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Составитель
Российская Академия ДНК-генеалогии

Оформление издания
Anatole A. Klyosov
Павел Шварев

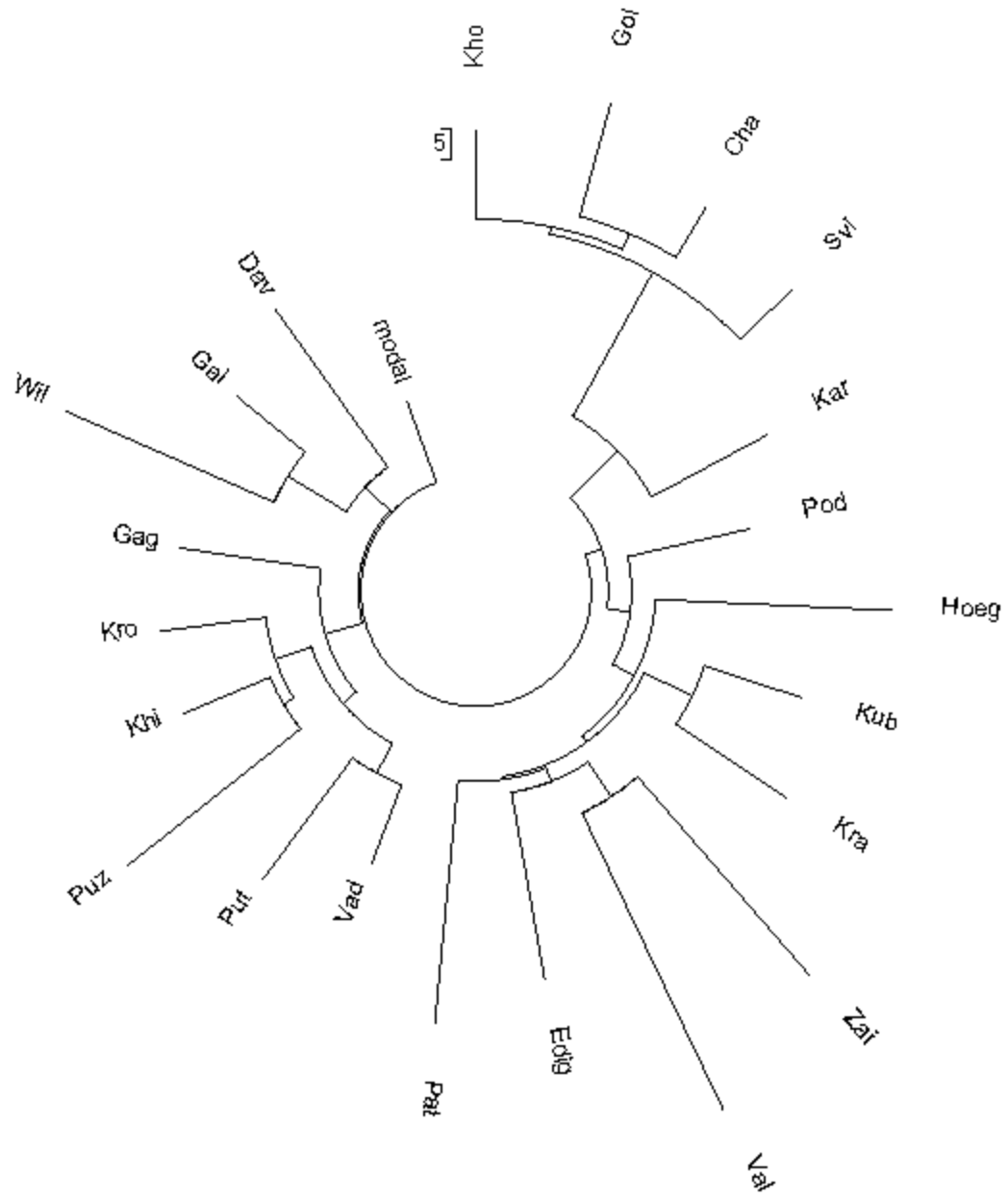
СОДЕРЖАНИЕ НОМЕРА

Еще раз о ДНК-генеалогии русских князей гаплогруппы N1c1 и им «сопутствующих»

А.А. Клёсов
http://aklyosov.home.comcast.net

Эта тема была довольно подробно рассмотрена в февральском выпуске Вестника (Клёсов, 2011a), где показано, что среди обилия гаплотипов гаплогруппы N1c1 есть ветвь с общим предком, который жил 1250±250 лет назад, и которую образуют князья Гагарин, Кропоткин, Хилков, Путятин, Пузына и Вадбольский. Это не значит, что в этой ветви больше никого не может быть, просто доступные гаплотипы других в эту ветвь не попадали. Эти люди входят в Российское Дворянское собрание, управляемое Императорским Домом Романовых, и определенно принадлежат к одной ДНК-генеалогической линии. Здесь следует сделать примечание, что поскольку В. Кубарев (см. статью Клёсов, 2011a) предоставил неправильный гаплотип одного из князей, датировка «княжеской ветви» в цитируемой статье оказалась завышенной, и в настоящей статье (включая датировку выше) она исправлена, и ниже приведено исправленное дерево гаплотипов.

Следует также отметить, что 67-маркерные базовые гаплотипы «княжеской» ветви и ветви «Гедиминовичей» различаются на 17.6 мутаций, что разводит эти ветви «по горизонтали» на 4300 лет, и помещает их общего предка примерно на 3035 лет назад. То есть они никак не родственники, даже в историческом смысле. Они родственники только по гаплогруппе, куда входят десятки миллионов людей.



Дерево 67-маркерных гаплотипов 22 человек гаплогруппы N1c1, по версии В. Кубарева принадлежащих «потомкам Рюрика». Расшифровка всех фамилий дана в работе (Клёсов, 2011а). Видно, что гаплотипы относятся по меньшей мере к четырем линиям, общий предок которых жил примерно 3200 лет назад. Шесть гаплотипов слева (Гагарин, Кропоткин, Хилков, Пузына, Путятин, Вадбольский) имеют общего предка, который жил 1250±250 лет назад; семь гаплотипов справа внизу – примерно 2325 лет назад. Четыре гаплотипа справа вверху (плоская ветвь), предположительно «Гедиминовичи», общий предок жил 520±170 лет назад, 15-й век плюс-минус один-два века.

Надо сразу сказать, что ДНК-генеалогия не может подтвердить или опровергнуть, относятся ли эти люди к «рюриковичам», в ДНК это не записано. Это могут быть потомки некоего знатного рода, общий предок которого по данным, «записанным» в ДНК, жил во второй половине 1-го тыс нашей эры. В этом отношении датировка вовсе не является уникальной или какой-то выделяющейся. Как показано в недавней работе по детальному анализу сотен гаплотипов гаплогруппы N1c1, есть масса ДНК-генеалогических линий, общие предки которых жили в 1-м тысячелетии нашей эры, в середине или в конце. Одна из них – ветвь приведенных здесь имен русских князей. Поэтому ДНК-генеалогия просто фиксирует данный факт, что предок данной линии руских князей жил в середине 1-го тысячелетия плюс-минус три века (столь широкий доверительный интервал обусловлен малым числом гаплотипов ветви), и что перечисленные люди действительно образуют родственную группу. Это уже очень немало. Что же касается фамильного происхождения этой группы – то здесь слово остается за «классической» генеалогией, хрониками, архивными материалами и так далее.

В данной работе я взгляну еще раз на эту группу и ее место среди «попутчиков», которые либо претендуют быть в родстве с русскими князьями, либо считают, что они и есть «истинные рюриковичи». В цитированной выше работе (Клёсов, 2011a) было показано, что в данной гаплогруппе есть отдельная ветвь, в которую входит «активист» и скандально известный «претендент на трон» В. Кубарев, и общий предок которой жил примерно 2125 лет назад. Ясно, что эта группа к описанной группе русский князей никакого прямого отношения не имеет. Их общий предок жил не менее трех тысяч лет назад, и Рюриком быть никак не может. Есть еще ветвь предположительно Гедиминовичей, с общим предком примерно 520 лет назад. Есть и еще отдельные гаплотипы, которые попали на анализируемое дерево просто потому, что их предложил тот же активист Кубарев. В этом смысле на дерево гаплотипов мог попасть любой из тысяч, а то и из миллионов носителей гаплогруппы N1c1, и для каждого нашлось бы место и ветвь. Только к русским князьям подавляющее большинство не имело бы прямого отношения.

В данном, новом рассмотрении будет применен новый прием, который позволяет почти «навскидку» разделить ветви «родственников» и выявить тех, присутствие которых под вопросом. Этот новый метод не заменяет детальный анализ 67-маркерных гаплотипов, использованныый в работе (Клёсов, 2011a), но делает его более наглядным. Оказалось, что в 67-маркерных гаплотипах есть короткие фрагменты, которые характерны для той или иной ветви. И простой взгляд на эти фрагменты уже позволяет

понять, насколько родственны расматриваемые гаплотипы, а значит, и их носители.

Деревья этих коротких фрагментов гаплотипов были детально рассмотрены в работе (Клёсов, 2011b), и было показано, что большинство гаплотипов гаплогруппы N1c1 расходятся на две большие группы – угро-финскую и южно-балтийскую. Обе они довольно молодые, обе образовались в 1-м тысячелетии нашей эры. Каждая из них включает несколько подветвей, и если эти подветви «огрубить», сложить, то эти две большие ветви имеют следующие базовые гаплотипы, угро-финский и южно-балтийский, соответственно:

14 24 14 11 11 13 11 12 10 14 14 30 – 17 10 10 11 12 25 14 19 30 13 13 14 14 – 11 11 18 19 14 15 18 19 36 36 13 10 – 11 8 15 17 8 8 10 8 11 10 12 21 22 14 10 12 12 17 7 13 20 21 15 12 11 10 11 11 12 11 (**угро-финский базовый гаплотип**)

14 **23** 14/**15** 11 11 13 11 12 10 14 14 30 – 17 **9 9** 11 12 25 14 19 **28 14 14 15 15** – 11 11 18 **20** 14 15 **17** 19 36 36 13 10 – 11 8 15 17 8 8 10 8 11 10 12 21 22 14 10 12 12 17 7 13 20 21 **16** 12 11 10 11 11 12 11 (**южно-балтийский базовый гаплотип**)

Между этими ветвями на вид 10 мутаций, на самом деле 7.82 мутации, поскольку некоторые мутации при усреднении дробные. Это разводит обе ветви латерально («по горизонтали») на 1725 лет, и помещает общего предка обеих ветвей на 2400 лет назад. Но это в первом приближении, потому что сами ветви состоят из подветвей разного количества и разного размера. Если все это учесть, то общий предок всей гаплогруппы N1c1 по доступным гаплотипам опускается во времени до 4200 лет назад.

В данном контексте эти детали не столь важны, поскольку для цели настоящей работы нам важно знать, что ведущими признаками угро-финской ветви (в которой большинство финнов) и южно-балтийской ветви (в которой большинство русских, украинцев, белорусов, поляков, литовцев, латышей, эстонцев) служат двойка 10-10 (в DYS459) и четверка 13-13-14-14 (в DYS464) в первой, и двойка 9-9 и четверка 14-14-15-15 во второй [на самом деле и четверки здесь являются дуплексными двойками, 13-14 и 14-15, но для целей настоящей работы это не важно]. Эти признаки не являются абсолютными, как не являются абсолютными понятия «финн» и «русский», но в целом корреляция между ветвями и самоотнесениями к национальностям есть. Есть еще один признак – это снип-мутация L550+ в южно-балтийской ветви, и ее отсутствие, L550-, в угро-финской ветви, но пока такое тестирование проведено всего для 10% участников проекта N1c1.

В основном этот снип сопровождается двойкой 9-9 и четверкой 14-14-15-15 в указанных маркерах.

Теперь можно приступать к основному вопросу настоящей работы. Перед этим дадим краткие сведения о князьях этой отдельной ветви на дереве гаплотипов, основываясь на справочниках:

Вадбольский - ветвь белозерских рюриковичей.
Пузына – потомок князя Черниговского (ум. 1246).
Гагарин – от князей Стародубских.
Кропоткин – от князей Смоленских, рода Мономаха.
Путятин – от князей Друцких, потомков князя Слонимского.
Хилков – потомок князя В.Д. Хилкова, боярина и воеводы, внука основателя рода, ум. 1602 г., то есть относительно поздно по сравнению с «временами Рюрика»)

Никто из них документально не подтвержден как прямые потомки Рюрика, хотя все они считают число колен от последнего. Собственно, в данной работе нам это не важно, цель ее – показать, что они действительно относятся к одной ДНК-генеалогической линии.

Все шестеро князей (Гагарин, Кропоткин, Хилков, Путятин, Пузына и Вадбольский), которые образуют отдельную ветвь на дереве гаплотипов, все имеют двойку 9-9, и четверо имеют четверку 14-14-15-15, кроме князя Гагарина, у которого 14-15-15-15, и князя Пузыны, у которого 14-14-14-14. Это вполне приемлемо, поскольку у всех в гаплотипах имеются мутации, и то, что выше – однократная палиндромная мутация. Она могла произойти когда угодно в последние столетия. Более того, у всех шести – одна и та же двойка 15-18 в DYS395S1, в парном «медленном» маркере. Мутация в этом маркере обычно – в среднем - остается на многие тысячелетия, и часто является ветвеобразующей или даже родообразующей. В принципе, мутация может произойти и в этом маркере, но это случается редко. Вот у родоначальника князей она и произошла. Во всей гаплогруппе N1c1 только 8% гаплотипов имеют пару 15-18, у остальных 92% там 15-17. Поскольку мутация редкая, то эта пара – важный признак данной княжеской ветви.

Итак, имеем три признака княжеской ветви: 9-9, 14-14-15-15 (или однократная мутация в данной четверке), и 17-18 в указанных маркерах. Это – принадлежность не к угро-финской, а к южно-балтийской ветви. Можно сказать – славяне, а не финны.

Посмотрим, что у других заявленных (в основном, заявленных «активистом» В. Кубаревым) претендентов на княжескую ДНК-родословную.

Молодая ветвь «гедиминовичей», в которую по 67-маркерным гаплотипам были отнесены четыре гаплотипа - Голицина, Свистунова, Чарторицкого и Хованского. У всех четверых – другие характерные признаки, хотя по двойке 9-9 и четверке 14-14-15-15 они тоже относятся к славянской, южно-балтийской ветви. Но у них у всех «медленная» двойка 15-17, в отличие от 15-18 у княжеской ветви. Это – другая ДНК-генеалогическая линия. Далее, в отличие от княжеской ветви у них еще одно отличие – у всех четверых DYS19 = 15, а не 14, как у князей. Это довольно быстрая мутация, она не является характерным признаком. Но в данном случае это уже второй признак отличия от княжеской ветви, что переводит эти отличия из случайных в закономерные.

Карцев не попадает ни туда, ни сюда. У него 9-9, 14-14-15-15 и 15-17, как у большинства в южно-балтийской ветви, и DYS19 = 14, отличающий от гедиминовичей, но обычный как для южно-балтийцев, так и для финнов (см. базовые гаплотипы выше). Иначе говоря, Карцев относится просто к большинству южно-балтийской ветви.

Остальные «претенденты» на дереве гаплотипов – полный разнобой. Это – обычные гаплотипы гаплогруппы N1c1, не образующие ничего характерного в данном контексте. Давайте посмотрим.

Кубарев, Кравжик, Зайцев, Подольский, Эдигей, Валихан и Патракка – все имеют нечто среднее между финно-угорской и южно-балтийской ветвями. У всех семерых двойка 10-10, что типично для угро-финской ветви, но четверка 14-14-15-15 (у Зайцева 14-15-15-15 и у Валихана 15-15-15-15, что опять просто одношаговые мутации), как в южно-балтийской ветви. То есть это то ли славяне с мутацией в финскую сторону, то ли финны с мутацией в славянскую сторону. У всех «медленная» двойка 15-17, что характерно для большинства как угро-финнов, так и южно-балтийцев, но резко отличающая от «княжеской» ветвь, в которой 15-18.

