the Atlantic shore area between 7,000 ybp and 3,000 ybp. The Semitidic languages gave many loanwords especially to the IE western languages. They influenced superstratically, i.e. by means of loan "cultural" terms for animals, advanced cattle breading, city, buildings, warfare, society organization, the IE languages of the North-West Europe, especially the Germanic languages. Also, they influenced substratically, i.e. by means of loan terms for plants, animal and herding, the coastal IE languages, especially the Insular Celtic, beginning about 7,000 ybp. From about 7,000 ybp onward the Semitidic peoples, apparently, bearers of the megalithic culture, moved north along the Atlantic coast, reaching Great Britain and Ireland about 6,000 ybp and Sweden about 5,000 ybp.

According to Baldi et al. [17], weak points of this theory are that, up to now, the megaliths cannot be dated longer before the Bronze Age (3,500 – 2,800 ybp); it requires a Celtic presence in the British Islands about 7,000 ybp, contrary to the traditionally accepted evidence that the Celts settled the British Islands not earlier then about 4,000 ybp; the building of megaliths by Semitidic settlers is opposed by Renfrew and other mainstream archaeologists. Vennemann [16] assumes that the Picts of Northern Scotland was an Atlantic population or at least a population speaking an Atlantic language.

A similar hypothesis, according to which the Picts were a NIE population, was set out by Zimmer [22] on the basis of the Pictish customs of tattooing and the matrilineal social organisation. Literature concerning the Picts was published by Wainright [23] and Jackson [24]. Vennemann assumes no genetic connection between IE languages and Vasconic and Semitidic languages. The expansion of the OE toward the North Europe was restricted by the expansion of IE populations which adopted the Vasconic toponyms, hydronyms and other lexical items related to the natural environment. The Basques, now living in a restricted region between France and Spain, is the people speaking the only descendant language of the OE or, according to Trask [25], [26], a patchwork of NIE languages sometime largely extended, sometime not, yet sometime interrelated between them, and sometime not.

Kuzmenko [27] has reviewed lexical borrowings to Indo-European languages of Europe from an "unknown substrate". In his opinion, despite lack of consensus in that regard between linguists for the last 120 years, most of the linguists agree on a contribution of a yet unknown substrate not only to German languages but rather to all European IE languages. Kuzmenko finds a merit in a hypothesis of Vennemann [16] that Basque language (the Vasconic) is the only survived representative of that European substrate.

The Vasconic and Afro-asiatic substratum theory: A view of MLS paradigm

The Vasconic and Afro-asiatic substratum theory is partially in agreement with the MLS paradigm.

The assumption of the theory according to which NIE populations initiated to settle central and northern Europe starting from its Southern portion after the end of the last Ice Age about 10,000 ybp is not supported by the MLS paradigm according to which the Arbins (R1b) moved to Europe by several routes (Northern Africa and Pyrenees, Mediterranean and the Apennines, Pontic steppes) between 4,800 and 4,500 ybp (Klyosov [12]). However, the Vasconic as a descendant of the ancient Arbin language is in agreement with MLS paradigm. Concerning the European toponyms, hydronyms as well as floral and faunal names which sometimes survived up to our times the hypothesis of Venneman that they are NIE is more acceptable in the light of the MLS paradigm. It is in a general agreement with the hypothesis of Krahe that they are OE because, according to the MLS paradigm, the Arbins (R1b) and their NIE languages migrated as Bell Beakers culture (mainly R1b) and apparently dominated in Europe between 4,500 and 3,500-3,000 ybp, and up to the first half of the 3rd millennium bp. In this respect, however, Krahe [18], [19] appears right in assuming that said toponyms and hydronyms were imposed before the 3,500 ybp.

The assumptions of the existence of a Vasconic language family of the NIE populations that imposed said toponyms and hydronyms, and of the Basque language as the only surviving language of this family are supported by the MLS paradigm. According to the paradigm, the Vasconic language family would be nothing else than another term for the NIE languages of the Arbins (R1b) and the NIE Basque language of the present Basques of the R1b haplogroup it is very likely a surviving descendent language of the NIE languages of the ancient Arbins (R1b). A common ancestor of the present day Basques of haplogroup R1b lived around 3,700 ybp, which reflects a population bottleneck of the R1b people who lived 4,800 years ago (Klyosov [12]).

The vigesimal counting system used both by the Basques and by Caucasian populations is supported and explained by the MLS paradigm as a characteristic showing a connection that existed between the corresponding ancient Arbins (R1b) that migrated along the Northern route across the Caucasus, the Mediterranean islands and northern Africa to Central Europe and the pushing and relegation of the Arbin ancestors of the Basques in the Pyrenees region.

Concerning the Semitidic, or Atlantic group of languages mentioned by Vennemann [16], according to the MLS paradigm, they might indeed have survived until the 1st millennium AD, and could have been spoken by the Picts of Northern Scotland. The haplogroup of the Picts is unknown, but it might have been I1 or I2 (as well as anything else, listed above), because both can be met in the Isles today. The great majority of nowadays population in the Isles bears R1b haplogroup, which came to the Isles after 4,200 ybp. The three groups of languages IE, NIE and Semitidic, or Atlantic, apparently belonged to Aryan tribes (R1a), Arbin tribes (R1b), and Semitidic, or Atlantic tribes (I1/I2/G2), which represent completely different tribes with a common ancestor of around 55,000 ybp (Klyosov and Rozhanskii

[1]). Therefore, a suggestion of Vennemann that there were no genetic connection between IE languages and Vasconic and the Semitidic or Atlantic languages seems to be justified.

The Anatolian theory: The linguistic view

Renfrew [28], in summarising the Anatolian theory, affirms that the PIE language, or the PIE linguistic family of languages, or the pre-PIE languages (Diakonov [29]), formed in the Central Anatolia in the Neolithic time, about 9,000 ybp, and that the PIE or IE languages diffused in Europe from West Anatolia in parallel with the diffusion of the agriculture. More precisely, the Anatolian theory proposes that:

- linguistic families that have large diffusion in Europe have distributions corresponding to the economic, social and demographic consequences, that the diffusion of the agriculture produced in their development areas;
- the language or languages spoken in said areas were established either by demic diffusion of the archaic PIE populations, or by non-demic linguistic changes due to linguistic contacts;
- the archaic PIE language after its separation from the pre-PIE in Anatolia evolved and modified itself through the diffusion of the agriculture in Europe – Phase I of the PIE.

Renfrew [28] explains that reliable radiocarbon datings have permitted to establish that the domestication of plants and animals from West Anatolia reached Greece and Crete around 8,500 ybp. Linguistic changes in Greece and the Danube and the Balkan areas were due mainly to demic migrations during the 9th and 7th millennia bp. At the same time, for other European areas, i.e. on the West in the present-day Dalmatia, Germany and France, South Italy and Sicily, and on the East in Hungary, Bulgaria and Ukraine, the changes were mainly due to linguistic contacts. The diffusion of the agriculture further East from what is now Ukraine could have brought to the formation in the Chinese Sinkiang of an IE peoples, that around 3,500 ybp spoken Tocharian.

Renfrew [28] observes that:

- Gray et al. [14], [30] on the basis of 87 languages and 2,449 lexical items and further datasets indicated an initial IE divergence between 11,800 and 9,800 ybp, which is consistent with said separation of the archaic PIE from the pre-PIE;
- Ryder et al. [31] indicate a unimodal posterior distribution for the PIE at about 10,400 ybp, which supports the Anatolian theory;
- other linguistic studies by Sturtevant [32], Dolgopolsky [33], [34], Gamkrelidze and Ivanov [35], [36], Pringle [37] and Bouckaert et al. [15], this last based on the spatial diffusion of infectious diseases, also support the Anatolian theory.

Renfrew [28] affirms that a first advergence linguistic area formed itself in the Balkan region in the period between 7,000 and 5,000 ybp - Phase II of the PIE. Some linguistic characteristics of the Celtic languages and the Tocharian languages indicate that they do not taken part in the Balkan linguistic advergence area. The disaggregation of the Balkan advergence linguistic area, around 5,000 ybp, indicates the end of the Phase II of the PIE and the separation of the Greek or proto-Greek from the proto- Thracian, proto-Dacian, proto-Phrygian and others. In the same time there would be also the separation of the proto-Indo-Iranian spoken in the Northern area of the Black Sea and its diffusion toward the Iranian plateau and India. The linguistic similarities between Greek, Armenian and Sanskrit – Phase III of the PIE – represent a result of said Balkan linguistic advergence area, which does not require languages or dialects as proto-Slavic, proto-Baltic, proto-Greek, Proto-Indo-Iranian, already distinguished within the PIE or pre-PIE. Concerning the other languages Renfrew [28] affirms that they were developed in different advergence areas were now their descendant languages are spoken.

The Anatolian theory: A view of MLS paradigm

The Anatolian theory is generally compatible with the MLS paradigm, although the theory is silent about the evolution of the PIE language before about 9,000 ybp.

As it was described above, the proto-Aryans (R1a) migrated westward across Anatolia around 10,000 - 9,000 ybp, which fits the linguistic estimates of 9,000 ybp (Renfrew [28]; Diakonov [29]) or 11,800 - 9,800 ybp (Gray et al. [14], [30]). "Diffusion of agriculture", "demic diffusion" or "non-demic diffusion" are concepts beyond the MLS paradigm. According to the MLS paradigm, the migrations of the proto-Aryans (R1a) from Anatolia to the Balkans about 9,000 – 8,000 ybp could represent the Phase I of the PIE, the later spreading of the Aryans (R1a) along with their IE languages over Europe about 8,000 – 5,000 ybp could represent the Phase II of the PIE, and then their migration eastward to the Russian Plain and their split into at least four migration routes to South, South-East, South East-East, and East about 4,500-4,000-3,500 ybp toward India could represent the Phase III of the PIE.

The affirmation of the Anatolian hypothesis that the Tocharian languages did not taken part in the Balkan linguistic advergence area, at the moment, cannot be decided on the basis of the MLS paradigm. The Tocharians were ascribed to the "Europeans" (Gray et al. [14]; Li et al. [38]) mainly on the basis of their somatic features, their haplogroup R1a and their clothing which, of about 4,000 ybp, looked "like Scottish plaid". On the language tree by Gray et al. [14], the Tocharian languages represent a very archaic branch, around 7,900 ybp, which were spoken by populations in the Tarim Basin. The linguistic distance of the Tocharian A, B with respect to the other IE languages (Tomezzoli and Kreutz [39]) demonstrates them to be the closest to Slovene and Venetic, and the most distant from the Anatolian languages Hittite and Luwian. Thus, according to the MLS paradigm two explanations would be possible:

- either the proto-Tocharians migrated westward to Europe and the Russian Plain together with the proto-Aryans (R1a), which probably brought the way of producing said clothing to Europe and Scotland and then, at about 4,000 ybp, they arrived from the Russian Plane to the Tarim Basin as part of the stream of the R1a people reaching India;
- or the proto-Tocharians did not migrated westward to Europe and the Russian Plain together with the proto-Aryans (R1a); they migrated from the Altai region or North China to the nearby Tarim Basin and remained there forming the autochthonous R1a peoples of Central Asia, and have never been in Europe. In any case very recent evidences (http://pereformat.ru/klyosov/) permit to state that the present Altai male populati-

on has R1a haplotypes which are very similar with the excavated R1a haplotypes in the Khakass-Minusinsk Basin (Adronovo) and Tagar (Tochar ?) cultures dated 3800-3400 ybp and later. They descended from the same common ancestor who lived 4500 ybp on the Russian plane.

Anatolia cannot be considered the homeland, or “Heimat” of the IE languages because according to the MLS paradigm, IE and NIE languages had no homelands, they migrate over thousands of miles and over thousands of years together with the R1a bearers.

According to the MLS paradigm, the predecessors of IE languages might have migrated some 50,000 ybp and further on from the birthplace of the β-haplogroup, the birthplace of which is unknown as yet, however, it might have been Europe or the Russian Plain, to South Siberia in which they arrived some 40,000-35,000ybp and then they migrated westward from 20,000 ybp along with the R1a haplogroup via Anatolia, which might have been just a passing point, to the Balkans, another passing point to the Russian Plain and Pontic steppes, yet another passing point, to the Middle East, Middle Asia, Iranian plateau, Ural mountains, Hindustan, South Siberia again, North China, Mongolia. All of them are in fact some passing points, and not homelands for the predecessors of the IE languages.

The Kurgan Theory: The linguistic view

During the Mesolithic and the Neolithic, NIE and IE peoples during the dry and cold period of the Younger Dryas 12,800 – 11,500 ybp settled along the shores of the Black Sea. The PIE formed in this area. At about 7,600 ybp (Ryan [40]), due probably to a cataclysm, the waters of the Mediterranean Sea entered the Black Sea through the Bosporus, causing in a short period, the raising of the water level to the present level and the submersion of many settlements. This event caused migrations toward the Balkan Region, the Central Europe and the formation of the Neolithic cultures of Vinča and of the Linearbandkeramic (LBK).

Gimbutas [41] defined Ancient Europe as the European Culture developed between the 9th and the 7th millennia bp in the area of the Balkans, Greece, Adriatic region, Moldavia and Ukraine before the arrival of the IEs. Gimbutas [42] provided a comprehensive description of the cultural level of the Ancient Europe characterized by well organised settlements, mixed horticular economies, elevated quality of the sculpture and the ceramics, and elaborated religious traditions. This materialized in the cultures of Bükk, Butmir, Cucuteni-Tripolye, Dimini, Karanovo, Lengyel, Petreşti, Vinča and the Linearbandkeramic (LBK). The attempts of writing by these cultures would predate by two thousand years the Sumerian writing. The discovery of a large number of female figurines, sometime crowned, together with other archaeological, mythological, historical evidences, brought Gimbutas to consider the women as the prominent players in the social life of the cultures of the Ancient Europe, which were characterised by matriarchy and egalitarism. She considered a Goddess or Big Goddess as principal religious symbol not only of fertility and procreation, but also of ruler of all what existed on the Earth.