У Хоэгсета – «южно-балтийская» четверка 14-14-15-15 и «угро-финская» двойка 10-10, как у семерых выше, но нестандартная тройка 15-18, как у «князей» То есть это просто отдельная ДНК-линия в гаплогруппе N1c1.

У Гэлбрейта и Давидсона – типичные «южно-балтийские» 9-9, 14-14-15-15 и 15-17, как у большинства, с разнообразными случайными мутациями, опять как у большинства. Непонятно, что их в «претенденты» привело. Кто

привел – понятно, тот же «активист» Кубарев. Видимо, были свои соображения.

То же самое и некто Уилсон, у него «южно-балтийская» двойка 9-9 и угро-финская четверка 13-13-14-14, то есть довольно типичный случай мутаций между этими двумя ветвями. Таких много.

Вот, собственно, и все «претенденты». В отношении «княжеской» ветви вывод остался тем же – это, безусловно, княжеская ветвь, но кто был ее общим предком в 1-м тысячелетии нашей эры – вопрос открыт. Это был, скорее всего, профессиональный военный, часть элиты общества, который дал потомственных профессиональных военных, опять же продолживших элиту. Был ли это Рюрик, или кто другой – вопрос опять же открыт. Да, наверное, это не столь важно. Потомками были люди, служившие России. Военно-боевой состав высшего звена.

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Haplogroup R1b as a carrier of Proto-Türkic languages, aka Dene-Caucasian languages, aka Erbin, that is a non-IndoEuropean language in its dynamics during 16,000 to 3,000 years before present

Anatole A. Klyosov
http://aklyosov.home.comcast.net

Foreword

This article in its earlier version was published in Proceedings of the Russian Academy of DNA Genealogy, vol. 3, No. 1, 2010 (in Russian), and then it was translated (with my permission) by the publishers of the Turkic History site http://s155239215.onlinehome.us/turkic/60_Genetics/Klyosov2010DNK-GenealogyEn.htm. For the past year I have received many letters from readers, mostly (or only) positive and appreciative. However, when I was talking to linguists, I felt that the word "Turkic" in the context of the article could be misleading, since the contemporary linguistics consider Turkic languages as young ones, which arose in the 1st millennium AD, as reviewed in this article. In their paradigm the term "Turkic" is not applicable to languages which have apparently were in use thousands years ago. My explanations that I was talking about proto-Turkic languages, as it was emphasized in the introduction to the paper, were repeatedly and consistently falling to deaf ear. I have tried to explain that I was talking about languages of bearers of haplogroup R1b, who had been migrating across Eurasia between 16 and 5 thousand years before present, and those languages were not Indo-European languages, they were not present-day Turkic languages, of course, however, they eventually brought about present-day Turkic languages. Those languages were in use many thousand years ago between South Siberia (maybe Yenisei), Altai, Xinjiang, across Central Asia to Middle Volga River, where Chuvash, Bashkir and Tartar people speak Turkic languages nowadays, then across the Caucasus to Anatolia, where present days Turkey people live, and further on through Middle East to Europe, where the Basques speak their isolated language which some linguists describe as Sino-Caucasian and as Dene-Caucasian languages. In place of "Proto-Turkic" I could have used "Dene-Caucasian" language, or whatever it could be called. It could

be called "Erbin", since the R1b bearers were speaking it for thousand years. Apparently, the very archaic form of that language was brought to America by ancient migrants, and now it is called Na-Dene languages. This is the same ancient language, which does not have a consensus name between contempotrary linguistics. Let it be Erbin.

This Erbin language was apparently brought to Europe by R1b1a2 people, who came to the Pyreneees after crossing the Gibraltar Strait some 4800 years before present, and as the Bell Beakers they moved up North to the European continent and eventually populated Europe, along with displacing (and apparently eliminating) many other inhabitants of Europe, such as of I1 and I2 tribes, and R1a1 people, and maybe a majority of G people as well. Maybe that is why I1 and R1a1 almost completely disappeared from Europe between 4500 and 4000 ybp, and repopulated it again starting at the end of the 2nd millennium BC (I1) and in the first half and the middle of the 1st millennium BC (R1a1). All European populations of I1 have a common ancestor around 3300 ybp, and most of R1a1 lineages in Europe have appeared there between 2700 and 2500 BC and later. At the same time, as R1a1 started repopulating Europe, R1b1a2 have gradually picked IndoEuropean languages.

The oldest Indo-European language in Europe among ancestors of the present-day R1b1a2 people was carried by the Celts, who suddenly appeared in Europe in the middle of the 1st millennium BC. However, they apparently were not those Celts who we believe were R1b1a2 bearers. The first Celts very likely were R1a1, who, according to some historians, have arrived to the Alps from the East European steppes. There were no R1b1a2 in the steppes by that time, however there were plenty of R1a1. They apparently brought their Indo-European language to Central Europe, as a thousand years before that, in the middle of the 2nd millennium BC, they, R1a1, brought the Indo-European, which was the Aryan language, to Iran and India. It seems that R1b1a2 people in Europe have acquired that IE language in the middle of the 1st millennium BC, and carried it around, calling themselves the Celts and the Gauls, as it was noted by Julius Caesar in the first lines of his "The Gallic Wars".

Now, when most of Europe speaks Indo-European languages, the mainstream of linguists truly believe that ancestors of R1b1a2 people spoke IE languages in Europe 4000 years ago and earlier. It is simply not substantiated. They spoke a variety of non-IE languages in Europe. One of very few of those ancient R1b1a2 languages is still in use in Europe as the Basque language (Basques are predominantly (around 90%) R1b1a2 people). The very term "Celtic languages" was coined only in the beginning of the 18th century.

This article tells the story on ancient migrations of R1b and R1a people and about their languages, as it is reconstructed by means of DNA genealogy. It is of no

doubt that the story will be refined and detailed along with appearance of new data, however, the core of the story is expectedly would not change much.

Introduction by the Turkic History site

(the author of this study is not responsible for this excessively positive description)

Whoever reads this, is blessed with a first, real, groundbreaking treatise on Türkic genetics that has a vision equipped with professional tools and not burdened with a load of preconceived notions and institutional restrictions. Even if the future establish that not all hypothesis and explanations in the following are correct, the principles and vision would be a ratchet that would not allow a slide backwards. This is a new page in Turkology.

The adjective Türkic and the noun Türk are used to denote the global world of the Turkic community that includes Turkish and Turks as one of the constituents; Türk is a noun of which Türkic and Turkic are adjectival derivatives needed for translation from Russian, which has four distinct designations for four phenomena. To designate a biased advocate of Türkic studies is used a word Türkist, a mirror of the word Iranist, vs. Turkologist whose specialty is impartial Türkic studies. The semantics of the above terminology in English and Russian is a result of their national histories.

* * *

SUMMARY

Based on the data of DNA genealogy, a concept was formulated and substantiated that in the ancient times, until the middle of the 1st millennium BC, two linguistic fields - the Türkic (Proto-Türkic) and Indo-European, the languages of the haplogroups R1b and R1a respectively, dominated in their turns over the whole Eurasia reaching the Atlantic Ocean in the West. With a time difference of 1-2 thousand years, people of these haplogroups were migrating in opposite directions, mostly crossing the same territories, which confused present day linguists and archaeologists, and led to the fundamentally erroneous "Kurgan" and "Anatolian" theories of the “Indo-European homeland".

The modern Uigurs, Kazakhs, Bashkirs, and some other peoples of Siberia, Central Asia and the Urals descend in part from the ancient R1b1 branch, and by now retain the same haplogroup for 16,000 years. The "ProtoTürkic-lingual" haplogroup R1b expanded from the South Siberia, where it formed some 16,000 years ago, across the territories of the Middle Volga, Samara, Khvalynsk (in the middle course of river Volga) and the Ancient Pit Grave ("Kurgan")

archaeological cultures and historical-cultural complexes (8-6 thousand years ago and later; the common ancestor of the ethnic Russians with haplogroup R1b1 lived 6,775 ± 830 years ago), northern Kazakhstan (for example Botai culture dated by the archaeologists 5,700 - 5,100 years before present (ybp), in reality must be much older), passed through the Caucasus to Anatolia (6,000 ± 800 ybp by the dating of R1b1b2 haplogroup of the modern Caucasians), and through the Middle East (Lebanon, 5,300 ± 700 ybp; the ancient ancestors of the modern Jews, 5,150 ± 620 ybp), and Northern Africa (Berbers of the R1b haplogroup, 3,875 ± 670 ybp), crossed over to the Iberian Peninsula (4,800 ybp, present day Basques have a common ancestor of 3625 ± 370 ybp, apparently, after passing a severe populational bottleneck between 4,800 and 3,625 ybp) and further on to the British Isles (in the Ireland 3,800 ± 380 and 3,350 ± 360 ybp for different R1b1a2 populations), and to the continental Europe (Flanders, 4,150 ± 500 ybp, Sweden 4,225 ± 520 ybp).

The path from the Pyrenees to the Continental Europe was the path and period of the Beaker Culture, the ancestors of the Pra-Celts and Pra-Italics as we know them today. It seems, however, that “Pra-Celts” in the Pyrenees 4,500 ybp and actual Celts in the Alps, who spoke Indo-European language 2600 ybp, were different people. Those “Pra-Celts” in the Pyrenees were R1b1a2, Bell Beaker people, and the Celts in the Alps 2600 ybp were R1a1 people, recently migrated from the East, from the Russian Plain, in the middle of the 1st millennium BC, and brought with them IndoEuropean language. Soon, it spread over Central and Western Europe. On the Russian Plain the IE language was spoken since at least 4800 ybp, and from there it was brough to Anatolia and Mitanni, India and Iran ~ 3500 ybp.

In parallel, the traces of the ancient R1b carriers are found in the Balkans (4,050 ± 890 ybp), separately in Slovenia (4,050 ± 540 ybp), Italy (4,125 ± 500 ybp). That was the beginning of the ProtoTürkic languages' time in Europe, and the disappearance there of the "Proto-Indo-European" haplogroup R1a1, which populated Europe from the 8th millennium BC. The haplogroup R1a1 was practically saved by the event that 4,800 years ago, in the beginning of the third millennium BC, its bearers moved from Europe to the Eastern European Plain (aka Russian Plain), and settled the territory from the Baltic to the Black Sea. As soon as 4,500 ybp they were already in the Caucasus, 3,600 ybp they were in Anatolia (according to the haplotypes of the R1a1 haplogroup in modern Anatolia). Meanwhile, across the Eastern European Plain they migrated to the southern Ural, and around 4,000 ybp on to the southern Siberia, at that time they established the Andronovo archaeological culture and populated Central Asia (4,000 - 3,500 ybp), and approximately 3,500 ybp a part of them went to India and Iran as the Aryans, bringing along the Aryan dialects, which effectively closed the linguistic link with the Aryan languages (R1a1) and led to the emergence of the Indo-European family of languages.

4,500-4,000 years ago the R1a1 disappeared from the Western and Central Europe, the Europe became non-IndoEuropean (ProtoTürkic-speaking) with the arrival of the people carrying the R1b haplogroup (at the beginning of the 3nd millennium BC), and that lasted until the middle of the 1st millennium BC (3,000-2,500 years ybp), when the haplogroup R1a1 re-populated the Western and Central Europe, and came about a reverse replacement of the ProtoTürkic languages to the Indo-European languages. That linguistic and haplogroup, or tribal (in terms of DNA genealogy) striations of the Eastern European Plain, in the Near East, and in Europe has led to erroneous linguistic and archaeological concepts such as the "Indo-European Kurgan Culture" with its transposed languages (postulated" Indo-European", when it was a ProtoTürkic language), the wrong direction of movement (the "Proto-Indo-European" was moving eastward, not westward, as did the ProtoTürkic (the westward movement was seen by the creators and supporters of the "Kurgan Culture" as the "Indo-European" movement, which was 180 degrees wrong), wrong periods (the Proto-Indo-European language advanced eastward across the Eastern European Plain in the 3rd millennium BC, while the ancient Pit Grave, or the "Kurgan" culture are mainly dated by the period of the 4th-3rd millenniums BC, and were moving westward and southward).

Something similar also happened to the "Anatolian theory", where a separate (Trans-caucasian) branch of the Aryans' route, the southward movement of the R1a1 haplogroup carriers across the Eastern European Plain (4500-3600 ybp) was mistaken for the "Indo-European homeland" in Anatolia, in addition to another "IndoEuropean homeland" there some 9,000 ybp, according to different scholars. That led to a conceptual distortion and misunderstanding of the fundamental role of the ProtoTürkic languages in the Eastern European Plain (at least from the time 10,000 years ago), and in the Europe, where it continued for one and a half thousand years (from the beginning of the 2nd millennium to the middle of the 1st millennium BC).

IMPORTANT PREFACE NOTE

What the article calls "Türkic" or "ProtoTürkic", or "ancient Türkic" language is based only on the fact that Turkologists call it Türkic. Analyzing the ancient texts (see below) they see specifically the agglutinative Türkic language, the Türkic ethnonyms in Europe. It is possible that this is a misunderstanding, and what they see is an agglutinative language of the haplogroup R1b ancient carriers, which can be called "Erbin" (after R1b). It could be, but not necessarily, a basis, a ground, a substrate for the modern Türkic languages; it could just be a related, lateral branch of the ancient Türkic language. It could be the agglutinative language of the ancient Basques. Was that Türkic language or not is a matter for the linguists to decide. In any case, it does not affect the discourse and

conclusions of the article. Those who find the term "Türkic language" or “ProtoTürkic language” in this context (as a pre-IE language in Europe, employing by R1b bearers 4500-2500 years before present, and some later) not acceptable may substitute it with the term "Erbin", and read on.

INTRODUCTION

For more than a hundred years the "Iranists”, or more commonly "Indo-Europeanists" on one side, and Turkologists on the other side, completely deny the contribution of the opponent's linguistic group into the Eurasian linguistic landscape in antiquity (from the beginning of our era and older), asserting that in the Europe and Asia was either a continuous "Indo-Iranian" substrate, or conversely continuous Türkic substrate. They do not compromise. Examples are given below.

However, the explanation is quite simple. Both sides are right, but on their own half. The two major Eurasian haplogroups, R1a and R1b, diverged (or rather, formed and diverged) 20-16 thousand years ago, evolved linguistically from the common Nostratic languages, respectively into the Pra-Aryan (later called "Proto-Indo-European") and the Proto-Türkic, and then into Türkic. Because the paths of the haplogroups R1a and R1b carriers in Eurasia significantly transversed in the same territories, often with a gap of a millennia or two (R1a migrations are older in Europe, R1b migrations are older in Asia), they left "substrates" superimposed one on another, and intertwined in many ways. Since the agglutinative ProtoTürkic and Türkic languages are probably less subjected to temporal changes than the flexive Indo-European languages, the Turkologists derive with ease almost all "Iranisms" from the Türkic languages. They are finding in works of historians of antiquity many examples of Türkisms, in the proper names and in the names for the objects, and in separate terms. The Iranists in response brush them aside, and cite their own versions, in accordance with which certainly no Türkisms existed in the Eurasia during the past era and even less so before that. Or they ignore it, or undertake repressive measures in science. Any Turkologist can cite many examples of that kind.

This article, introductory to the problem, is to show that many thousands years ago both the ProtoAryan (or Aryan), that is Proto-Indo-European languages, and the Proto-Türkic (or Türkic), non-IndoEuropean languages have existed. They simply were carrying by different haplogroups (as tribes), the first by the tribe R1a1, the second by R1b1, and perhaps by the kindred tribes Q and N (all of them split from the “upstream” tribe-haplogroup NOP some 50,000-45,000 ybp).

The concept, naturally, is awaiting for a deeper linguistic studies. But the beginning, as can be seen, is established.

The next section relays the story about of opposition between "Iranists" and "Türkists". Actually, the opposition does not exists literally, it is rather a figure of speech. Too unequal were both sides to call it an "opposition". But this figure of speech reflects the essence of the problem. Ever since the beginning of the 1950s, the official historical science postulated that the Scythians were "Iranian speaking". The issue was not to be discussed any more. Any arguments and scientific evidence on the subject were not acknowledged by the official science (and that the official science exists is beyond discussions; at least it have existed in the Soviet Union where linguistics was totally controled by the government; Josef Stalin himself was a self-appointed linguist, the author of "Marksism and Problems of Linguistics" (Pravda, June 20, 1950) which was then published as a book by millions of copies), or reacted to with dead silence for at least the last 60 years.