The languages spoken in the Ancient Europe were NIE, as testified by surviving of NIE agricultural, technological and social terms, toponyms, personal and tribe names. The Ancient Europe about between 7,500 and 6,300 ybp developed an advanced civilization, including metallurgy and writing. The Model of the steppe, or the Kurgan model, or the Kurgan hypothesis, or the Kurgan theory developed mainly by Gimbutas [43], [44], see the synthesis by Marler [45], proposes the formation, about in the 7th millennium bp, of territorial, nomadic, pastoral peoples speaking PIE languages, collectively named Kurgan Culture, in the area of the Dnepr and Don basins, the middle and lower Volga basin, the Caucasus and the Ural mountains. The tombs, covered by round tumuli named kurgans contained often weapons and other artefacts indicating a set of cultures marked by: a pastoral economy with a rudimentary agriculture, territorialism and nomadism, the domestication of the horse which happened around the 7,000 ybp (Bököny [46]; Gimbutas [42]) between East Ukraine and Kazakhstan, a patriarchal, patrilineal hierarchy and a secondary social role of the women.

The fact that the Kurgan culture had characteristics different from those of the cultures of the Ancient Europe, indicated that it was not developed from the cultures of the Ancient Europe.

A first migration of Kurgan culture peoples, according to the theory, took place about during 6,400 – 6,300 ybp, due to the progressive drying of the steppes during the 8th and the 7th millennium bp, towards Bulgaria, the Danube basin, and Central Europe. This was not a mass migration, but a migration of small bands, letting the original population of the Ancient Europe as majority. This migration is testified by the increasing of kurgan tombs, discovered between the egalitarian tombs of the Ancient Europe cultures, the fortification of the settlements, the damages to the settlements of the Varna, Karanovo-Gulmenița, Vinča, Lengyel and LBK cultures, and the substitutions or dissolution of some Ancient Europe cultures in new Kurgan cultures. The development of IE languages was due to language substitution and bilinguism.

A second migration took place around 5,500 ybp from the area north of the Black Sea through Ukraine toward Poland, Central and East Germany. In this period the four wheel wagon appeared in Europe, along with the plow and the metallurgy of bronze, which was interpreted as the activity of surviving Ancient Europe cultures, absorbed by Kurgan cultures. This second migration led to the formation of hybrid-cultures: the Baden complex in the middle Danube basin, having the Vinča culture as substrate, the Ezero culture in Bulgaria, having the Karanovo culture as substrate, the Globular Amphora culture in Rumania, West Ukraine, Poland, and Germany, having the Trichterbecherkultur (TBK) as substrate. In parallel with the development of said hybrid-cultures, took place the fragmentation of the PIE into the IE languages. The appearance of a religious solar symbolism and armoured IE deities were rather typical for this migration.

A third migration took place about between 5,000 and 4,800 ybp, from the Volga steppes. It was more massive than the other two as witnessed by the numerous Yamnaya culture burials in the Balkan region and East Hungary. This migration caused the displacement of the hybrid cultures of Central Europe, originated mainly by the second migration, toward the Northern Europe, Southern Scandinavia, Baltic area, and Central Russia. The

Minoan civilization in the Aegean Sea reached its culmination during the first half of the 4th millennium bp, i.e. before the arrival of the IE Mycenaeans. This last migration was followed by a period of stability characterized by the formation of cultural groups (Gimbutas [43], [44]) which were speaking separated IE languages.

The Kurgan theory: A view of MLS paradigm

The Kurgan theory appears incompatible with the history of Europe based on the MLS paradigm.

According to the MLS paradigm, PIE arrived to the Balkans after a long migration from Central Asia, as described above in this paper. Boric and Price [47]) has shown, using strontium isotopic measurements, a significant increase in non-local individuals in the Balkans from ~ 8200 ybp. This generally coincides with timing of the arrival of R1a peoples and IE languages to the Balkans. Thus, both them did not come from the Pontic steppes.

The MLS paradigm indicates a migration of R1a peoples eastward, from Europe to the Russian Plain about between 4,600 and 4,000 ybp, i.e. a direction opposite to the direction of the migrations suggested by the Kurgan theory, and a migration of R1b peoples southward earlier, between 7,000 and 5,000 ybp and westward, about between 5,500 and 5,000-4,500 ybp.

The Kurgan theory has completely distorted the whole pattern of what has happened in Europe and in the Russian Plain about between 5,000 and 3,000 ybp. Besides, contrary to what is proposed by the Kurgan:

- The PIEs and the corresponding PIE language did not settled or formed along the shores of the Black Sea about between 12,800 and -11,500 ybp. Actually, the PIE language formed or rather evolved along said southern Black Sea shores, or steppes north of them, witnessed only the late period of settling the IE languages around 4,500 ybp, i.e. when IE languages were already split. At the moment, it is unknown which haplogroups, if any, were the most affected by the Black Sea cataclysm. It might have been G2a, E1b, F, I1, I2, etc., with survivors which moved westward, to Europe.
- Ancient Europe cannot be considered as the European culture developed between the 9th - 7th millennia bp in the area of the Balkans, Greece, Adriatic region, Moldavia and Ukraine before the arrival of the IEs. In fact, the IEs (R1a) arrived to the Balkans and further in Europe between the 10th - 8th millennia bp.
- The languages spoken in the Ancient Europe were not totally NIE, in fact, the arriving IEs (R1a) between the 10th - 8th millennia bp introduced their IE languages. The presence of surviving NIE agricultural, technological and social terms, toponyms, personal and tribe names cannot be considered as a valid argument supporting an Ancient Europe totally NIE, since between said period in Europe both IE and NIE languages co-existed.
- The Kurgan theory is in error in proposing the formation of territorial, nomadic, pastoral populations speaking PIE languages, collectively named Kurgan culture, in the 7th millennium bp in the area of the Dnepr and Don basins, the middle and lower Volga basin, the Caucasus and the Ural mountains. In fact, there were no PIEs (R1a) at those

times on said territories. Actually the Kurgan theory describes here NIEs (R1b) who migrated westward by the northern route. The Kurgan theory apparently has mixed and inverted the roles of the NIEs (R1b) and the IEs (R1a).