About confrontation between "Iranists" and "Türkists". Solely quotes.

Yu.N. Drozdov "Türkic ethnonyms of ancient Europeans" (2008) [a new edition "Turkic-speaking Period of European History" (Moscow, 2011) was published, ISBN 978-5-904729-20-2]:

"*... Here we present the results of ethnonymic studies of ancient European tribes and peoples according to the ancient and early medieval written sources. It was established that the ethnonymy of these tribes and peoples was Türkic-lingual*" (annotation for the book).

Ibid: "*The results give reasons to believe that a vast majority of the European population from the ancient times to the 10-12 centuries AD was Türkic-lingual*".

Ibid, p. 5: "*The Antiquity and Early Medieval written sources in Greek, Latin and Arabic cite a large number of names for the ancient European tribes and peoples. Not a single name that could be derived from Greek, Latin, or any other modern European language was found among them ... The linguistic analysis of the ancient European ethnonyms shows that all of them are distorted Türkic-lingual words*".

Ibid, p. 5-6: "*The results of the study showed that neither the Hebrew, nor the Greek language had any relation to the (Christian) terminology (two millennia ago). It also was entirely Türkic-lingual*".

Ibid, p. 8-9: "*In accordance with the concept of the modern historical science, all of these (Scythian) tribes are considered to be Iranian speaking (more accurately, Persian speaking). Moreover, this view has acquired a status of a static axiom ... (To the contrary)*

a number of scientists and experts provably state for already quite a long time that all Scythian and Sarmatian peoples were Türkic-lingual".

V.I. Abayev "Ossetian Language and Folklore" (Moscow-Leningrad, 1949, pp. 239): "*... We have received a certain amount of positive, solid and indisputable results which can not be changed by any future explorations and discoveries. These results characterize the Scythian language as an Iranian language, with features of peculiar and well-defined individuality*".

Yu.N. Drozdov, p. 9: "*... The modern historical science adopted this conclusion of V.I. Abaev as axiom, resulting that the ethnogenesis of all European nations does not find an intelligible and logical explanation.*"

M.Z. Zakiev "Origin of Türks and Tatars" (Moscow, 2003, pp. 139-140): " *The theory of exclusive Iranian linguality of all tribes united by the common name of the Scythians seemed plausible when the Iranists conducted etymological studies of the Scythian written sources by picking only selected words (ethnonyms) with solely Iranian roots. However, a circle of researchers of these sources is extending. The problem was also approached by non-Iranists, in particular Turkologists and other linguists. Words with non-Iranian roots, especially with the Türkic roots were introduced into the scientific circulation, indicating the presence of Türkic-lingual people in the union of Scythian tribes ... The result is a vicious circle: archaeologists are guided by the opinion of linguists who attribute the archaeological culture of the Scythian and Sarmatian period to the Iranian-speaking tribes, and the linguists-Iranists for confirmation of their theory refer to the conclusions of the archaeologists*".

M.Z. Zakiev, ibid: "*Notably, all the Turkologists that reached the Scythian materials and studied them themselves, unequivocally recognize the Türkic-linguality of the main composition of the Scythians and Sarmatians, and prove that with linguistic, ethnological, mythological, and archaeological evidence*".

I.M. Miziev "The History Nearby" (Nalchik, 1990, cit. per T.A. Mollaev "A new perspective to the history of the Ossetian people, 2010, p. 6):

Scythians	**Medieval Türkic peoples**	**Ancient and Medieval Indo-European peoples**
Kurgans (Timuli)	**+ + +**	**- - -**
Funeral carts, timber graves, dugouts	**+ + +**	**- - -**
Felt in the graves	**+ + +**	**- - -**
Embalming corpses	**+ + +**	**- - -**
Grave lined with wood, bedding of	**+ + +**	**- - -**

bark, reeds, log ceiling over grave		
Round-, pointed-, egg-shaped-bottom ceramic	+ + +	- - -
Bone and copper horse mouth gears	+ + +	- - -

T.A. Mollaev, "A new perspective on the history of the Ossetian people", 2010, p. 6): "*This table shows irreconcilable difference between the ethnic passports of the Scythians, represented in the archaeological materials, and the Indo-European peoples ... And also a complete equivalence in the corresponding characteristics of the medieval Türkic peoples with the Scythian nations in antiquity.*"

TA Mollaev, ibid, p. 9: "*The "Iranists" explained the Scythian words in the following mode: they would take any anthroponym, ethnonym, etc. recorded by the ancient written sources, then a lexical unit from Ossetian or other Iranian language and even from other Indo languages, phonetically more or less suitable, was arbitrarily sought, and after that they insist that the result of that comparison points at the lexical unit of the Scythian words to belong to the Iranian languages. With that method, and with the same success, any Scythian word and its lexical units can be "found" to belong to any other languages in the world. And then, having that phonetical "resemblance", they would declare the Scythian words as certainly derived from those languages.*

Thus, the absence of an appropriate scientific methodology, or more accurately, ignoring any proper methodology, allowed the above theory to appear and penetrate into historiography. The founders of the theory were three very bias minded Indo-Europeanists of the 19th century (J.G.Klaproth, K.V.Mullengof, V.F.Miller). Using identical method and having a certain desire, any word can be etymologized in any language of the world".

T.A. Mollaev, ibid, p. 11: "*That would remain immaterial if their "scientific explorations", or more accurately fakes, were not represented at an official level as solid scientific arguments. And after that many others were duped by the "Iranists": both specialists and regular folks would start to believe that the Scythian tribes (ancestors of the Türkic people), indeed spoke Iranian languages.*"

D. Verkhoturov (cited per T.A. Mollayev, ibid, p. 15): "*If to believe the Iranian theory, it follows that around the middle of the 1st millennium AD the Türks "moved" from the Altai, quickly captured and Türkified a huge "Iranian world", and did it so well that no trace and fragments of the old world have remained.Meanwhile, it is perfectly clear that the formation of such vast Türkic world took millennia. There is an absolutely definite archaeological complex of the steppe peoples, first of all kurgan burials in timber graves, burials with horse, etc., which in the archaeological materials of the Eurasian steppe zone clearly continue their descent in the culture of the undeniably Türkic peoples. The beginning of the continuity ascend at least to the beginning of the 1st millennium BC.*"

I.M. Miziev and K.T. Laypanov "On the origin of the Türkic peoples" (Nalchik, 1993, cit. per T.A.Mollayev, p. 20): "*Scythologists B.N. Grakov, M.I. Artamonov, A.P. Smirnov, I.G. Aliev, V.Y. Murzin, and many other honest archaeologists fell into the "trap" of the Iranist linguists. They knew, that according to archaeological and other materials the Andronovans, Scythians, Sakas, Massagetes, and Alans were not Iranians, however "since linguists proved their Iranian-linguality", they were forced to recognize these tribes as Iranian-speaking.*"

Yu.N. Drozdov, page 10: "*... despite a large number of works produced to demonstrate that the Scythian-Sarmatian people were indeed Türkic-speaking, the conclusions of those authors have not yet been accepted by the modern historical science. Perhaps their arguments were not found to be convincing, or more likely their findings did not fit the commonly accepted historical concept.*"

The books of Yu. Drozdov and T. Mollayev supply a wealth of materials for the Türkic ethnonymy of the European and Eurasian tribes, nations, of historical figures, and mythical characters; the material was collected by the authors themselves, as well as by their predecessors. The quoting can be extended to infinity, and the following are but a few examples. Concluding the series of descriptions on mutual pricking between Iranists and Turkists related to the Scythians, the following example is cited by the both authors. Herodotus lists several legends about the origin of the Scythians. According to one of them, the ancestor of the Scythians was a man named Targitai, who had three sons, Lipoksai, Arpoksai and Kolaksai. Herodotus noted that Lipoksai was an ancestor of the Avhatai Scythians, then from the middle son Arpoksai descended Katiars and Traspians, and from the youngest Kolaksai descended Paralats. "*Alltogether they are called Scolots, Greeks call them Scythians*" (Herodotus).

All these names and ethnical terms were deciphered by the turkologist M. Zakiev based on the Türkic language (described in detail in N. Drozdov, p. 15), and T. Mollaev adds that the names of both father and son are listed in a long series of the 13th century Türkic names in the annals of Rashid al-Din, for example Actai, Ashiktai, Gurushtai, Buruntai, Daritai, Oiratai, Kamtai, Kutai, Kutuktai, Kyahtai, Subektai, Tubtai, Uigurtai, Usutai etc. (Mollaev, p. 52). It should be added that since tai/sai/thai is "clan" in Turkic, said etymology is totally transparent for the tribal descent: those are clans from Dari, Oirat, Kithai, Kuyan, Suvar, Tuba, Uigur, Usun.

Yu.N. Drozdov (2008) systematically examines ancient authors, and also examines in detail virtually all regions and known tribes of the ancient Europe, and finds layers of Türkic-lingual ethnonymy everywhere, among the Scythians, Sarmatians, Goths, Huns, Avars, Enets and Venets, Sklavens, Antes, Vandals, Baltic tribes, both in the Dnieper area and east of Dnieper area, among the Germans, Scandinavians, Franks, Gauls and Celts, ancient Britons, inhabitants of

the Apennines, the Khazars, Burtas, Bulgars, and tribes of the Volga and Kama.

In the conclusion of the book, Yu.N. Drozdov wrote: "*The ethnonymic analysis of the ancient European tribes and peoples, and also their names and separate terms according to the Greek, Latin and Arabo-Persian Classical and Early Medieval written sources demonstrated that they all were Türkic-lingual. That suggests that the population of Europe in the period under consideration was Türkic-lingual ... Currently, however, virtually all European nations speak in different flexive languages that have nothing in common with the Türkic languages. Only in the extreme east of Europe, a few Kama, Volga and North Caucasian peoples have preserved the ancient European Türkic language. So, at some time period in the past, the bulk of the European nations switched from the Türkic to other languages, which presently are known as the European languages*" (p. 352).

Further on: "*It seems that the languages of the Türkic linguistic group were spread throughout Eurasia (and it seems not only there) from a very distant period in time, beyond the historical memory of the modern humanity*" (ibid.).

And further on: "*A careful analysis of available written sources in order to identify any evidence that would allow, at least in a first approximation, to understand when, how and from where the European nations received new flexive languages did not produce any results so far*" (p. 353) .

Further, Yu.N. Drozdov estimates that the period of final change from the agglutinative Türkic to the flexive Indo-European languages in Europe, namely to French, Germanic, Danish, and Slavic falls in the period between the 9th and 13th centuries AD (p. 357). But a significant number of the Türkisms remains, though they are phonetically deformed under the influence of the modern languages (pp. 357-358), and, we add, due to rules of dynamics of languages.

More on the confrontation between "Iranists" and "Türkists". A novel view at resolution of the conflict. The emergence of the flexive Aryan and agglutinative Türkic languages in Asia and Europe

As it was noted above, the continued *de facto* opposition between Iranists and Türkists already crossed over into the 21st century, it leads to obvious mutual excessives. As the Iranists not give an inch of ancient Eurasia to the Türkic languages (see the previous section), the same way the Turkologists in the example of Yu. Drozdov (in this particular case) do not see the Indo-European languages in Europe at that same time and later, including the whole first millennium of our era, excepting the Greek and Latin (from the middle of the last millennium BC [p. 352] or the end of the last centuries BC [p. 356]). Although, as

Yu. Drozdov pointed out, "*to ascertain the carriers (of the Latin) was impossible so far*" (p. 352).

It commonly does not happen that both sides were so mistaken. This article attempts to show that both sides are in a way correct, each on its own half. As states the famous saying attributed variously to A. Einstein or I. Newton, "The Nature is cunning, but not malicious." And here the nature has played a cunning joke with the linguists. It seems that the two Caucasoid (Europeoid) brotherly tribes, or haplogroups, R1a1 and R1b1, that came about 60 thousand years ago to the Eastern European Plain as an upstream tribe CT (or maybe arose as that CT tribe at the Russian Plain, contemporary science does not know it as yet), and then went to the Southern Siberia at least 50,000 years ago as the NOP tribe, and then as a split P tribe (45,000 years ago), and finally arose as R1a1 and R1b1, have dispersed over time and over territories, as relayed below, carrying two quite different languages, ProtoIndoEuropean and ProtoTurkic, respectively.

In other words, one of those post-Nostratic languages was a flexive Aryan language (language of the R1a1 tribe), which later became to be called Proto-Indo-European, and the other was an agglutinative Proto-Türkic language (language of the R1b1 tribe). Both types arose in the Southern Siberia.

The R1b1 tribe, a carrier of the agglutinative, ancient ProtoTürkic languages. The path from Asia to Europe, with the arrival at the turn of the 3rd-2nd millenniua BC

The modern Uigurs, Kazakhs, Bashkirs, and some other peoples of Siberia, Central Asia, and the Urals, descend in part from the ancient R1b1 tribe, and by now retain the same R1b1 haplogroup for about 16,000 years. That tribe historically was moving from east to west, leaving their descendants along their migration route.

Those are the present-day peoples of Siberia, Volga, Kama, Central Asia, and the ancient peoples of the Middle Volga, Samara, Khvalyn, the ancient Pit Grave or "Kurgan" archaeological cultures, cultural and cultural-historical communities, and some Caucasian peoples that partially retained the haplogroup R1b1, which by the time of 6,000 years ago has become a downstream haplogroup R1b1a2 (carryingt mutations M269 and L23 or L49 according to the modern nomenclature), and the peoples of the Turkey and Middle East, whose populations retained in their DNA many structural segments of the same haplogroup R1b1, see the table below (Abu-Amero et al, 2009; except the new data on the Assyrians).

Country	A fraction of R1b1a2, %
Assyrians	**30**
Anatolia	**15**
Iraq	**10**
Iran	**8**
Lebanon	**7.3**
United Arab Emirates	**3.7**
Pakistan	**2.8**
Egypt	**2**
Saudi Arabia	**1.9**
Qatar	**1.4**
Jordan	**1**
Oman	**1**

The Assyrians are considered to be descendants of ancient Sumerians, and they have their R1b1a2 haplogroup as the dominating one among others, lagging far behind. Notably, the "indigenous" Caucasians, the descendants of the haplogroup R1b ancient tribes, have no further recorded downstream subclades of their haplogroup R1b1a2 (with mutation M269) or R1b2a2a (with mutation L23), which are typical for the Western and Central Europeans. In other words, the subdivision to suclades, of course, exists, but no one has yet studied it for the Caucasians (as inhabitants of the Caucasus). It seems that the fragmentation in the Caucasus went the other way, forming other "downstream" mutations that have not yet been identified. On the contrary, the Europeans for identification of the downstream "European" mutations threw in large forces of specialists, and their R1b2a2a-L23 in the subsequent move from the Caucasus to Europe already has 83 subgroups identified by the end of September 2011 (there were 34 of them when the first edition of this article was published in 2009, and the list is growing at the rate of two dozen R1b1a2 subclades a year). In an abridged version, without side branches, the subsequent, post-Caucasian development of the subgroups looks as follows:

- **R1b1a2a** L23/S141, L49.1
  - **R1b1a2a1** L150
    - **R1b1a2a1a** L51/M412/S167
      - **R1b1a2a1a1** L11/S127, L52, L151, P310/S129, P311/S128
        - **R1b1a2a1a1a** M405/S21/U106
        - **R1b1a2a1a1b** P312/S116
          - **R1b1a2a1a1b3** S28/U152
          - **R1b1a2a1a1b4** L21/M529/S145, L459
            - **R1b1a2a1a1b5** L238/S182

Here subclades and their respective SNP (Single Nucleotide Polymorphic) mutations are shown. Some subclades have multiple SNP mutations, all of them are characteristic for the subclades, though all they were formed at different times. Some indexes, such as P312/S116, are the same thing, but identified in different laboratories, and in the cited case P designates University of Arizona, and S – Edinburgh University.

Since those SNPs are practically irreversible, they serve as clear "markers" that allow tracing the carriers of the R1b migration (and migrations of all haplogroups and their subclades, on that matter) throughout the whole Europe and the world, to the most remote corners.

Considering the ancient migrations of the haplogroup R1b in Asia, eastward of Anatolia (15% of R1b1a2) the share of the R1b1a2 noticeably falls (8%): it is 2.8% in Pakistan, alongside with 4.6% of the ancient Asian line R1b1a1. We see that the most ancient R1b left (in a very little amounts nowadays) closer to their place of origin, though they could have moved for thousands of years. In Central Asia, their downstream R1b1a1-M73 in Pakistan (as well as among Uigurs, Tuvans, Kazakhs and other Central Asians) exceeds their further downstream R1b1a2-M269, which grow higher in their share starting from Iran (still not much) and Anatolia, and further westward. In the British Isles, for example, R1b1a2 reaches >90%, as well as among the Basques in Iberia.

- **R1b** M343
  - **R1b1** L278, M415, P25_1, P25_2, P25_3
    - **R1b1a** P297, L320
      - **R1b1a1** M73, M478
      - **R1b1a2** L265, M269, M520, S3, S10, S13, S17
        - **R1b1a2a** L23/S141, L49.1

Very little, only 0.8% of the last ancient Asian line (R1b1a1-M73) is found in Anatolia (Abu-Amero et al, 2009), as also elsewhere outside of the Central Asia. However, we are now talking only on adding some SNP mutations to the DNA of those ancient people, who continued to move thousand years ago from Central Asia westward without any knowledge of their subclades and haplogroups. They continued to carry their ancient (ProtoTurkic) language from Central Asia to Europe by relaying if from generation to generation over hundreds of generations, and why would not they? They continued to speak in their ProtoTürkic language, which, naturally, was changing in accordance with the laws of linguistic dynamics. Of course, their ProtoTurkic language in Central Asia 14,000 years ago and their ProtoTurkic language on Middle Volga 9,000 years ago, and their language in the Caucasus 6,000 years ago and in Sumer 5500 years ago, and in Iberia 4500 years ago, and among the Basques nowadays – of

course they were and they are now tremendously different languages.

Therefore all those "objections" that we cannot call all of those languages as "Turkic", are irrelevant. None of languages can be called a single name during 16,000 years or so. All that linguists can do is to look at assorted fragments of an ancient language which was evolving in its continuiety over thousands and thousands of years, and call those fragments by different names, such as "ProtoTurkic", "Dene-Caucasian", "Sino-Caucasian", "Na-Dene", "Enisseian", "North-Caucasian", "Iberian", "Sumerian", "Basque", and other agglutinative, non-IndoEuropean languages. In fact, it might well be the same language in its historical dynamics, and DNA genealogy points in this direction, telling linguists – just look better, now you do know where to look and what at. That is why in order to avoid confusions I suggest to call this language "Erbin", as being attributed to the abcient R1b tribe in its historical dynamics.

From Anatolia, which the carriers of the R1b1a2 characteristic mutation (SNP), together with their agglutinative language, reached 6,000 ± 800 years ago (Klyosov, 2008a, b), they continued moving westward toward Europe by two routes. One route went through the Balkans, where the haplogroup R1b1a2 are identified (by a pattern of mutations in their Y-chromosomal haplotypes) at about 4,000 years ago (a formal calculation gives 4050 ± 890 years ago). In Sardinia, it dates at 5,025 ± 630 years ago, Sicily 4,550 ± 1020 years ago, in Italy 4,125 ± 500 years ago, in Slovenia 4,250 ± 600 years ago. Another route went through the Middle East (the common ancestor of the modern carriers of the haplogroup R1b1a2 in Lebanon dates back to 5,300 ± 700 years ago, among the nowaday Jews 5,150 ± 620 years ago), then across the North Africa (Algerian Berbers 3,875 ± 670 years ago) to the Atlantic Ocean and across Strait of Gibraltar to the Iberian Peninsula (4800 years ago), and further up North to the continental Europe (Klyosov, 2009a). Approximately 3,600 years ago that haplogroup has reached the British Isles. This is the movement of Beaker culture - from the Iberian Peninsula to the British Isles and on the European continent. On the overall, the peopling of Europe by the carriers of the haplogroup R1b1a2, who were speaking the ancient Türkic languages, occurred between 4,800 and 3,300 years ago. They were the ancestors of the present 60% of population in Europe.

The R1a1 tribe, carrier of the flexive, Aryan languages. The path from Asia to Europe and back East in the 3rd-2nd millenniums BC

Between 10 and 5 thousand years ago Europe was populated (although with low density in those times) by bearers of haplogroups R1a1, G2, I1, I2, J2. The last four probably came to Central Europe in Upper Neolith, in the pre-glacial period, and R1a1 came from Asia around 11-9 thousand years ago. It was much earlier than the arrival time of R1b1a2 about 4800 years before present.

Haplogroup R1a, as it was mentined above, arose in South Siberia. "Arose" in the sense that one of haplogroup R1 bearers acquired a certain SNP mutation (see the diagram below) in his DNA Y-chromosome, and after many generations those who survived from his tribe had exactly that mutation, possibly along with some other, "parallel" mutations (parallel not in time, but in the final result).

R M207/Page37/UTY2, P224, P227, P229, P232, P280, P285, S4, S9, V45
- **R1** M173/P241, M306/S1, P225, P231, P233, P234, P236, P238, P242, P245, P286,
  - **R1a** L62/M513, L63/M511, L145/M449, L146/M420
    - **R1a1** L120/M516, L122/M448, M459, Page65.2/SRY1532.2/SRY10831.2
      - **R1a1a** L168, L449, M17, M198, M512, M514, M515
        - **R1a1a1** L457, M417, Page7
          - **R1a1a1a** M56
          - **R1a1a1b** M157.1
          - **R1a1a1c** M64.2/Page44.2, M87, M204
          - **R1a1a1d** P98
          - **R1a1a1e** PK5
          - **R1a1a1f** M434
          - **R1a1a1g** M458
            - **R1a1a1g1** M334 (position relative to L260 uncertain)
            - **R1a1a1g2** L260
          - **R1a1a1h** L176.1/S179.1
            - **R1a1a1h1** L175
          - **R1a1a1i** L365
          - **R1a1a1j** L366
          - **R1a1a1k** P278.2
          - **R1a1a1L** L342.2

It was a pure coincidence. Those SNP mutations that defined the haplogroup R1a1 provided no advantage for survival, as far as (current) science tells us. The carriers of another mutation could have survived, and then we would now state that survived carried a mutation XYZ. Anyway, those who survided and continued life of the tribe with their descendance, we now call R1a1. They were descendants of the same upstream tribe R1, and spoke the same language, at least at the time when the new SNP mutation appeared which now defines R1a haplogroup.

This R1a haplogroup appeared about 20,000 years ago (Klyosov, 2009b), in any case there are no other data. I use here designations R1a and R1a1 interchangeably, since we do not have data whether they were distant in time or have appeared almost at the same time, within a few generations. Apparently, it was some 4,000 years before the appearance of the R1b1 haplogroup. It seems that by the time when R1b arose, bearers of R1a1 have already left those places.

Four thousand years is a long period, within which is quite conceivable for a tribe to move to a new territory. For what reason the common language of R and then R1 diverged into the flexive (R1a1) and agglutinative (R1b1) language families we do not know.

The base for both languages was Nostratic, or Boreal language, or whatever name can be invented, it will not change anything. There were many "Nostratic" levels of languages, starting at least from ~ 65,000 years before present, the times of the upstream haplogroup BT, then its downstream CT, then IJK, which as IJ or I separately, migrated west to Europe, then K gave NOP, which around 50,000 years ago went eastward, split to NO and P, and some of them arrived to Southern Siberia about 45,000 years before present.

NOP was certainly a source of Nostrac language (from 50,000 years and onward), and, when split, N (arose ~ 20,000 years ago) gave an Altaic, Uralic, and Finno-Ugric languages; O (arose ~ 23,000 years ago) gave the Dene/Sino-group of languages, such as Sino-Tibetian and other languages resulten in languages of China, Japan, Korea, and many East Asian regions. P gave Q and R haplogroups (~40,000 years ago), of which Q populated Siberia (including many Mongoloid tribes) and the Americas (including many carriers of Amerindian agglutinative languages), and R produced R1a and R1b, which currently populate Werstern, Central and Eastern Europe, and who now speak Turkic (in Asia) and IndoEuropean languages (mainly in Europe). All those languages have their roots in Nostratic languages back to 50-10 thousand years ago, and particularly 13-15 thousand years ago when R1a and R1b were migrating across Eurasia, westward to Europe. It seems that initially haplogroups NOP spoke an agglutinative language(s), including R1, however, on some reason not understood as yet, R1a1 spoke a flexive, proto-IE language. It was identified as early as 10-9,000 years before present in Anatolia (Gray and Atkinson, 2003). Later it became the signature language of R1a1 haplogroup in Europe, a Proto-Indo-European Aryan language, which was brough to the Russian Plain at 4800 ybp, and then to India and Iran at about 3500 ybp.

The exact path of the haplogroup R1a1 to Europe remains unknown, however, we can see a trail of R1a1 haplotypes from South Siberia (the Altai and Xingjiang regions) across India, Pakistan, Iran, Anatolia and the rest of Asia Minor to the Balkans. The oldest dates of R1a1 populations in Europe go back to 10-11 thousand years ago, that is immediately after the melting of the glaciers. By some indications, its place was in the Balkans. That is also in agreement with some linguistic data about the landscape of the Indo-European "homeland", although this term is inherently flawed if applied to Anatolia and anywhere in Europe. At any rate, as we observe, it was not an "ancestral home", and they were not "Indo-Europeans", but the R1a1 tribe, at the time they were Pra-Indo-Europeans. As will be seen later, that tribe migrated from the Russian Plain to India and Iran in

the middle of the second millennium BC under a name of the Aryans, bringing along their Aryan flexive language. From that period the language acquired a status of "Indo-European". Prior to that it was the Aryan language, a language of the haplogroup R1a1.

So, the carriers of the haplogroup R1a1 remained (apparently) in the Balkans from about 10-11,000 years ago, and quite possibly were populating the Europe. They could have trade and other relations with the southern Europe, including Anatolia and in general with the Asia Minor, Greece, and initiated, alone or in association with the people of the haplogroup I, what later was named Balkan Archaeological Cultures. The early dating of these cultures are about 8-9 thousands years ago (6th-7th millenniums BC), which does not contradict the dating of DNA genealogy for the haplogroup R1a1 in Europe as 11-10,000 years ago. The archaeology testifies about excavated (typically) material traits, and not about the time of the arrival there of an ancient migrants. The 2-3 thousand years that separate the appearance of R1a1 in the Balkans, from the dates of the Starcevo, Keresh, and then Tripolie-Cucuteni cultures is quite reasonable.

So, what linguistic landscape was in Eurasia from 16 to 6 thousand years ago (4th millennium BC)? Before answering that question, we roll back to the more ancient times, and present, inevitably in general terms, the concept of the world status with respect to humanity for the previous 60-50 thousand years, as it is presented by the modern DNA genealogy.

The linguistic landscape in Eurasia by 6 thousand years ago (4th millennium BC), and in the next 2,000 years

Let us return to the subject of our review. By the 6 thousand years ago the carriers of the haplogroup I, divided into two main subgroups I1 and I2, lived in Europe for more than 30 thousand years. They barely left the European continent. What language they had is unknown, but it is possible that the Basque language is an ancient language of the carriers of the haplogroup I. This is currently a totally groundless suggestion, and I list it just for the record. It is known though that the Basque language is a non-Indo-European language. Currently, it is considered to be unclassified, agglutinative language. If it also would turn out not to be a Pra-Türkic, has no connections whatsoever with said Caucasian languages, as well as with any ancient languages in Asia, it is likely that it was the language of the ancient carriers of the haplogroup I. But if an unbiased study would find the elements of the ProtoTürkic, agglutinating languages, it is the language of the ancient R1b1a2, Erbin.

The carriers of the haplogroup R1b1a2, as was mentioned above, arrived to the Iberian Peninsula 4800 years ago [presen-day Basques have a common ancestor who lived 3,625 ± 370 years ago, and among the Basques the haplogroup R1b1a2 is the majority, with its 93% (Adams et al, 2008)], and arrived via the Caucasus, where they lived 6,000 years ago, with a follow up migration to Europe along several directions. In this connection it is important that some linguists are attributing the language of the Basques to the Sino-Caucasian or Dene-Caucasian linguistic macrofamily, which includes Caucasian, Tibetan, Yenisei, Chinese and Burushaski languages. Here we definitely see the reflection of the haplogroup R1b path during the ancient times, from the southern Siberia (Yenisei and Chinese languages) across the Caucasus (6,000 years ago) to the Pyrenees (Basques). So, the conjecture that the Basque language is the ancient language of the haplogroup R1b is not devoid of a connection with the classification of the linguists. Moreover, the Basque language has the same vigesimal (20-base) numeral system like the Caucasian languages, and has common elements with the Semito-Hamitic world, as well as with the Sumerian, and Hurro-Urartian (private communication of Dr. I. Byzov). This again points at the path and the environment on the way of the haplogroup R1b to Europe.

The carriers of the haplogroup R1a1 were the Aryans, considering that it was them who came to India and Iran about 3,500 years ago. In the 4th millennium BC they began spreading across Europe, and 4,750 ± 500 years ago came to the Eastern European Plain. In the next few centuries, they settled from the Baltic to the Caucasus, about 4,500 years ago they were recorded in the Caucasus, and about 3,600 years ago were already in Anatolia. This is consistent with the linguistic and archaeological results, and documentary evidence. The Anatolia in no way can be considered a "homeland" of the Indo-European language not only because the notion of the "ancestral home" in this context at totally wrong, but also because Anatolia and the surrounding regions were among the territories which the Aryans visited during the colonization and settling of the Eurasia. From the Anatolian side, it is unlikely that the Aryans advanced far to the east, and in any case not to the India and not to the eastern Iranian Plateau. These were the local places of the Aryan stay (haplogroup R1a1).

The phrase above, "consistent with the linguistic and archaeological results, and documentary evidence" should not be understood that that picture is consistent with a modern interpretation of these results by the linguists and archaeologists. This is a synthesis by the author of the findings by the archaeologists and linguistics, often dispersed, scattered, and reconciling them with the findings of the DNA-genealogy. The modern archaeology, as is known, over the past decades was not inclined to consider migrations of the ancient people, its methodological arsenal is not too suitable for the studies of the migration. Their classic slogan, known to every archaeologist, is "The pots are not people" (read: "and we are doing the pots"). In their paradigm, the transmission of the cultural

and material traits are passed along the "chain", not necessarily by the migrations. On the contrary, the DNA genealogy is focused precisely on migrations, because the markers in the form of the DNA mutations are characteristic in different parts of Eurasia, together with dating that follows from the accompanying faster mutations in different loci of Y chromosome. That is, the places of migrations are detected rather directly, and the datings are calculated by mutations in those loci. From that, a picture of the migrations such as presented in this article is deduced.

Archaeologists usually assert that in those times, in the 3rd millennium BC there were no migrations to the east, because they were not recorded in the written sources, there are none in archeology. Let's glance at the following specific experimental buttressing.

4000 years ago, the carriers of the haplogroup R1a1 already established the Andronovo archaeological culture and reached southern Urals. The archaeological excavations in the south of Krasnoyarsk region revealed that the bone remains dated by 3,800-3,400 years ago have characteristic mutations of the haplogroup R1a1 (Keyser et al, 2009). Moreover, the haplotypes of these remains easily appended into the haplotype tree for the modern ethnic Russians from Ivanovo, Penza, Tver, Lipetsk, Novgorod and Ryazan regions. In other words, these remains and modern ethnic Russian had one and the same common ancestor, who lived, as we already know, about 4,800 years ago.