- The Kurgan theory is in error in ascribing kurgans, nomadism, and domestication of horse around 7,000 ybp between East Ukraine and Kazakhstan to the IEs. Instead, these cultural features should be ascribed to NIEs (R1b) who migrated westward by the northern route.
- The three waves of IE migrations to Europe – the first about between 6,400 and 6,300 ybp, the second about between 5,500 ybp from the area North of the Black Sea, and the third about between 5,000 and 4800 ybp, which originated in the Volga steppes appear not sustainable. Apparently, there was no IEs (R1a) in the Volga steppes about between 5,000 and 4,800 ybp and earlier, they arrived later about between 4,600 and 4,300 ybp and if there were, unlikely, IEs (R1a) they were moving in the opposite direction, that is from Europe eastward. What the Kurgan theory actually conjectured, was related to the migrated westward of NIEs (R1b) by the northern route.

The Palaeolithic Continuity Theory: The linguistic view

Concerning the Kurgan theory, Alinei [48] observes that a great IE invasion in the Chalcolithic, with total ethnic and linguistic substitution on continental scale, is simply unconceivable. He suggested that the evidence that the greater part of common Neolithic IE lexicon, i.e. the set of loan words designating innovating devices like the plow, the yoke, the wheel, some domesticated animals, plants and some metals, was already diversified in almost all the IE languages indicates that the IE languages were already diversified in the Mesolithic and the Neolithic.

Concerning the Anatolian hypothesis, Alinei [48] observes that few millennia in the Neolithic and the limited migrations in the Balkans and Central Europe from Anatolia are not sufficient for the development and differentiation of the IE languages in Europe. Moreover, according to Alinei [48], they cannot explain the relatively big number of NIE toponyms in the Aegean area and the NIE words in Greek and other languages of South Italy, Sicily, Sardinia, Corsica and Spain. These observations, according to Alinei, support the hypothesis that the populations coming from Anatolia were NIEs and that the Neolithic in Europe was a period of complex acculturation and geographical differentiation in which small migrating groups played a limited role with respect to the populations already inhabiting Europe.

The fact that the greater portion of the grammatical structure of the Celtic, Germanic, Italic, Greek, Illyrian and Balto-Slavic do not belong to the common IE means that they could not be formed in the Chalcolithic or Eneolithic. In this situation, Alinei [48] affirms that the only solution is offered by the Continuity Model, or Palaeolithic Continuity Theory (PCT) supported by the recent acquisitions of the paleoanthropology which is arrived to the conclusion that not only *Homo erectus* but also *Homo habilis* and perhaps some kind of *Australopitechus* were able to talk (Tobias [49]). Moreover, the cognitive sciences have reached the same conclusion, i.e. for explaining the innate character of the language in the humans it is necessary that the language be connected with the *Australopithecus* (Pinker [50]). Thus, the structural portions of the human languages, including the PIE languages, i.e. words, affixes, syntax formed long time ago in Africa in connection with the human evolution.

Alinei [48] considers that Europe would have been occupied by IE, NIE and Uralic peoples as soon as the archaeology, the paleoanthropology and similar sciences permit to establish. The NIE peoples would have played a peripheral role influencing the IE languages by contact and adstrates. Although by excluding a massive invasion of Europe during the Chalcolithic or Neolithic, Alinei [48] accepts all the migrations and invasions attested by archaeology and considers them as important factors of hybridization. An important hybridization took place at the beginning of the Neolithic in South Europe by infiltration of NIE populations and by the migrations of the Kurgan peoples, of Turkic culture, during the Chalcolithic. Other hybridizations took places during the Bronze Age. However, these hybridizations would have only superstratically altered the languages and cultures of the IE populations. Concerning the Uralic peoples, speaking Finno-Ugric and Samoyeds languages, in the North West Europe and North West Asia, Alinei [48] considers them as a branch of the *Homo sapiens* coming from South and settling in North-West Europe during the Mesolithic.

Alinei [48] considers that the sedentarysation of the IE populations would have started in Northern Europe during the Mesolithic and in Central and Southern Europe during the Neolithic. The Baltic, North-Germanic, North-Celtic populations of fishers and hunters were the first to settle in the territories free from ice, followed by the Southern-Greek, Slavic, Illyrian, Italic populations which developed Neolithic forms of production, and then the Northern-Slavic, Southern-Germanic and South-Celtic groups. Alinei [48] considers that in northern Europe, the Baltic Sea was a cultural border between Baltic, Slavic, Germanic and Uralic populations. During the Mesolithic, it was the border between the Uralic culture of Kunda on the northern coast and the Maglemose and Nemunas cultures on the southern coast. During the Neolithic, it was the border between the Uralic cultures of Narva on the northern coast and the IE cultures of Nemunas, Comb and Cardial Ceramics, Globular Amphorae and the Ship form Axe on the southern coast. In Central Europe, a border existed in Switzerland, Alsace and Belgium between Germanic and Latin groups, which coincided with the border between the LBK culture and the Cord impressed Ceramics.

Alinei [48] considers that Celtic and Northern-Celtic peoples occupied Western Europe, including Brittany and Ireland, as long ago as before the retreat of glaciers, and they created the Megalithism and the TBK cultures. The Italide or Italoide ethnolinguistic peoples occupied southern Europe, from the Iberian Peninsula to Dalmatia, during Palaeolithic. During the Neolithic, the Balkan area was influenced by NIE migrant groups of farmers, which created the *Balkan Sprachbund*, i.e. the Balkan group of languages: Greek, Serbian, Bulgarian, Macedonian, Albanese and Rumanian which shared some basic features. The exceptional stability of the Balkan area is witnessed by the tells, artificial hills built by rests of sedentary life, and the lack of deep differences between the Slavic languages. Some isoglosses connecting the East and the West Slavic, with the South Slavic would be caused by two migrations of South Slavic farmers: one to the East generating the Tripolye culture, the other to the West generating the Lengyel culture.

Alinei [48] suggests that the aggressive migrations of the Chalcolithic as well as of the Bronze and Iron Ages, were caused by elitarian IE and NIE peoples, as the Etruscan, generated hybridization processes without changing the ethnolinguistic IE frame of the ancient Europe. The Chalcolithic Kurgan culture and the Srednij Strog culture, through which it developed, should be considered as Altaic, Turkic cultures and so were all the nomadic, pastoral cultures which developed the domestication of the horse up to the Medieval Kurgans and the Huns. The Kurgan culture introduced Turkic, not Iranian, influences on the IE languages, and the border between the Tripolye and Srednyj Strog cultures would represent the border between Slavic and Turkic cultures. The late Combat Axes peoples would be the IE peoples influenced by the Kurgan culture. The Europe of the Bronze Age would correspond to the Modern Europe in that sense, according to the Uniformity Principle of the Historical Linguistics which suggests that the areas of the Bronze Age civilizations correspond to the dialectal language areas, which in turn correspond to each IE language.

The PCT: A view of MLS paradigm

The PCT appears incompatible with the history of Europe based on the MLS paradigm.