Approximately 3,600 years ago a part of the Aryans (haplogroup R1a1) left the southern Ural Mountains and moved to India. About at the same time the Aryans from the Middle Asia, where they lived at least for five hundred years, moved to Iran. The common ancestors of the Indians and Iranians with the haplogroup R1a1 lived 4,050 and 4,025 years ago, respectively (Klyosov, 2009b, g), which is 800 years "younger" than the common ancestor of the modern ethnic Russians with the haplogroup R1a1. The haplotypes of the modern Eastern Slavs (haplogroup R1a1) are almost identical with the haplotypes of the Indians and Iranians, even in the 67-marker haplotype format, i.e. to almost a maximum resolution of the modern DNA-genealogy. Let us take a look at them. They show a striking illustration for a joint history of common ancestors of the Russians and the Indians.

The following 67 marker haplotype is of the author of this paper, a Slav with the R1a1 haplogroup:

13 24 16 11 11 15 12 12 10 13 11 30 -- 16 9 10 11 11 24 14 20 34 15 15 16 16 -- 11 11 19 23 15 16 17 21 36 41 12 11 -- 11 9 17 17 8 11 10 8 10 10 12 22 22 15 10 12 12 13 8 15 23 21 12 13 11 13 11 11 12 13

and below are three quite typical 67 marker haplotypes of Indians randomly taken from the Indian database FTDNA. Mutational differences between them are shown in bold:

13 24 **17 10** 11 14 12 12 10 13 11 **32** -- 16 9 10 11 11 24 14 20 **31** 12 15 15 16 -- 11 **10** 19 23 **16** 16 **17 20 33 34 13** 11 -- 11 8 17 17 8 **11** 10 8 11 10 12 22 22 15 10 12 12 13 8 14 23 21 13 13 11 13 11 11 12 **13**

13 24 16 11 11 14 12 12 10 13 11 **31** -- 16 9 10 11 11 24 14 20 **33** 12 15 15 16 -- **10** 12 19 23 15 17 18 **18** 35 **41 15** 11 -- 11 8 17 17 8 12 10 8 11 10 12 22 22 15 10 12 12 13 8 **13** 23 21 **12 12** 11 13 **10** 11 12 12

13 **23** 16 11 **12 15** 12 12 10 13 11 **30** -- 16 9 10 11 11 24 14 20 **30** 12 **16 16** 16 -- 11 12 19 23 15 16 18 **21** 35 **39 12** 11 -- 11 8 17 17 8 12 10 8 11 10 12 22 22 **16** 10 12 12 13 8 14 **24 22** 13 13 11 13 11 11 12 12

The four haplotypes are obviously similar to each other. A number of mutations between the Indian haplotypes (pair-wise) equals 27 - 30, and that between the Slavic haplotype of the author and to each of the Indian haplotypes equals 25 - 30. In other words, the Slavic haplotype is closer to the Indian haplotypes than the Indian haplotypes between each other. In fact, those differences are within the margins of error, and all four haplotypes are equally similar to each other.

This can be compared to a typical Western European base haplotype of haplogroup R1b1a2, which (and its variants) make around 60% of Western and Central Europeans, and up to 90% (and higher) population in the British Isles:

13 24 14 11 11 14 12 12 12 13 13 29 -- 17 9 10 11 11 25 15 19 29 15 15 17 17 -- 11 11 19 23 15 15 18 17 36 38 12 12 -- 11 9 15 16 8 10 10 8 10 10 12 23 23 16 10 12 12 15 8 12 22 20 13 12 11 13 11 11 12 12

The number of mutations between the European R1b1a2 base haplotype and the Indian (and the Russian) haplotypes shown above is around 50. This is of no surprise, since their common ancestors are separated by at least 30 thousand years. There are almost no haplotypes of the R1b haplogroup in India and Iran. It looks like there were no bearers of the R1b haplogroup, that is, ancestors of the majority of nowadays Western Europeans, among the Aryans 3500 years ago. It should also be noted that the upper castes of India in the present time consist of up to 72% of bearers of haplogroup R1a1, particularly among Brahmins (Sharma et al, 2009). At the same time not a single Brahmin among 367 tested ones belonged to haplogroup R1b (ibid.).

On that basis it should be asserted that the Aryans of the 2nd millennium BC, the bearers of the haplogroup R1a1, without a doubt were the descendants of those

same ancestors as the present day ethnic Russians. At present, in India live not less than 100 million men who are descendants of the Aryans from the Eastern European Plain, and before that from the Balkans. Up to 72% of the higher castes in India belong to the haplogroup R1a1 (Sharma et al, 2009).

These ancestors of the modern Russians, as well as of many modern Ukrainians, Belarusians, Lithuanians, Estonians, Tajiks, and Kyrgyzes, those who are carriers of the haplogroup R1a1, brought to India and Iran their Aryan flexive language, which also bridged the linguistic link between Europe and India-Iran, and manifested the beginning of a new linguistic family, the Indo-European languages.

As long as 150 years ago, A.F. Hilferding in his work "On the affinity of the Slavic with Sanskrit" (1853) wrote: "*... Slavic language, taken in its entirety, does not differ from the Sanskrit by any permanent, organic phonetical change. Some distinction, found in it, like some lisping "r" of the Czechs and Poles and others, have developed already in the later, historical era, and belong to only a few of their vernaculars. I repeat that in the overall the Slavic language does not have any particular distinctions alien to the Sanskrit. The Lithuanian language shares with it this property, whereas all other Indo-European languages follow different phonetical laws, which are exclusively peculiar to each of them separately. Thus, in the lexical relation the Slavic and Lithuanian languages are very closely kindred to Sanskrit, and together in the Indo-European tribe they make up something like a separate family, outside of which stand the Persian and Western Europe languages.*"

At the present time, we know that the Persian or Iranian languages also were basically brought to the eastern part of the Iranian Plateau by the Aryans, the carriers of the haplogroup R1a1, and around the same time as to the India, but the Aryans that had lived at least for several hundred years (probably for at least 500 years) in the Middle Asia. The starting time for the ancient Iranian languages is the middle of the 2nd millennium BC. According to S.A. Starostin (1989), the modern Russian and Persian languages have 28% pairwise matches in the Swadesh 100 word list, from which with the value of the "rate of loss of words factor" (per Starostin) equal to 0.05, S.A. Starostin arrived at

$$t = \sqrt{\frac{\ln(100/28)}{2x0.05}} = 3.6$$

i.e. 3,600 years from the time of of the divergence, the split of these languages (S.A. Starostin, ibid.) This coincides quite precisely with the Aryans' arrival time to Iran, and the outset of the ancient Iranian languages. S.A. Starostin believed that that value "is made younger" and wrote that he would prefer to have this value by the 4th millennium BC, i.e. about 6,000 years ago, believing that that

should be the time of the collapse of the Indo-European languages. But without realizing it, he has received a reliable dating in respect to the time of the difference of the Aryan or "Pra-IE" and Iranian languages.

Thus, the words of Yu.N. Drozdov "*Under the concept of the linguistic science, the languages of the modern European nations belong to the linguistic family called "Indo-European", although you can not find a single ancient source which would have recorded any trace of Indians or their kindred peoples in the European territory*" reflect the already mentioned above categorical stand of the Turkologists (and equally of the Iranists) in respect to the opposing science, and clearly outdated views of the linguists, where the "Indians" (or as much the "Iranians") have already formed as an ethnic group, and should have been the primary bearers of the Indo-European languages in Europe. On the contrary, the Indians, like the Iranians, were the recipients, and not the donors of these languages. The "Indo-European" languages at that time were generically the Aryan languages.

Thus, 6000 years ago, or at the turn of the 4th and 5th millenniums BC, the linguistic landscape in Europe was the ancient Aryan, the language of the R1a1, and perhaps to some extent the language (or languages) of the ancient European haplogroups I and G. The language of these haplogroups could also be the ancient Aryan, or could be pra-language of the current Basques, or be an unknown now tongue. The Türkic language was brought over by the haplogroup R1b1b2 only about 4 thousand years ago, at the turn of the 2nd and 3rd millennia BC.

Approximately 4,500-4,000 years ago something happened in Europe, resulting in the haplogroup R1a1 virtually disappearing from Europe (see below). As, incidentally, at the same time also disappeared haplogroup I1 and largely the haplogroup I2. At the same time or a few centuries earlier, Europe was settled by the carriers of the ProtoTürkic R1b (mainly by its subgroups R1b1a2). Two hypothetical reasons could be at the root, either an almost complete extermination of the other haplogroups by the carriers of the R1b, or between 4,000 and 4,500 years ago Europe had suffered a major natural cataclysm, and the Türkic-lingual R1b1a2 settled in the almost deserted Europe, if had arrived some later. Evidence can be found in favor of the first and the other possibility. The possibility of the first is supported by the numerous finds in Scandinavia of ancient human remains with crushed skulls belonging to approximately the same time, which even received a conditional designation of the "period of crushed skulls". Characteristically, many findings uncovered fractured skulls of women and children (Lindqvist, 1992, 1993, 1994, 1997, 1998). That finding is echoed the finding in Germany of a group of 13 people, most of whom children and women, most (including children) with crushed skulls and stone arrowheads stuck in the bones, dating by 4,600 years ago. Two boys (aged 4-5 and 8-9 years) and a men aged 40-60 years were successful identification of their

haplogroups, and all three were R1a (Haak et al, 2008). The analysis of the site revealed that the women, elderly and children were killed during an absence of the adults, apparently by a hostile tribe.

Apparently, under the standard scheme the period of the "fractured skulls" is linked with the "Indo-European invasion," not realizing that the "Indo-Europeans" already lived in Europe for many thousand years, and no their "invasion" from the west ever happened. Later, from the end of the 3rd millennium BC and for the next one and a half millennia, before their migration to India and Iran, the vector of their migration was directed to the east. The so-called "Kurgan theory" to the "Indo-Europeans", i.e. to the bearers of R1a1, to the Aryans, had no relation whatever, but it is applied to the bearers of R1b, which were Türkic-speaking, and indeed were moving westward and then southward through the Caucasus to the Asia Minor and Europe, as was described above; moreover, a thousand years or more ahead of the Aryans of 4000 ybp. To the "Indo-" they, too, had no relation, neither linguistically, no migrationally, and it remains only to wonder how such a theory could emerge at all. Like, however, also the "Anatolian" theory" of Indo-European Urheimat. This will be discussed below.

In its entirety, the theory of "Kurgan Culture" as an "Indo-European" was one continuous mishap. It transposed migratory flows, their directions (westward and eastward), timing of these flows (6-5 thousand years ago and 5-3 thousand years ago), origin (ancestral affiliation) of the migrants (R1a and R1b), their linguistic classification (Aryans and ProtoTürks). It seems that the desire of the authors and supporters of the Kurgan theory as "Indo-European" to persuade others in their accuracy did not allow them to consider alternatives, as is due in science. Naturally, that mishap could not address the ancestral affiliation, such information did not exist then.

In Europe 4,500-4,000 years ago, the scenario about extermination of the haplogroups R1a1 and I bearers, has a historical basis. Moreover, in Scandinavia the haplogroup I1 was (then and now) particularly common, so that the fractured skull in Sweden could primarily belong to them. But we can not exclude a major natural disaster in Europe between the 4,500 and 4,000 years ago, and that has numerous literature that is so vast that we are not getting into details now. Instead, we will refer to the geophysical work (Keenan, 1999) with hundreds of references on this topic. According to the author, it probably was a largest destructive event in the history of civilization since the Ice Age, and it "*encompassed the greater part of the northern hemisphere*" (ibid.)

Whatever the reason, the haplogroup R1a1 virtually disappeared from Europe at about 4,500-4,000 years ago, and the ProtoTürkic-speaking carriers of the haplogroup R1b1a2 colonized the deserted Europe. Or they had made it devoid

of other haplogroups. As it is shown several lines below, virtually all modern branches of the haplogroup R1a1 in Europe are dated from the 2,900-2,500 years ago and later. At the same time, there is evidence that haplogroup R1a1 was in Europe from 11-10,000 years ago. Then the archaeological excavations found the haplogroup R1a1 in Europe (Germany) 4,600 years ago (see above). In other words, a gap for R1a1 in Europe exists starting from the middle to the end of the third millennium BC (4,500-4,000 years ago) that is lasted for 1,000 - 1,500 years. At the same time no gap exists in Europe with respect to the R1b1a2, their settling goes in a continuous stream from the 4,000-4200 years ago, without any stops.

Apparently, as a result of it Europe became ProtoTürkic-speaking. The R1a1 people remained only on the Eastern European Plain, they were the descendants of people who moved there about 4,800 years ago. Within a few centuries, about 3,500 years ago, the surviving descendants of the extinct in Europe haplogroup R1a1 would bring their haplotypes, and their preserved Aryan language to the Urals and Middle Asia, to the India and Iran, and to Siberia. The common ancestor of all these branches of the haplogroup R1a1 lived on the Eastern European Plain 4,750 ± 500 years ago. These are again the results of the DNA-genealogy with the inevitable conclusions of the linguistic nature. It is known that the Aryan, or the Proto-Indo-European language was brought over to India and Iran. It is unlikely that the same R1a1 tribe at the same time brought to the Urals and southern Siberia some other language.

The repopulation of Europe by the bearers of the R1a1 happened between 3,000-2,200 years ago, that is from the beginning to the middle of the first millennium BC and later on. Here are the distances to lifetimes of the common ancestors of the major European DNA-genealogical branches (Rozhansky and Klyosov, 2009, and updated since the publication), time is shown in years before present:

- European north-west 2,800 ± 400
- European north-west 2,500 ± 400
- Northern European 2,900 ± 400
- Western Slavic 2,600 ± 300
- Central European 3,000 ± 400
- Northern Eurasian 2,200 ± 250
- Baltic-Carpathian 1 2,700 ± 300
- Baltic-Carpathian 2 2,500 ± 300
- Young Scandinavian 2,300 ± 300
- North-Carpathian 2,150 ± 300
- Western Eurasian 1 2,600 ± 300
- Western Eurasian 2 2,000 ± 300

- Western Carpathian 2,000 ± 300
- South Eurasian 2,550 ± 320

That was a return of the carriers of the flexive, Indo-European languages to Europe. As can be seen, for a large part of Eastern and Central Europe it was the end of the last era (of non-IE languages) and the beginning of our era (of IE languages). As a result of this migration the ProtoTürkic, non-IndoEuropean European languages were replaced with Indo-European languages, and that tilted the balance in the direction of the current European languages. However, this replacement left many Türkisms in the personal names, designations for the objects, and some individual terms.

Since many historians consider that the first Celts in Europe (around 2500-2600 ybp) have appeared as migrants from South-Russian steppes, they were likely R1a1 settlers, who moved as R1a1 tribes westward, which names and dates list in the above table. In this case it is quite understandable why the first Celts spoke Indo-European languages, languages of R1a1. I could not find in the literature any indications which would make me believe that the first Celts were R1b1a2, and that the R1b1a2 in general spoke Indo-European language(s) before 3000 ybp. All references to IE languages in Europe in the 1-2 millennium BC point at those first Celts in the middle of the 1st millennium BC. They seemed to be totally disconnected from R1b1a2 in Europe, from the Bell Beakers – by origin and by language.

It is unlikely that the displacement of the ProtoTürkic languages by the Indo-European in the Western and Central Europeans was quick and without a good reason. Typically, in such transitions a number of factors, especially military, economic and political (ideological) are acting together. The military factor is not always necessary, or rather, is not decisive, but the last two factors are mandatory. Apparently, the arriving carriers of the Indo-European languages from the east convincingly (this is a wide concept) demonstrated to the ProtoTürkic-lingual population of the past era last millennium Europe the benefits of their organization, the advantages of producing or more progressive economy (trade), education and culture. Only that could lead to the assimilation of the alien (for then-Türkic population of Europe) material culture and to the transition to a different language. This area still awaits its researchers.

That the branches of R1a1 haplogroup were returning to Europe indeed from the Eastern European Plain is evidenced by the fact that all of these combined European and Eurasian branches indicate the haplotype of the ancestor from the Eastern European Plain, and the same age, about 4,900 years ago, to their common ancestor (Rozhansky and Klyosov, 2009). Thus, reciting the statement of Yu.N. Drozdov "*...you can not find a single ancient source which would have recorded*

any trace of Indus or their kindred peoples in the European territory" it is worth noting that despite the ancient sources and their interpretation, kindred to "Indus" carriers of the haplogroup R1a1 with their flexive "Indo-European" language, more accurately, languages of that time, by the beginning of our era returned to Europe and brought back their languages.