The PCT places the origin of the PIE language in Europe to the Upper Palaeolithic, minimum 10,000 ybp, and linked it to the arrival of people in Europe from Africa and proposes the continuity of peoples and languages in Europe for the last at least 10,000 ybp, generally from Palaeolithic times. But this view does seriously collide with the MLS paradigm.

The only parts of the PCT which find support by the MLS paradigm are the following:

- The PIE languages arrived in Europe around 10,000 ybp; although they did arrive not from Africa, but from Asia, via Anatolia.
- Words designating innovating devices, domesticated animals, plants and some metals, were already diversified in IE languages, and were not brought by R1b "invaders" which arrived in Europe only in the beginning of the 5th millennium bp.

However, according to the MLS paradigm, peoples, meaning also genealogical lineages or haplogroups, and languages in Europe have not shown a continuous pattern. In fact, according to the MLS paradigm:

- IE (R1a) populations fled from Europe to the Russian Plain around 4,600 ybp. There were at least ten of R1a peoples each with a distinct subclade/SNP and/or a branch of haplotypes, which migrated back to Europe since the beginning of the 3rd millennium bp.
- Haplogroup G populations were almost completely eliminated in Europe about between 4,500 and 4,000 ybp, apparently by the arriving of the Arbins (R1b), and survivors fled to Asia Minor, Mesopotamia and the Caucasus. The excavated haplotypes of E-V13 showed the dating of 7,000 ybp, however, the current E-V13 has a common ancestor of only 3,500 ybp indicating a population bottleneck.

- Haplogroup I1 populations were almost completely eliminated in Europe about between 4,500 and 4,000 ybp, and went through a severe population bottleneck around 3,600 ybp; in other words, the date of 3,600 ybp was the "new beginning" for I1 haplotypes in Europe.
- Haplogroup I2 populations were almost completely exterminated in Europe around 4,500 ybp, and the survivors fled to the Isles and to the Eastern Europe, their present day populations have common ancestors at 4800 ybp and 2300 ybp, respectively.
- NIE (R1b) arrived to Europe, at the Pyrenees as Bell Beaker culture, around 4,800 ybp and at the Apennines and the Balkans, and from the Pontic steppes from the East, around 4,500 ybp and caused the major disruption to populations and languages of the Old Europe.

Besides, in the PCT there are some other points that are questionable in the light of the MLS paradigm:

- The proposal of the PCT that few millennia in the Neolithic and the limited migrations in the Balkans and Central Europe from Anatolia were not sufficient for the development and differentiation of the IE languages in Europe is questionable. In fact, IEs (R1a) were in Europe from about between 10,000 and 9,000 ybp up to between 5,000 and 4,500 ybp, that is for a period of about 4.4-5.0 millennia. Thus, it cannot be assumed that there was a too short time for "development" and "differentiation" of the IE languages.
- The proposal of the PCT that the arrival of IE languages from Anatolia "cannot explain the relative big number of NIE toponyms in the Aegean area and the NIE words in Greek and other languages of South Italy, Sicily, Sardinia, Corsica and Spain" is questionable. The IEs (R1a) did not come to an empty Europe, there already were NIE populations of haplogroups E, F, G, I1, I2, J2, K, etc. So, IE languages were very likely introduced in a NIE speaking Europe. Moreover, the PCT assumption that "These facts support the hypothesis that the populations coming from Anatolia were NIEs" is contradicted by the MLS paradigm. It might well be, though, that some other haplogroups/tribes speaking NIE languages also migrated to Europe about between 10,000 and 9,000 ybp, however, it would not change the language landscape of the ancient Europe.
- The suggestion of the PCT that "the structural portions of the human languages, included the PIE languages, i.e. words, affixes, syntax, formed long time ago in Africa in connection with the human evolution" appears erroneous and unsupported. Nobody can responsibly exclude that *H. habilis* and *Australopithecus* were able to talk, however, DNA genealogy has shown that non-Africans do not have "African" SNPs in their Y chromosomes (Klyosov and Rozhanskii [1], [2]). The Africans and non-Africans do have plenty of SNP-mutations from a common ancestor of humans and chimpanzee; however, apparently, non-Africans have not received them from the Africans (ibid.). As consequence of this lack of hybridization, it is hard to imagine that African languages, as for example the click languages, could have evolved to the PIE languages.
- The suggestion of the PCT that "Celtic and Northern Celtic populations occupied Western Europe, including Brittany and Ireland, as long ago as before the retreat of

glaciers, and they created the Megalithism and the TBK cultures" appears erroneous and unsupported. According to the MLS paradigm, Celtic populations and Celtic IE languages reached the Isles in the 3rd millennium bp and the Celtic languages were imposed to the NIEs (R1b). This explains why Celtic languages are spoken up today in the British Islands by R1b populations (around 90% and above of today populations) plus a little amount (singular per cent) of R1a, I1, I2 and other minor haplogroups populations on the Isles.

The earlier genetic studies

There were many errors made by the founding fathers and population geneticists in what they have called "genetic genealogy", or "population genetics" in the 1990-s and 2000-s as highlighted by the DNA-genealogy. They claimed, for example, that bearers of R1b lived in Europe 30,000 ybp (Wells et al. [51]; Wells [52]), or between 40,000 and 35,000 ybp years ago (Semino et al. [53]). The main reason was, apparently, that if R1b populations live in Europe now, then, in their minds, they lived there practically always. This erroneous idea of about 30,000 ybp for R1b tribes in Europe, stuck for 15 years and continuous to stick nowadays in population genetics literature. This date was cross-cited hundreds times in academic publications. However, according to the MLS paradigm, R1b tribes have arrived to Europe by the northern route only around between 4800 and 4500 ybp.

They claimed that R1a haplogroup arose in South Russian steppes 15,000 ybp (Wells et al. [51]). Then the date was changed to 10,000 years (Wells [52]), with no explanations, also because the first one was practically invented. They claimed that the oldest R1a bearers survived the Ice Age in some "Ukrainian refuge" (Semino et al. [53]) without any ground for this assumption. As a result, the R1a was called for years without ground "Ukrainian haplogroup" (Wiik [54]).

They claimed that genetic data showed the African origin of man, and that man left Africa some 70,000 ybp (other dates were of 50,000 or 60,000 ybp, and around) without any ground (Klyosov and Rozhanskii [2]). They made no calculations or no appropriate calculations based on Y chromosome. The main reason was that the African Y-chromosomes are more "diverse" compared to non-African Y chromosomes. However, diversity as criterion of "age" is valid only in closed systems. In open systems, such as Africa in this particular case, diversity is a consequence of mixing of Y chromosomes. Unfortunately, those dates flooded the academic literature from the 1990-s to our times, and they continue to flood. More recent genome studies have only shown that the African genome has a wide gap with respect to non-African "generalized" genome, as shown in Fig. 1. There are no indications that non-Africans descended from the Africans also because African SNPs are absent, for example, in Europeans (Klyosov and Rozhankii [1], [2]). Klyosov and Rozhanskii [1] have shown that the stream of SNP mutations from a common ancestor with chimpanzee goes to the α-haplogroup, from which the African lineage (haplogroup A) split around 120,000 ybp, and evolved separately as Y-chromosomal lineage from the

Europeid lineage. Another archaic African lineage split even earlier, some 200,000 ybp or still earlier some 350,000 ybp (Mendez et al. [55]), and goes to Africa. In other words, the "Out of Africa" hypothesis has presented a distorted pattern of the origin of man and its languages (Klyosov and Rozhanskii [2]).