The formation and divergence times of the Türkic languages', and glottochronology of Türkic languages

When do experts think the Türkic languages were formed? The following is an excerpt from a paper written by a corresponding member of the USSR Academy of Sciences, Orientalist S.E. Malov in 1952: "*Some oldest Türkic words and even a whole phrase ("Hunnish") are in the Chinese records at the beginning of our era. And the Türkic languages in the writings of the Türks are known to us from approximately 5th-6th cc. of our era.*" According to other sources, the beginning of the Türkic languages is associated with the appearance of the European Huns on the historical scene, i.e. the end of the past - the beginning of common era. The same is also evidenced by the glottochronology, that is not "evidenced", but in fact is postulated by the will of those who decided to use it to resolve this problem. Let us briefly review that.

Nearly all works in glottochronology of the Türkic languages are written in Russian, and all with a notation "preliminary analysis", are connected with the name of M.T. Diyachok. Those preliminary analyses were carried out rather recently, mostly in 2001. Example - (Diachok, 2001, "Glottochronology of Türkic languages (preliminary analysis)." Let us look at this work. It provides a classification of the Türkic languages suggested by A.N. Samoylovich (1922), as well as the works of N.Z. Gadjiyeva (1980, 1990). According to that classification, based on the phonetic and morphological principles, the Türkic linguistic group comprises six subgroups (sometimes Sakha/Yakut is defined as a separate subgroup):

1. Bulgar (Bulgar, Chuvash).
2. Uigur (Ancient Uigur, Khakas, Shor, Tuvan, Tofa, Yakut, Dolgan).
3. Kypchak (Tatar, Bashkir, Kazakh, Kirgiz, Altai, Karachai-Balkar, Kumyk, Crimean Tatar).
4. Chagatai (modern Uigur, Uzbek).
5. Kypchak-Turkmen (Western dialects of the Uzbek language).
6. Oguz (Turkish, Azeri, Gagauz, Turkmen).

It is noted that despite numerous languages of the Türkic group, many are very close to each other (Tatar and Bashkir, Kazakh and Karakalpak; Tuvan and Tofa,

Sakha and Dolgan), although it is mentioned that in areas close to the Türkic ancestral home (Southern Siberia and northern China), the classification is developed insufficiently, and "*it is quite possible that among them may be found fairly archaic elements*".

Regarding the glottochronology, it turns out that M.T. Diyachok simply postulated that the laws of the of linguistic dynamics are the same for flexive and agglutinative languages, and took the same constant for the retaining of the vocabulary as it is employed for the Indo-European languages (even though it is floating there from situation to situation, as pointed by S.A. Starostin, from 0.14 by the initial Swadesh "dropping out average rate constant", to the 0.03 used by other authors). But if S.A. Starostin, in his paper "Comparative-historical linguistics and lexicostatistics" (1989) went through a lot of options for the constant for retaining of the language, and was comparing results with considerations about the suitability of the options, and in which cases the constants should be changed and adapted to the real situations, M.T.Diyachok did not bother with such matters. He decided that "*in accordance with the methodology, of S.A. Starostin ... the factor of lexical preservation was taken to equal 91% per millennium.*" And that was it.

Apparently the subject here was not the "coefficient of lexicon preservation", but its double value for the intersection of two 100 word lists. The 91% preservation of lexicon in the 100 word list corresponds to the coefficient of the linguistic dynamics equal to 0.047 (in S.A. Starostin for a number of languages it was 0.05, and, by his remark, "it slightly varies from 0.04 to 0.06). For the intersection 100 word lists this constant should be doubled.

Be that as it may, it remains unclear on what grounds M.T. Diyachok stopped at the same constant for a totally different linguistic system, agglutinative instead of flexive. No such equality for the two constants was ever demonstrated. Moreover, there are assertions of the Turkologists that the Türkic languages are much more stable than the Indo-European languages. Examples:

(Zakiev M.Z.): "*In the agglutinative languages the roots of the words almost do not change over time, because in the process of application (i.e. grammatical changes) they do not lose their original phonetic form. The modern phonetic form of the words in the agglutinative languages (hence in the Türkic language) we also can find in the ancient written sources*" ("Genesis of the Türks and Tatars", Moscow, 2003. p. 79).

(Yu.N. Drozdov): "*The root part of the Türkic words phonetically remains permanent by definition (otherwise it would be either meaningless, or another word). The affix system is also phonetically conservative and has no exceptions to the rules for its use. And on the whole this means that the phonetics of the Türkic-lingual lexicon should not significantly change over time, unless it would be influenced by other languages. This*

phonetic stability of the Türkic-lingual lexical units is its unique distinction..." (pp. 11-12).

(T.A. Mollaev): "*Due to specifics of the grammatical structure, the Türkic languages are preserved marvelously, and remain mutually intelligible with each other*" (p. 50).

And what M.T. Diyachok has obtained? It can easily be predicted that if the Türkic languages and their lexemes are stable, and considerably more stable than the flexive languages, the stability of the Türkic 100-word lists or other comparison texts will inevitably be interpreted, on the basis of the same coefficients of the linguistic dynamics as for the flexive language, that the Türkic languages are young and diverged relatively recently.

Exactly that conclusion was made (see table below). Data from (M.T. Diyachok, 2001) [years are rounded to the nearest century].

Compared languages	**Number of words**			**% of total words**	**Divergence year (AD)**
	Total	**Different**	**Common**		
Turkish - Yakut	**91**	**23**	**68**	**74,7**	**100**
Turkish - Tatar	**93**	**12**	**82**	**87,2**	**800**
Turkish - Uzbek	**90**	**7**	**83**	**92,2**	**1000**
Turkish - Chuvash	**90**	**19**	**71**	**78,9**	**300**
Turkish - Salar	**92**	**14**	**78**	**84,8**	**600**
Turkish - Tuvinian	**92**	**22**	**70**	**76,1**	**200**
Sakha - Tuvinian	**92**	**22**	**70**	**76,1**	**200**
Turkish - Khakas	**94**	**16**	**78**	**83,0**	**500**
Tatar - Uzbek	**93**	**4**	**89**	**95,7**	**1300**
Tatar - Kazakh	**86**	**2**	**84**	**97,7**	**1500**
Turkish - Kyrgyz	**94**	**12**	**82**	**87,2**	**800**
Turkish - Turkmen	**92**	**8**	**84**	**91,3**	**1000**
Turkish-Azeri	**93**	**9**	**84**	**90,3**	**900**

The main conclusion made by M.T. Diyachok is the following: "*The results of the glottochronological analysis agree surprisingly well with the known history, and therefore can be regarded as reliable.*"

Another conclusion: "*The division of the Türkic languages into the four most ancient branches (Sakha, Tuva, Bulgar and Western) occurred almost simultaneously during the first three centuries of our era.*"

All of these conclusions that include a time component are resting on a shaky postulate about applicability of the linguistic dynamics constant, or the

"coefficient of preservation of language", or "loss of words rate factor" (per Starostin) established for flexive languages to the agglutinative languages. And not only on that constant, but also on a premise that for the agglutinative languages the square root equation is working in the same way at that for flexive languages, which also nobody demonstrated so far. It may be so, however, it should be examined and verified.

The catch is that if the loss of words from the 100-word list proceeds according to the first order kinetics, i.e. it depends only on its "internal" behavior, and is not subject to outside influence, the rate equation which relates the proportion of the remaining words and the constant of the linguistic dynamics will be as follows:

$[\ln (100 / N)] / k = n$

where:
N - number of words preserved in a 100-word glossary,
k - constant of the linguistic dynamics (loss of words rate factor),
n - number in thousands of years after which N words will remain in the 100 word list.

For example, with k = 0.05, a half of the words in 100 word list will survive after

$\ln 2/0.05 = 13.9$ thousand years.

A half the same (overlapping) words in two 100 word lists will still be the same after

$\ln 2/0.1 = 6.9$ thousand years.

But because in reality this does not occur with the Indo-European languages, and loss of words there is much faster, then without any quantitative reason, purely empirically, a square root was introduced into the above equation. This way the desired result is achieved, that is to get a faster rate for the loss of of the words, and to get a shorter period for the erosion of the language "core". For the Indo-European languages in this case it is

$$t = \sqrt{\frac{\ln(100/50)}{2x0.05}} = 2.6 \text{ thousand years}$$

or, which is the same thing,

$t = \sqrt{6.9} = 2.6$

which means that half of the words in the two 100 word lists remain unchanged after 2,600 years.

Naturally, this square root is just a fix for the desired result, and with a caveat that at the wish of the researcher the constant of the linguistic dynamics is also changing, any desired result can be obtained. Nevertheless, because in reality the Indo-European languages are fairly well known, examples are plentiful, in other words the linguistic field is fairly well studied, the glottochronology methods turned out to be useful for justification of, generally, what is already known. By the way, my professional field is chemical kinetics (the science of reaction rates), and I spent a fair amount of time of my life working with similar (and much more complex) equations (see, for example, I.V. Berezin and A.A. Klyosov, Practical course of chemical and enzymatic kinetics, Moscow University Press, Moscow, 1976, 320 pages; A.A. Klyosov, Enzymatic catalysis, Moscow University Press, Moscow, 1984, 214 pages; along with dozens of peer-review papers on chemical and biological kinetics).

The glottochronology of the Türkic languages, however, is an unexplored field, time constants are unknown, and it is unknown what to adjust to what. So, in reality we see an adjustment of glottochronology data to the main provisions of the contemporary views on the Türkic languages. The conclusion is that glottochronology supports those views. That is not the best approach in science.

The table above shows that in the Sakha and Turkish languages, of the 91 words 68 are common. If the empirical assumption about the square root in Turkic languages is wrong (and those languages are in fact more stable compared to IndoEuropean languages), and the constant of linguistic dynamics is not 0.05, as for the flexive languages, but say, only half as fast, then we obtain

[ln (91/68)] / 2x0.025 = 5, 800 years.

That is, then the Sakha and Türkish languages would have diverged 5,800 years ago. Since the carriers of the R1b began their journey from the Southern Siberia 16,000 years ago, and arrived to the Asia Minor 5,500 years ago, the calculated divergence time of 5,800 years ago is quite possible. It is not necessarily so, it is just an example showing how rickety is the stand of glottochronology when applied to an uncharted field of ancient Turkic languages.

There are publications on the relationship of the Türkic languages and Sioux of the American Indians, on the affinity of the Türkic languages and Mayan languages (see, for example,

http://www.varvar.ru/arhiv/texts/karimulin1.html), but the author of this work is not a linguist, and can not properly appreciate reliability of the cited study. If these results were confirmed, it would not superfluous to state that the Ural-Altaic peoples have a significant trace of the same haplogroup Q as the majority of the American Indians. The same haplogroup have the Maya, and the great majority of South American natives. Thus, if these findings were to be confirmed, they would have a solid foundation within the framework of the DNA-genealogy.

About the "Kurgan Culture" as an "Urheimat of the Indo-Europeans", the "Anatolian theory of the Urheimat of the Indo-Europeans", and how this could happen that were confused not only the "Urheimats", but the “ProtoTürks” (R1b) and the "Indo-Europeans" (R1a)

In the eyes of the author of this work, there were two main reasons for the confusion and the resulting incorrect postulates. The first and foremost is that at a time when these theories were developing, the science did not operate with the concepts of tribes in terms of DNA-genealogy, that is the presence of a marker in the DNA of its bearers. These markers cannot be “assimilated” as are assimilated and over time become blurred the cultural traits, languages, ethnic characteristics, even the anthropological, morphological features of the skeleton. The analysis of these markers, called SNPs, which determine the nature of their carrier and allow to trace the migration paths of each SNP-tribe separately, and with a calculation of the residence time for each tribe in the course of the migration, quickly demonstrated the both fallacy of the "Kurgan theory", and the partial, limited significance of the Anatolian theory.

I will not dissect the pros and cons of the Anatolian theory. That could continue indefinitely, which is exactly what observed in the literature for decades if not centuries, when one uncritical "argument" is advanced in opposition to another uncritical "argument", and so on. The analysis of the haplogroups (based on SNPs as collective characteristics of Y chromosome our ancestors and their descendants) and haplotypes (individual characteristics of Y chromosome of the ancestors who lived thousand years ago, and their presend-day descendants) has helped to establish several important factors.

First - the present day bearers of the haplogroup R1a are descendants of the very same "Proto-Indo-Europeans", some of them migrated to India and Iran about 3,500 years ago, in the middle of the 2nd millennium BC, it is they who under a name (or self-name "Aryans") brought to India their Aryan language, which after millennia received the titles of "Proto-Indo-European" and "Indo-European". It is their descendants who comprise 48% of the ethnic Russians (haplogroup R1a1) in Russia in general, and 62% in the southern regions of Russia, such as Orel,

Belgorod and adjacent territories, and up to 72% in the highest Hindu castes. The modern ethnic Russians with the haplogroup R1a1 have a common ancestor who lived on the Eastern European Plain about 4,800 years ago, and he belonged to the Aryan haplogroup, or the haplogroup of the future Aryans, that depends on the definitions, the essence is the same.

The tribe R1a1, with its Aryan language, moved to the Eastern European Plain, presumably from the Balkans, in the early 3rd millennium BC. The vector of the migration was to the east, although the path from the Carpathians to the southern Urals, and to Central Asia for the haplogroup took fifteen hundred years. It is clear that they were not nomads. It was a slow but steady settling across the Eastern European Plain and further South, East, and South-East. It was a spread of the Aryan language from the West to the Baltic to the Caucasus, and later to the South Caucasus, to Anatolia, to the Hittites and Mitanni. In those regions the Aryan, Proto-Indo-European language arrived, judging by the mutations in the haplotype, about 3,600 years ago. It remained in that region, and if moved, it was not to the East, but to the South toward the Arabian Peninsula. The fraction of the R1a1-M17 in Russia, Iran, Middle East and the Arabian Peninsula (according to Abu-Amero et al, 2009; Underhill et al, 2009), comprises the following figures:

Country	**Share of R1a1-M17, %**
Russia, South	**62**
Russia avarage	**48**
Iran	**10-14**
Oman	**9.0**
UAE	**7.4**
Iraq	**6.9**
Anatolia	**6.9**
Qatar	**6.9**
Saudi Arabia	**5.1**
Egypt	**3.0**
Lebanon	**2.5**
Jordan	**1.4**

Any noticeable moves to the north or east from the Asia Minor the Pra-Indo-European for R1a1 were not recorded. The South Caucasus, western Azerbaijan or western Iran, and the whole Asia Minor were just "dead-end" regions of the migrating "Proto-Indo-Europeans" 3,600-3,000 years ago. The Aryans came there once again, in the first millennium BC, already from the their area in Iran,

expanding the territory of their empires to the Caucasus and Assyria.However, it was already at the time of the ancient Iranian languages, with a transition to the Middle Iranian languages. Remember that the haplogroup R1a1 was found in the Andronovo archaeological culture, and the haplotypes were typical for the modern haplotypes of the ethnic Russians (Klyosov, 2009c, and references therein; Klyosov, 2009b, h).

With that, the "Anatolian theory" is over with, if dated by 4-3 thousand years ago. In reality, it could relate to the Nostratic languages in the same region, but that was 12-9 thousand years ago.

The linguistic and temporal space of the haplogroup R1b were different, but the territories were largely the same. This led archaeologists and linguists to a complete confusion, confounded the ProtoTürks for the "Indo-Europeans". As was already noted, at first the Proto-Türkic haplogroup R1b appeared in Southern Siberia about 16,000 years ago. After a long period of time the carriers of that haplogroup expanded, bringing along with their language, to the Middle Volga and Volga-Kama region, which now also abounds with the carriers of the haplogroup R1b, which constitute a substantial proportion of their ethnic groups (Lobov, 2009). Generally, the ethnic Russians (i.e., those who are speaking Russian for many generations and consider themselves to be Russians at least for three generations), 5% of whom have R1b1 haplogroup, have a common ancestor who lived 6,775 ± 830 years ago, much earlier than time of the "Proto-Indo-European" haplogroup arrival to the Eastern European Plain.