In the same way, the "evolution tree" designed by Cavalli-Sforza and Edwards [56] and Cavalli-Sforza [57], and which indicated that the most ancient peoples that separated first were those of the islands, Sardinia and Iceland, and isolated social groups like Lappishes and Basques, could not hold the scrutiny of examination. In fact, the Basques (R1b) have their common ancestor around 3,700 ybp. The error was probably induced by the use of the method of principal components, which is based on very arbitrary multiple assumptions.

Conjectures by Richards et al. [58] and Sykes [59] based on mtDNA considerations suggested that the actual European populations are the results of the settlement of Anatolia in the Upper Palaeolithic are questionable. Anatolia was not an isolated spot but since at least 40,000 ybp a crossroad or passing point for many haplogroups, among them E, F, G, J, K, R1a, R1b. Of course, Anatolia was very important for development of civilization, but it was not a cradle of the actual European populations. It seems that haplogroup I, or the possible combined haplogroup IJK, moved from the Russian Plain westward some 45,000 ybp and so contributed to the European settlement.

The population geneticists of the 1990-s – 2000-s, apparently, have tried to please historical considerations of that time by bending their DNA-based exercises accordingly. They uncritically considered "gradients of frequency", which can always be found for whatever reason, including population bottlenecks, ignoring the existence of downstream subclades. In many studies (Hammer [60]; Underhill [61]; Zhivotovsky [62]) erroneous "mutation rates" were employed, such as "population rate constants" or "Zhivotovsky mutation rates" which increased the actual datings by 350-400%. As a result, the "age" of populations are inflated by 3.4-4.0 times, IE population in India becomes the age not of 3,500 ys but of 14,000 ys.

Similarly, Semino et al. [53] concluded, that European peoples are genetically different with respect from other Europeans like the Basques. This appears totally wrong, since the Basques, as already seen, in their majority have a common R1b haplogroup and dated by the same time as about 60% of Europeans, and typical phrases such as "Concerning in general the genetic structure of the European populations, the Neolithic genetic components are prevalent in the Southern Europe and the Palaeolithic genetic components are prevalent in the Northern Europe" are not are erroneous, since the authors did not knew which "genetic component" was really Neolithic and which Palaeolithic. In fact, the Southern Europe has many Palaeolithic haplogroups, such as E, F, G, K, J, some of them passed a severe population bottleneck around 4500 ybp apparently a result of the Arbins (R1b) arrival to Europe. Similarly, the Northern Europe has Palaeolithic haplogroups, such as I1, which passed the same bottleneck.

Conclusion

To sum it up, the earlier genetic studies of the origin of Europeans often presented superficial conclusions based on scarce data without a serious scientific scrutiny. DNA genealogy has started only in 2009 and before that date any historical considerations based on DNA cannot always be assumed as valid. The DNA genealogy brought us to the construction of the MLS paradigm for Ancient Europe which has permitted to put the current main linguistic theories under scrutiny and to disprove the Kurgan theory and the PCT and in some way to correct and complete the Vasconic theory and the Anatolian theory. In addition, DNA genealogy has permitted also to put in question some aspects of the "Out of Africa" hypothesis.

Bibliography

1. Klyosov, A.A., Rozhanskii, I.L., Ryanbchenko, L.E. (2012) Re-examining the Out-of-Africa theory and the origin of Europeoids (Caucasoids). Part 2. SNPs, haplogroups and haplotypes in the Y chromosome of Chimpanzee and Humans. Adv. Anthropol. 2, 198-213.
2. Klyosov, A.A., Rozhanskii, I.L. (2012) Re-examining the "Out of Africa" theory and the origin of Europeoids (Caucasoids) in light of DNA genealogy. Adv. Anthropol. 2, 80-86.
3. Benazzi, S., Douka, L., Fornai, C., Bauer, C.C., Kullmer, O., Svoboda, J., Pap, I., Mallegni, F., Bayle, P., Coquerelle, M., Condemi, S., Ronchitelli, A., Harvati, K. (2011) Early dispersal of modern humans in Europe and implications for Neanderthal behavior. Nature, 479, 525-528.
4. Higham, T., Compton, T., Stringer, C., Jacobi, R., Shapiro, B., Trinkaus, E., Chandler, B., Groning, F., Collins, C., Hillson, S., O'Higgins, P., FitzGerald, C., Fagan, M. (2011) The earliest evidence for anatomically modern humans in northwestern Europe. Nature, 479, 521-524.
5. Prat, S., Pean, S.C., Crepin, L., Drucker, D.G., Puaud, S.J., Valladas, H., Galetova-Laznickova, M., van der Plicht, J., Yanevich, A. (2011) The oldest anatomically modern humans from far Southeast Europe: direct dating, culture and behavior. PLOS ONE, 6, No. 6, e20834.
6. Anikovich, M.V., Sinitsyn, A.A., Hoffecker, J.F., Holliday, V.T., Popov, V.V., Lisitsyn, S.N., Forman, S.L., Levkovskaya, G.M., Pospelova, G.A., Kuzmina, I.E., Burova, N.D., Goldberg, P., Macphail, R.I., Giaccio, B., Praslov, N.D. (2007) Early Upper Paleolithic in Eastern Europe and implications for the dispersal of modern humans. Science, 315, 223-226.
7. Bednarik, R.G. (2012) The origins of human modernity. Humanities (ISSN 2076-0787), 1, 1-53.
8. Bednarik, R.G. (2013) Pleistocene palaeoart of Africa. Arts (ISSN 2076-0752), 2, 6-34.
9. Sharma, S., Rai, E., Sharma, P., Jena, M., Singh, S., Darvishi, K., Bhat, A.K., Bhanwer, A.J.S., Tiwari, P.K., Bamezai, R.N.K. (2009) The Indian origin of paternal haplogroup R1a1* substantiates the autochthonous origin of Brahmins and the caste system. J. Human Genetics, 54, 47 - 55.
10. Rozhanskii, I.L., Klyosov, A,A. (2012) Haplogroup R1a, its subclades and branches in Europe during the last 9000 years. Adv. Anthropol. 2, 139-156.
11. Kayser, C., Bouakaze, C., Crubezy, E., Nikolaev, V.G., Montagnon, D., Reis, T., Ludes, B. (2009) Ancient DNA provides new insights into the history of south Siberian Kurgan people. Hum. Genet. 126, 395-410.
12. Klyosov, A.A. (2012) Ancient history of the Arbins, bearers of haplogroup R1b, from Central Asia to Europe, 16000 to 1500 years before present. Advances in Anthropology, 2, No. 2, 87-105.
13. Lacan, M., Keyser, C., Ricaut, F.-X., Brucato, N., Tarrús, J., Bosch, A., Guilaine, J., Crubézy, E., Ludes, B. (2011) Ancient DNA suggests the leading role played by men in the Neolithic dissemination. Proc. Natl. Acad. Sci. US, 108, No. 45, 18255-18259.
14. Gray, R.D., Atkinson, Q.D. (2003) Language-tree divergence times support the Anatolian theory

of Indo-European origin. Nature 426, 435-439. On line at http://www.nature.com/nature/journal/v426/n6965/full/nature02029.html .