That was the time of the Middle Volga, Samara, Khvalyn archaeological cultures, and the ancient Pit Grave, or "Kurgan" culture. Neither the R1a1, nor the "Indo-Europeans" had any relations to them except sharing the same upstream haplogroup R1. Though the advance of the Kurgan Culture was to the west, or more accurately, to the west and south, they were not carrying along the Indo-European languages. They were carrying the Pra-Türkic or Türkic languages, the term is also a matter of definitions.

The aforementioned work of the USSR Academy of Sciences corresponding member S.E. Malov "Ancient and new Türkic languages" (1952), although states that "*the Türkic languages in the writings of the Türks are known to us from approximately 5th-6th cc. of our era*", discussed in that part only the written materials. Indeed, the writing among the Türkic peoples is held to be late. But the language is not just the writing, though for unwritten languages archeology is practically helpless. So far one can only rely on common sense - if a tribe, a population identified by its haplogroup, that is by its ineradicable marker in the Y-chromosome, existed for many thousands years, and at times 20 and 16 thousand years respectively, as in the cases of the considered here "Proto-Indo-European" and "Proto-Türkic" haplogroups R1a and R1b, there is no reason to

believe *a priori* that their languages appeared only with the advent of the writing. The same common sense dictates that the time bar of their languages can be lowered down for many thousands years, to the same 20 and 16 thousand years, unless shown otherwise. Nobody has shown any contradictory data as yet.

S.E. Malov also writes the same, speaking of rock inscription monuments in the basins of the Enisei and Talas: "*about the Türkic languages we can conclude that before that they had quite a long history, it is not only difficult, but also impossible to admit the contrary.*" And S.E. Malov continues: "*The languages, judging by these monuments, are a result of a very long development, and therefore it can undoubtedly be presumed that the Türkic languages, which we know now and which we could easily understand, i.e. the Türkic languages in their present known to us composition and in the present constitution existed several centuries before our era, say for five centuries! We are not allowed by our knowledge, or rather by our ignorance, to further penetrate into the depths of centuries, into the the history of the Türkic languages. Of course, further into the depths of centuries the Türkic languages existed, but with our present knowledge we would not understand them, we would not know any phonetical transitions, special phonetic laws, and their vocabulary in those times, especially for specific realities of the ancient Türks*."

That's why I continue to believe that a strong likelihood exists that the Basque languages are ancient ProtoTürkic Languages of the R1b haplogroup, brought over to the Pyrenees about 5 thousand years ago, after a long circuitous route from the Altai, through the Volga-Urals and the southern steppes, across the Caucasus, Anatolia, and the Middle East, through the North Africa and on to Iberia. And the fact that the Basque language for many linguists remains "unclassified" reflects the position of S.E. Malov "*with our present knowledge we would not understand them, we would not know any phonetical transitions, special phonetic laws, and their vocabulary in those times, especially for specific realities of the ancient Türks*."

If the scheme proposed in this paper is more of less correct, then the answer to the following question of S.E. Malov "*I have unanswered question: who is older, the Bulgars-Chuvashes in the west (Danube and Volga), or the Uigurs in the East, in the Central Asia, or they belong to the same time*" is certainly determined: the Uigurs in the east are much older.

Haplotypes of the R1b carriers in the Eurasia

Let us compare haplotypes of the present day Uigurs on the one hand, and Chuvashes, Bulgars, and Hungarians on the other, all of them belong to the haplogroup R1b. The present day Uigurs usually have more ancient subgroup

R1b1a1, which predominantly remains in Asia. An another subgroup is a more recent haplogroup R1b1a2-M269, which begins in the Caucasus or some North-Eastern Caucasus, and tails off via Middle East and/or Asia Minor to Europe. The European common ancestors of R1b1a2 lived, as was noted above, 6,000 years ago in the Caucasus, 5,500 years ago in Anatolia, 5,300 years ago in the Middle East, and 4,500-4,200 years ago in Europe. The European haplotypes of the R1b1a2 group are so young (in terms of the DNA genealogy) that many individuals still retain the ancestral haplotype of 4,000 years ago (shown here in the 25 marker format):

13 24 14 11 11 14 12 12 12 13 13 16 – 17 9 10 11 11 25 15 19 29 15 15 17 17

It is the most widespread branch of R1b1a2 in Europe, so-called P312 subclade. By many indications it was an ancestral haplotype of the Bell Beakers who arrived to Iberia some 4800 years ago, went almost to extinction, or, in terms of DNA genealogy, went through the population bottleneck, resurfaced about 4200-3600 ybp, and populated Europe between 4000 and 3000 ybp. Sometimes the above ancestral haplotype (or base haplotype, in terms of DNA genealogy, which means a "deduced ancestral haplotype") is called the "Atlantic modal haplotype", because it was first identified in the study of the British Isles haplotypes. Generally, the term "modal" is a slang, and it is often referred to a mix of haplotypes picked in a certain area or in a certain population. If often represents some "phantom", a heterogeneous population, such as the "Cohen Modal Haplotype". One might like to come up with a "Boston Modal Haplotype". On the contrary, the "base" haplotype is a deduced ancestral haplotype identified with all possible precautions of DNA henealogy.

For example, a series of 750 haplotypes of the R1b1a2 haplogroup in the Iberian peninsula (in the 19-marker format, showed in [Adams et al, 2008]) 16 haplotypes still retain the ancestral sequence, and are identical to each other in that series. Using the same method shown above for the glottochronology, we can calculate that the starting time for the divergence of these haplotypes, or in other words the time when it was a common ancestor of these haplotypes is

[ln (750/16)] / 0.0285 = 135 → 156 generations ago,

that is ~ 3,900 years to the common ancestor (Klyosov, 2009a). Here 0.0285 is the average rate of mutations per haplotype per generation of 25 years (the duration of the generation here is a mathematical parameter, not connected with the actual duration of the generation, which is a "floating parameter"), and 135 → 156 is a correction for reverse (back) mutations. Since the same series of 750 haplotypes has 2,796 mutations from the base haplotype, simple calculations provides 2796/750/0.0285 = 131 → 150 generations, that is 3,750 ± 380 years to the common ancestor. The closeness of the dates ontained by the logarithmic and the

“linear” methods shows that the kinetics of mutation accumulation in the dataset follows the first order kinetics, and the calculations are essentially correct, within a certain margin of error. Hence, the base haplotypes shown above is close (or identical) to the ancrestral haplotype of the population to the best of our knowledge.

Much more extended 67 marker haplotype dataset gives similar number of years to the common ancestor, which slightly vary depending on a dataset, albeit withing a margin of error. For example, 464 of 67 marker haplotypes result in 3950 ± 400 years, 337 haplotypes give 3525 ± 360 years, 273 haplotypes give 4200 ± 430 years, etc. On average, those dates group around 4000 years to a common ancestor. The Basques in the Northern part of the Pyrenees have essentially the same base haplotype and the same timespan to their common ancestor. In the North Africa, among the Berbers, that value is about the same, 3,875 ± 670 years to a common ancestor, and the ancestral haplotype is also the same.

But the Asia, among Uigurs, and many Uzbeks, Tajiks, Tuvans, and Kazakhs the base haplotype is quite different (two lineages, each one with its base haplotypes are shown below):

13 19 14 11 13 13 12 12 14 14 13 16 – 17 9 9 11 11 23 15 19 33 12 15 15 16

13 24 14 11 11 14 12 12 12 13 13 16 – 17 9 10 11 11 25 15 19 29 15 15 17 17

Compared with the "Atlantic modal haplotype" (aka R1b1a2-P312) it differs by 24 mutations (20.5 mutations, if calculate properly, considering palindrome and fractional mutations), and knowing that each mutation on average happen once in a thousand years on the considered here time scale (that is, considering the effect of back mutations on that time scale), it can be seen how far back in time a common ancestor of the Asian and European bearers of the haplogroup R1b slived. More detailed calculations with these extended haplotypes showed that the common ancestor of both Asian and European haplotypes lived in Asia 16,000 years ago (Klyosov, 2011, Proceedings of the Russian Academy of DNA Genealogy, vol. 4, No. 8, pp. 1666-1668). That apparently is the minimum lower (tentative) limit for the Proto-Türkic languages.

Before continuing this review further, note that the first digit (allele) in the base haplotypes, which is 13 both in the "Atlantic modal haplotype", and in the Asian base haplotype, is very stable, and it mutates on average once in many millennia, that is once in hundreds of generations. It turned out that in the southern steppes, or perhaps even in the Middle Volga archaeological culture of 8-7 thousand years ago, this allele became "12", and many descendants who reached the Caucasus and advanced into Anatolia and on to the Middle East, and in the

Balkans, had the same "12" in the first allele of their haplotype. For example, among only four people from the Middle East at the site
http://www.familytreedna.com/public/sharifs/default.aspx?section=yresults

three have "12" in the first marker. Similarly, out of 11 people from Arab countries, nine have "12" in the first marker
http://www.familytreedna.com/public/r-arabia/default.aspx?section=yresults

In other words, this marker allows to distinguish the reasonably close descendants of the "ancient Pit Gravers", the "Kurganians". During migration to Europe, and on its way from the North Africa through the Pyrenees, the "12" was replaced and inherited by "13", as is observed in the "Atlantic modal haplotype". Using it as a marker allows us to distinguish separate migration streams.

For example, out of 750 R1b1a2 haplotypes on the Iberian Peninsula (with the common ancestor 3,750 ± 380 years ago), only 41 were "12", which is about 5.5%. Among the R1b1a2 haplotypes of the Central Europe (Flanders) the allele 12 is found only in 3% of the population. On the contrary, among the older R1b1 haplotypes of the ethnic Russians, the direct descendants of the ancient "Kurganian" Pit Gravers (common ancestor lived 6,775 ± 830 years ago) the allele" 12 "is encountered in as many as 37% of the population. This allele is advancing to the Caucasus, and in the Caucasian haplotype R1b1a2 the allele "12" is in more than 50% of haplotypes which coalescent to the base haplotype

12 24 14 11 11 14 12 12 12 13 13 16 -- 16 9 10 11 11 25 15 19 30 14 15 16 18

As one can see, this first marker yields the single difference of the ancient Caucasian subclade R1b1a2-L23 from the European group among he first 12 markers

13 24 14 11 11 14 12 12 12 13 13 16 – 17 9 10 11 11 25 15 19 29 15 15 17 17

and displays a continuity from the ancient "Pit Grave" haplotypes and the European R1b1a2-P312 haplotypes. The first 25 markers amount 6 mutation total, which separates the common ancestors of the Caucasian and Central European R1b1a2 haplotypes by 3725 years, and places THEIR common ancestor at 6800 years before present. This is suspiciously close to a timespan to the direct descendants of the ancient "Kurganian" Pit Gravers (common ancestor lived 6,775 ± 830 years ago, which actually is a timespan to the base R1b1 haplotype of the Russian Plain).

In this context it is important to add that the R1b haplotypes in the Balkans have "12" in that first marker in 50% of the cases, in Italy 27% of the cases. In Slovenia that parameter is 20%, with the "age" of the common ancestor 4,250 ± 600 years.

All these are a branch of the ProtoTürks, "Kurganians", "ancient Pit Gravers" people, that crossed from the Eastern European Plain either directly from the Black Sea region to the Balkans, and further on to the the Apennines, or through the Asia Minor to Europe. The others, as was noted, went to Europe via Anatolia through the Middle East and then on through the North Africa on the way to the Pyrenees. That was the future Beaker Culture. The have nothing to do with "IndoEuropeans", which at the times were R1a1 people.

The following are typical haplotypes of the Hungarian Seklers (Szeklers), who belonged to a service military class, and were recoeded in a 1602 Sekler military census (Klyosov, 2009d). 18% of the Seklers have haplogroup R1b1, 15% have haplogroup R1a1. The largest is a European group I2, to which 20% of the Seklers (rather, their descendants) belong. The haplogroup N haplotypes take only 2% of the Seklers, another one initial "ProtoTürkic" haplogroup Q takes 4%.

The typical Seklers' R1b1 haplotypes are:

001	12	23	14	10	11	14	12	12	12	14	13	16
002	12	24	14	11	11	14	12	12	12	13	13	16
003	12	24	14	11	11	14	12	12	12	14	14	16
004	12	25	14	11	11	14	12	12	13	13	14	16
005	13	23	14	11	11	14	12	12	11	13	13	15
006	13	23	14	11	11	14	12	12	12	13	13	16
007	13	23	14	11	12	12	12	12	13	14	13	16
008	13	23	15	11	12	12	12	12	13	14	13	16
009	13	24	14	10	11	11	12	12	12	12	13	16
010	13	24	14	10	12	14	12	12	13	13	13	17
011	13	24	14	10	12	14	12	12	14	13	13	17
012	13	24	14	11	9	14	12	12	11	13	13	16
013	13	24	14	11	11	11	12	12	11	12	13	16
014	13	24	14	11	11	13	12	12	12	13	13	16
015	13	24	14	11	11	13	12	12	12	13	13	16
016	13	24	14	11	11	14	12	10	11	14	13	16
017	13	24	14	11	11	14	12	12	12	13	13	16
018	13	24	14	11	11	14	12	12	12	13	13	17
019	13	24	14	11	11	15	12	12	11	13	13	17
020	13	24	14	11	11	15	12	12	11	13	13	17
021	13	24	14	11	12	15	13	12	14	13	13	15
022	13	24	14	12	11	14	12	12	12	13	13	16
023	14	23	14	11	11	14	12	12	11	13	13	16
024	14	23	14	11	11	14	12	12	11	13	13	16
025	15	23	14	11	11	13	12	12	11	13	13	16

This dataset presents different genealogical lines (all those haplotypes belong to the descendants of the Seklers recorded in the 1602 military Census). Indeed, the first four haplotypes have allele 12 in the first marker (16% of the total, much higher than the typical European 3-5%), which corresponds to the "Kurgan Culture" ancient haplotype. Apparently, that is the starting point of the Hungarian Seklers ancestral migrations. None of those haplotype has the typical Asian "19" in the second marker, all alleles are typical European late (timewise) alleles. The apparent ancestral haplotype for these haplotypes is determined by the twelve most frequent alleles (vertical columns of numbers) in the whole sample. That is

13 24 14 11 11 14 12 12 12 13 13 16

i.e. exactly the "Atlantic modal haplotype" (aka R1b1a2-P312), as shown above. This is the haplotype number 017 in the list above, it is preserved unchanged from the apparent ancestral haplotype of the majority of haplotypes shown above. In other words, the dataset has a small admixture of those ancient "Kurgan", or "Caucasian" haplotypes, but they are overshadowed by more recent European haplotypes that "pull the blanket over". As a result, the Sekler haplotypes of the R1b1a2 haplogroup already represent a younger age of these ProtoTürkic carriers of the R1b, which is predictably the common ancestors who lived about 4,000 years ago. In general, the Sekler haplotypes are shifted a little toward more ancient times because of the admixture of the ancient haplotypes.

Let us take a more close look at the above dataset. The most stable markers in the (apparent) ancestral haplotype are the third, seventh and 11th in a column counting from the left, they produced only 1, 1, and 2 mutations respectively in all 25 haplotypes in the above dataset from the ancestral haplotype (number 017) Overall, the dataset of 25 haplotypes has 82 mutations from the apparent ancestral haplotype.

This gives 82/25/0.022 = 149 → 175 generations from a common ancestor, that is 4,375 ± 650 years. Indeed, within the error margin it is in the same 4000-4500 year timespan.

We can present here Bulgarian haplotypes of haplogroup R1b. There are not too many of them; unfortunately, Bulgarians are not very enthusiastic to test their haplotypes.The haplotypes are very short, however, for our purpose it will suffice.