15. Bouckaert, R., et al. (2012) Mapping the origins and expansion of the Indo-European language family. Science 337 (6097), 957-960. On line at http://onlinelibrary.wiley.com/doi/10.1126/science.121.9669.
16. Vennemann, T. (2003) Europa Vasconica – Europa Semitica, Berlin.
17. Baldi, Ph., Page, R.B. (2006) Review Europa Vasconica – Europa Semitica. Lingua 116, 2183-220. ISSN 0024-3841. On line at www.sciencedirect.com .
18. Krahe, H. (1954) Sprache und Vorzeit: Europäische Vorgeschichte nach dem Zeugnis der Sprache, Quelle und Meyer, Heidelberg.
19. Krahe, H. (1964) Unsere ältesten Flussnamen, Harrassowitz, Wiesbaden.
20. Schmid, W.P. (1987) "Indo-European" – "Old European". – in: Skomal, S.N., Polomé, E.C. (Eds.). Proto-Indo-European: The Archaeology of a Linguistic Problem. Studies in honour of Marija Gimbutas. Institute of the Study of Man, Washington, 322-338.
21. Schmid, W.P. (2001) Was Gewässernamen in Europa besagen. Akademie-Journal 2, 42-45.
22. Zimmer, H. (1898) Matriarchy among Picts in Henderson, G., Zimmer, G. (Eds.), Leabhar nan Gleann. Norman Macleod Edinburgh, 1-42.
23. Wainright, F.T. (1955) The Picts and the problem. – in: Wainright, F.T. (Ed.). The problem of the Picts. Nelson, London, 1-53.
24. Jackson, K.H. (1955) The Pictish language. In: The problem of the Picts. Wainright, F.T. (Ed.). Nelson, London, 129-160.
25. Trask, R.L. (1995) Origin and relatives of the Basque language: review of the evidence. In: Toward a History of the Basque Language. Hualde, J.L. et al. (Eds.). Benjamin, Amsterdam, 65-77.
26. Trask, R.L. (1997) The History of Basque. Routledge, London, New York.
27. Kuzmenko, Y. (2011) Earlier Germans and Their Neighbours: Linguistics, Archaeology, Genetics" - Nestor-History, St. Petersburg.
28. Renfrew, C. (2001) Origini indoeuropee: verso una sintesi. In: Le radici prime dell'Europa Paravia, Bruno Mondadori Editori, 3-22.
29. Diakonov, J.M. (1984). On the Original Home of the Speakers of Indo European. Soviet Anthropology and Archaeology, 23(2), 5-87.
30. Gray, R.D., et al. (2011) Language evolution and human history: what a difference a date makes. Phil. Trans. R. Soc. B, vol. 366, no. 1567, 1090-1100.On line at http://rstb.royalsocietypublishing.org/content/366/1567/1090.abstract .
31. Ryder, R.J., Nicholls, G.K. (2011) Missing data in a stochastic Dollo model for binary trait data and its application to the dating of Proto-Indo-European. J. of R. Stat. Soc. C, (Appl. Statistics), vol. 60, Issue 1, 71-92. On line at http://onlinelibrary.wiley.com/doi/10.1111/j.1467-9876.2010.00743.x/abstract
32. Sturtevant, F.H. (1962) The Indo-Hittite Hypothesis. Language 38, 376-382.
33. Dolgopolsky, A.B. (1987) The Indo-European Homeland Problem. Mediterranean Archaeological Review, 3, 7-31.
34. Dolgopolsky, A.B. (1993) More about the Indo-European Homeland Problem.

Mediterranean Archaeological Review, 6-7, 251-272.

35. Gamkrelidze, T.V., Ivanov, V.V. (1984) Indoevropeiskij jazik i Indoevropeijcy. T'bilisi State University, T'bilisi
36. Gamkrelidze, T.V., Ivanov, V.V. (1995). Indo-Europeans and the Indo-Europeans. A Reconstruction and Historical Analysis of a Proto-Language and a Proto-Culture. Nichols, J., de Gruyter, M., Berlin-New York, 2 voll.
37. Pringle, H. (2012) News & Analysis: New method puts elusive Indo-European homeland in Anatolia. Science 337 (6097), 902. On line at http://onlinelibrary.wiley.com/doi/10.1126/science.337.6097.902
38. Li, C., Li, H., Cui, Y., Xie, C., Cai, D., Li, W., Mair, V.H., Xu, Z., Zhang, Q., Abuduresule, I., Jin L., Zhu, H., Zhou. H. (2010) Evidence that a West-East admixed population lived in the Tarim Basin as early as the early Bronze Age. BMC Biol. 8:15, doi: 10.1186/1741-7007-8-15.

39. Tomezzoli G.T., Kreutz J. (2011) The linguistic position of the Tocharian. Proceedings of the 9th International Topical Conference: Origin of Europeans. Ljubljana 03 June 2011, 67-86. Založništvo Jutro, ISBN 978-961-6746-52-6.
40. Ryan, W., Pittman, W. (1998) Noah's Flood. The New Scientific Discoveries about the Event that Changed History. Simon & Schuster. New York.
41. Gimbutas, M. (1991) The Civilization of the Goddess: The World of Old Europe, Harper. San Francisco.
42. Gimbutas, M. (1956) The Prehistory of Eastern Europe. Mesolithic, Neolithic and Copper Age Cultures in Russia and the Baltic Area. American School of Prehistoric Researches. Harvard University Bulletin, 20. Peabody Museum, Cambridge (Mass.).
43. Gimbutas, M. (1994) Das Ende Alteuropas. Archaeolingua, Budapest.
44. Gimbutas, M. (1997) The Fall and Transformation of Old Europe: Recapitulation. Institute for Study of Man, Washington (DC). Journal of Indo-European Studies, Monograph 18, 351-372.
45. Marler, J. (2001) L'Eredità di Marija Gimbutas: una ricerca archeomitologica sulle radici della civiltà europea. In: Le radici prime dell'Europa, Paravia Bruno Mondadori Editori, 3-22.
46. Bököny, S. (1997) Horses and Sheep in East Europe. Iin: Proto-Indo-European: The Archaeology of a Linguistic Problem. Studies in Honour of Marija Gimbutas, Skomal, S.N., Polomé, E.C. (Eds.). Institute for the Study of Man, Washington (DC), 136-144.
47. Boric, D., Price, T.D. (2013) Strontium isotopes document greater human mobility at the start of the Balkan Neolithic. Proc. Natl. Acad. Sci. US, 110, No. 9, 3298-3303.
48. Alinei, M. (2001) Un modello alternativo delle origini dei popoli e delle lingue europee: la "teoria della continuità". In: Le radici prime dell'Europa Paravia, Bruno Mondadori Editori, 177-234.
49. Tobias, P.V. (1996) The Evolution of the Brain, Language and Cognition. In Colloquium VIII: "Lithic Industries, Language and Social Behaviour in the First Human Form, Facchini, F. (Ed.), ABACO, Forlì, 87-94.
50. Pinker, S. (1994). The Language Instinct. The New Science of Language and Mind. Penguin Books, London-New York.
51. Wells, R.S., Yuldasheva, N., Ruzibakiev, R., Underhill, P.A. Evseeva, I., Blue-Smith, L., Jin, L., Su, B., Pitchappan, R., Shanmugalaksmi, S., Balakrishnan, K., Read, M., Pearson, N.M., Zerjal, T., Webster, M.T., Zholoshvili, I., Jamarjashvili, E., Gambarov, S., Nikbin, B., Dostiev, A., Aknazarov, O., Zallous, P., Tsoy, I., Kitaev, M., Mirrakhimov, M., Chariev, A., Bodmer, W.F. (2001) The Eurasian heartland: a continental perspective on Y-chromosome diversity. Proc. Natl. Acad. Sci. US 98, 10244-10249.
52. Wells, S. (2006) Deep Ancestry. Inside the Genographic Project National Geographic, Washington, DC, 248.
53. Semino, O., Passarino, G., Oefner, P.J., Lin, A.A., Arbuzova, S., Beckman, L.E., De Benedictis, G., Francalacci, P., Kouvatsi, A., Limborska, S., Marciki, M., Mika, A., Mika, B., Primorac, D., Santachiara-Benerecetti, A.S., Cavalli-Sforza, L.L., Underhill, P.A. (2000) The Genetic Legacy of Paleolithic Homo sapiens sapiens. In Extant Europeans: A Y Chromosome Perspective. Science, 290, 1155-1159.
54. Wiik, K. (2008) Where did European men come from ? J. Genet. Geneal. 4, pp. 35-85.
55. Mendez,F.L., Krahn, T., Schrack, B., Krahn, A.-M., Veeramah, K.R., Woerner, A.E., Fomine, F.L.M., Bradman, N., Thomas, M.G., Karafet, T.M., Hammer, M.F. (2013) An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree. Amer. J. Human. Gen., http://dx.doi.org/10.1016/j.ajhg.2013.02.002, February 28, 2013.
56. Cavalli-Sforza, L. L., Edwards, A. W. F. (1963) Analysis of Human Evolution. Proceedings of the 11th International Congress of Genetics, The Hague and Genetics Today (1965), 3, 923-933.
57. Cavalli-Sforza, L. L. (2001) Un approccio multidisciplinare all'evoluzione della specie umana. In: Le radici prime dell'Europa Paravia, Bruno Mondadori Editori, 3-22.
58. Richards, M., et al. (1996) Palaeolithic and Neolithic Lineages in the European Mitochondrial Gene Pool. Am. Journal of Human Genetics, 59, 185-203.

59. Sykes, B. (1999) The Molecular Genetics of European Ancestry. Phil. Transactions of the Royal Society of London, Series B, 354, 131-139.
60. Hammer, M.F., Behar, D.M., Karafet, T.M., Mendez, F.L., Hallmark, B., Erez, T., Zhivotovsky, L.A., Rosset, S., Skorecki, K. (2009) Extended Y chromosome haplotypes resolve multiple and unique lineages of the Jewish priesthood. Hum. Genet. , 126, No. 5, 707-717.
61. Underhill, P.A., Myres, N.M., Rootsi, S., Metspalu, M., Zhivotovsky, L.A., King, R.J. et al (2009) Separating the post-Glacial coancestry of European and Asian Y chromosomes within haplogroup R1a. Eur. J. Human. Genet., advance online publication, 4 November 2009, doi: 10.1038/ejhg.2009.194
62. Zhivotovsky, L.A., Underhill, P.A., Cinnoglu, C., Kayser, M., Morar, B., Kivisild, T., Scozzari, R., Cruciani, F., Destro-Bisol, G., Spedini, G., et al. (2004). The effective mutation rate at Y chromosome short tandem repeats, with application to human population-divergence time. Am. J. Human Genet. 74, 50-61.

Summary

This article attempts to merge data of contemporary linguistics and DNA genealogy in order to obtain a consistent Migration/Linguistic/Settlement (MLS) paradigm describing migrations and settlement of peoples and languages in Europe after the last Ice Age. In the MLS paradigm, three important players have been identified:

- R1a haplogroup bearers, conventionally indicated as the Aryans, which from around 20,000 ybp, during their migrations from the Central Asia and Altai along the southern route arrived to Europe around 10,000 ybp bringing proto-IE and IE languages and then migrated eastward from Europe to the Russian Plane and India as the legendary Aryans and in the first half of the 3rd millennium bp migrated with their IE languages back from the Russian Plain to Central, Western and South Europe bringing in Europe peoples later called Celts, Germans, Italics, Greeks, Illyrians and Balto-Slavs.
- R1b haplogroup bearers conventionally indicated as the Arbins, which from about 16,000 ybp during their migrations from the Central Asia to Europe along the northern route arrived to Europe around between 4,800 and 4,500 ybp bringing non-IE.
- E, F, G, J, I, K haplogroups bearers which migration routes and dates of arrival to Europe before 5,000 ybp remain obscure and spoken non-IE languages.

It seems that the arrival of the Aryans (R1a) in Europe was peaceful; at least, there are no indications that it might have been genetically violent. However, the arrival of the Arbins (R1b) to Europe was marked by almost complete elimination of the E, F, G, J, I, K haplogroups from Europe.

Concerning the current main linguistic theories it has been possible to ascertain that:

- the Anatolian theory is generally compatible with the MLS paradigm;
- the Vasconic and Afro-asiatic substratum theory is partially in agreement with the MLS paradigm;
- the Kurgan theory and the PCT appear incompatible with the history of Europe based on the MLS paradigm.

In addition errors made by the founding fathers and population geneticists in what they have called “genetic genealogy”, or “population genetics” in the 1990-s - 2000-s and in some aspects of the “Out of Africa” hypothesis as highlighted by the DNA genealogy are discussed.