001 13 24 14 11 13 13 16
002 13 24 14 11 13 13 16
003 13 24 14 11 12 13 16
004 13 23 14 10 13 13 16

005 12 24 14 11 13 12 16
006 14 24 14 11 13 13 16
007 12 25 14 11 13 13 16
008 12 23 14 10 14 14 15
009 12 25 14 11 14 13 16
010 13 22 15 11 13 13 16
011 13 23 15 10 13 13 16
012 12 24 15 11 13 13 16
013 13 25 15 11 13 13 16
014 13 24 15 11 13 13 17

Again, we see a rather extensive admixture of the ancient "12" allele in the first marker, it is five out of forteen, which is 38%, the same as in the Russian ancient haplotypes. There is a typical Asian "22" in the second marker (haplotype 010), the rest are typical European haplotypes. The ancestral, or, more precisely, "base" haplotype in this series is

13 24 14 11 X X X X X 13 13 16

where X is missing alleles in the standard 12 marker format. It is obvious that this is again the "Atlantic modal haplotype." The Asian haplotypes practically did not reach Europe.

Somewhat distorted (and again somewhat older, for reasons described above) timespan to a common ancestor can be obtained from the number of mutations in the dataset, calculated from the base haplotype. There are 29 mutations in all 14 haplotypes. This gives 29/14/0.013 = 159 → 188 generations, that is 4,700 ± 990 years before the common ancestor. Here 0.013 is the constant of the mutation rate for the 7-marker haplotype (Klyosov, 2009a), and the estimate of the error is given in (Adamov and Klyosov, 2009; Klyosov, 2009e, f). The base haplotype is a right one, but the date is partially "phantom", because of said admixtures. Hence, the large margin of error.

Let us consider several Gagauz haplotypes, more than 90% of whom speak Gagauz Türkic language

001 12 24 14 11 13 11 16
002 12 24 14 11 13 11 16
003 12 24 14 11 13 11 17
004 12 25 14 10 14 14 15
005 12 25 14 10 14 13 16
006 13 24 14 11 13 13 16
007 13 24 14 12 13 13 16
008 13 24 14 11 14 13 16

009 13 24 14 11 14 13 16
010 13 24 14 11 15 13 16
011 13 24 14 11 15 13 16

Here the ancient allele "12" takes almost half (45%) of the first markers, but the second allele is clearly not Asian, but European. Generally, it is again a mixture of descendants of the ancient and relatively recent ancestors, which gives a base haplotype slightly shifted away from the same "Atlantic modal haplotype". The third marker from the right is no longer predominantly 13, but also 14 and 15, which apparently reflects a more significant contribution of the ancient ancestor.

13 24 14 11 X X X X X 13/14 13 16

All 11 haplotypes have 26 mutations, which gives 26/11/0.013 = 182 → 222 mutations, which is 5,550 ± 1,120 years to a common ancestor.

The share of the haplogroup R1b1 among Gagauzes is 12% (Journal of the Russian Academy of DNA-Genealogy, Volume 2, No 1, p. 152). Thus, we have found that in Europe, including Hungary and Bulgaria, most of R1b1a2 haplotypes are those of the "new era", with common ancestors of the R1b1a2 populations who lived 4-5 thousand years ago. Among the ethnic Russians, the common ancestors are somewhat older, close to 7,000 years ago (6,775 ± 830 ybp), with base haplotypes which fit this time difference. These are of the same ancient Pit Grave, or "Kurgan Culture", and their predecessors, the ProtoTürkic-lingual bearers of those haplotypes.

The Türkic-speaking bearers of Asian R1b haplotypes and their descendants largely remained in Asia, the rest had moved to the Caucasus, the Middle East, ancient Europe. 5,700-5,100 years ago in the North Kazakhstan they established the Botai archeological culture, and according to the latest data, about 5,500 years ago horse was domesticated there (*Archaeology*, Jan-Feb 2010). In addition to the Botai settlement dated 3,700-3,100 BC (it certainly was the haplogroup R1b, since the carriers of the R1a1 appeared in those regions only 1500-2000 years later).

A summer camp dated 1,200-900 BC, i.e. 3,200-2,900 years ago, was found there. However, these were much more recent times, and the camp might have been established by the Andronovans, “Indo-European” R1a1, after a departure of a part of their tribe to India. They could also be the Türkic-speaking R1b1. The archaeologists, naturally, did not get into such distinctions. They simply noted that the camp belonged to the Bronze Age.

There is some data on the share of the R1b1 haplogroup among Bashkirs, which varies from population to population ranging from 7% to 84% (Lobov, 2009, p. 15). Among the Perm and Baimak Bashkirs this proportion is 84% and 81%

respectively. Among the Burzyan, Western Orenburg and Saratov-Samara Bashkirs it is 33, 23, and 18% respectively. Among the Eastern Orenburg and Abzelil Bashkirs it is 9% and 7% respectively. Among the Sterlibash Bashkirs in the East Urals the haplogroup R1b1 is absent. Perhaps linguists can compare this statistics with the presence of the Türkic languages in these regions, although the link may be very indirect, taking into account a great extent of multi-ethnicity among Bashkirs.

According to the data (Wiik, 2008) the following populations have the haplogroup R1b1 at these quantities (average):

Nation	**Proportion R1b1, %**
Bashkirs	**19**
Khanty	**10**
Komi	**16**
Mordovians	**13**
Chuvashes	**12**
Udmurts	**9**
Tatars	**6-9**
Mari	**5**
Russians	**5**

For comparison, the content of the haplogroup R1b1 in other countries is:

Country	**Share R1b1, %**
Hungary	**13-20**
Turkey	**6-10** **14-16** **(other data)**
Lebanon, Syria	**6-15**
Georgia (Gruzia)	**10-14**
Iraq	**11**

In Central Asia, the share of the haplogroup R1b in the populations is:

Nation	**Share R1b1, %**
Turkmens	**37**
Uzbeks	**10**
Uigurs	**8-19**
Kazakhs	**6**

As it can be seen, this "Türkic" haplogroup have been substantially displaced from the population with respect not only to the language, but also to the presence of the haplogroup. Perhaps they were interrelated processes. Generally, the S.E. Malov words "*The Eastern Türkic languages ... present a more ancient picture, older then the Western Türkic languages*" (1952) more than 50 years later still remain valid, although he added that "*initially, so to speak, they are not any less ancient than their eastern brethren languages, but many new elements now prevail in the western Türkic languages that replaced the ancient elements*" (ibid.). This is certainly true, but in antiquity the western languages are certainly younger compared to the eastern languages.

A NOTE added by the Turkic site:

(Within the context of this work, the accepted division of the Türkic languages into the Western Ogur and Eastern Oguz is not applicable; within the context of this work, both Ogur and Oguz are Eastern languages, with the Ogur being a Middle and Central Asian branch of the paternal Oguz language; within the context of this work, the Western Türkic language is the language(s) of the Western Timber Gravers, which upon joining with the Eastern Oguz language in the 7th c. BC produced the Ogur variety; and the language(s) of the Western Timber Grave R1b predecessors, starting with the R1a/R1b split 40 KYBP. The subject of prevalence and temporal pedigree is non-existent, in the Western and central Europe the (Western) Türkic languages were ubiquitously supplanted by the Indo-European languages, in the Eastern Europe they were supplanted first by the Oguz languages, then by a millennium-long predominance of the Ogur languages, and then again by the Oguz languages).

So, as follows inevitably from the above, the bearers of the haplogroup R1a1, or the Aryans, or the "Proto-Indo-Europeans", were moving eastward from Europe, most probably from the Balkans, from the beginning of the 3rd millennium BC, populating the European Plain (the age of the common ancestor of the [future] Aryans in the Eastern European Plain is about 4,750 years), and further on, establishing the Andronovo Culture 4,000-3,200 years ago, which overlaid the previous habitat of the haplogroup R1b1 that preceded R1a1 by 1500-2000 years (Botai archaeological culture 5,700-5,100 years ago) and R1a1 subsequently settled in the Southern and Eastern Urals, southern Siberia and Altai, reaching the northern China.

The haplogroup R1b migrated on an opposite course, but much earlier. It had arrived to the Eastern European Plain at least 8-6 thousand years ago, partially populating the Caucasus 6,000 years ago, and at the same time crossing into Anatolia and then the Middle East. Timewise, they practically did not intersect with the "Proto-Indo-Europeans", the carriers of the haplogroup R1a1, but transversed the same territories, especially territories of the ancient Middle Volga, Samara, Khvalyn, the ancient Pit Grave, Timber Grave, and Andronov

Cultures, the last one will develop as the R1a1 culture thousands year later. This led to misunderstandings of archaeologists and linguists about localization of the Indo-European homeland "in the southern steppes of Russia and as much in the Northern Pontic and Anatolia".

Theories of "Indo-European Urheimat" in light of DNA-Genealogy

Amazingly, all four main hypotheses localizing the "Indo-European homeland", namely "Circumpontic localization", "Kurgan", "Anatolian", and "Neolithic discontinuity" turned out to be wrong at their core. They could not explain the direction of "Indo-Europeans", including the path towards the India; they could not explain the timing of their movements and what preceded that movement; they were unable to point the location of the "pra-homeland" and from where the "Pra-Indo-Europeans" appeared there, especially since (the fallacious) very notion of "primordial homeland" does not point at the previous localizations, which is fundamentally wrong; they could not explain the prolonged contact of the "Proto-Indo-Europeans" with other language families (Kartvelian, North Caucasus, Semitic, Pra-Türkic), which clearly occurred in the 3rd and 2nd millennia, when the carriers of the haplogroup R1a1 reached the Caucasus about 4,500 years ago, then they reached the Near East around 3,800-3,600 years ago, and reached the territories of the ancient Pit Grave Culture, Andronovo Culture, and Central Asia, with their probable Türkic-lingual population (haplogroup R1b1) approximately 4,000-3,600 years ago.

1. The "Circumpontic localization" hypothesis (Merpert, 1974, 1976) erroneously places the "IndoEuropean homeland" in the Caspian-Black Sea steppes, and also erroneously times it by more than 5,000 years ago (second half of the 4th millennium BC). Apparently, here again the Türkic-lingual carriers of the R1b1 were mistaken for the "Indo-Europeans" (R1a1), who at that time were completing the movement across the Caucasus to Anatolia, and were already present in the Middle East where they arrived not later than 5500 ybp. Not accidentally, this hypothesis mentions the "*pastoral cultures of the Caspian-Black Sea steppes*".

In connection with that, the author of the hypothesis rightly talks about "continuity and cultural integration", from the zone of the ancient Pit Grave Culture to the Caucasus region and further to the south of the Black Sea, only that culture belonged to the Türkic-lingual R1b1. The Balkan-Carpathian region, where the Proto-Indo-Europeans (R1a1) came from, is not even considered in that hypothesis. The hypothesis does not also consider the spread of the "Proto-Indo-Europeans" (haplogroup R1a1) in all directions in Europe, from the Balkans to the Atlantic, to the Scandinavia, to the south to Greece and the

Mediterranean islands, all that mainly in the 4th millennium BC and earlier. That was the spread of the carriers of the Proto-Indo-European (R1a1) dialects.

2. "Kurgan theory» (Gimbutas, 1964, 1974, 1977, 1980, 1984) interpreted the materials about the "Indo-Europeans" totally opposite in comparison with the real movement of the "Indo-Europeans" (R1a1), which took place millennia later, and it in fact analyzed the most likely scenario of the southwestward move by the ProtoTürkic-lingual tribes (haplogroup R1b1). The concept of the Eurasian steppes as a homeland of the "Indo-European community" (R1a1) is totally counterproductive and incorrect. First, the "Proto-Indo-Europeans", whoever they could have been, could not appear in the steppes from a nowhere, and create there a "homeland language" out of the blue.

In fact, they have not appeared out of nowhere. The ProtoTürkic-lingual R1b1 migrated from the east, while the Aryan-speaking "Proto-Indo-Europeans" R1a1 migrated from the west. In the deep ancient, pre-glacial times, they both came from the Southern Siberia, or more generally, from Central Asia. The route of their arrival to the South Siberia is also adequately described in terms of the DNA genealogy. This does not mean at all that the actual material collected by M. Gimbutas is incorrect. On the opposite, it is precisely true (as can be true any archaeological material and data), such as the findings on the increase in the share of the animal husbandry relative to the agriculture in the region of the ancient Pit Grave culture, and the further movement of the "Kurganians", and the facts and conclusions about the type of the housing and settlements, about the physical appearance of the population, and the terminology related to the horse, but all that belongs to the ProtoTürkic-lingual R1b, and not to the "Pra-Indo-Europeans", about which M. Gimbutas apparently even did not suspect as the carriers of R1a1. The same applies to the physical appearance of the population, because both the R1a "Proto-Indo-Europeans", and the R1b "Pra-Türks» not only both are Caucasoids, but altogether belong both to the same upstream tribe R1. It is easy to confuse one of them for another, and that's what happened in the M. Gimbutas "Kurgan Theory".

Here is a core of the M. Gimbutas "Kurgan theory" (Gimbutas, 1994), in the quotation: "*The Proto- or Early Indo-Europeans , whom I have labeled "Kurgan" people, arrived from the east, from southern Russia, on horseback. Their first contact with the borderland territories of Old Europe in the Lower Dnieper region and west of the Black Sea began around the middle of the 5th millennium BC. A continuous flow of influences and people into east-central Europe was initiated which lasted for two millennia*".

The middle of the 5th millennium BC was about 6500 years ago. Those "Kurgan" people were certainly the ProtoTürkic-lingual R1b1, since the carriers of the haplogroup R1a1 did not exist there at that time, they appeared there some 1700

years later, and yet it took several hundred years more for them to reach the Volga region. M. Gimbutas had confused the ProtoTurkic R1b1 people, who indeed were moving west (and south) those times, and the IndoEuropean R1a1 people, who were moving east (and south, and southeast) from 4800 onward.

One more quotation: "*The material of the Volga-Ural interfluve and beyond the Caspian Sea prior to the 7th millennium BC are, so far, not sufficient for ethnographic interpretaion. More substantive evidence emerges obly around 5000 BC. We can begin to speak of "Kurgan people" when they conquered the steppe region north of the Black Sea around 4500 BC*" . Yes, it was not sufficient several decades ago, when M. Gimbutas was working on her concept, which appeared to be grossly distorted with respect to both the proto-IndoEuropeans (who turned out to be proto-Turks of the R1b1 tribe) and timing of their arrival fron the west more than 2000 years after "around 5000 BC).

M. Gimbutas had classified the "Kurgan people" as Kurgan I, Kurgan II and Kurgan III. "*Kugran I people were from the Volga steppe… 4400-4300 BC*", "*Kurgan II … developed in the North Pontic area … at c. 3500 BC*", "*Kurgan III people were again from the Volga steppe… soon after 3000 BC*". We see again that they could not have been the Indo-European R1a1 people who, again, came <u>from</u> Europe eastward and brought their IE language eventually to Anatolia and Mittanni, India and Iran all around 1600-1500 BC. M. Gimbutas wrote in fact about the proto-Turkic R1b1, who moved to Europe from the east, indeed, "*soon after 3000 BC*".

What M. Gimbutas had described, the "*carriers of the first wave of the Kurgan Culture*" developed from the Samara and Seroglazov periods of the Volga Basin. These were definitely the ProtoTürkic-lingual R1b1. To the "Proto-Indo-Europeans" (R1a1) they had no relation neither in time, nor place, nor origin, except they both belonged to the same upstream tribe R1 about 10 thousand years earlier. A recent paper (Vybornov, 2008) showed that radiocarbon dating of the Volga-Kama Neolithic pottery allows to date the encampments of the northern Caspian Sea area by the first half of the 6th millennium BC, that is about 8,000 years ago. The "Proto-Indo-Europeans" (R1a1) would appear there only 4,000 years later. The author (ibid.) notes that at the same time a Neolithic culture is being formed in the south of the Volga-Ural interfluve, which is where M. Gimbutas had placed the "homeland of the Indo-Europeans". A few centuries later (second half of 6th millennium BC) settlements in the Lower Volga region (ibid.) had appeared. Now we can definitely stipulate that all that was the areal of the ProtoTürkic languages.

Finally, as is known now, the domestication of horses came about in north of the Kazakhstan, in all certainty again by the carriers of the R1b1 about 5,500 years ago, long before the arrival of the R1a1 "Proto-Indo-Europeans" (*Archaeology*, Jan-Feb 2010), and the use of the horses in the household economy by the

"Kurganians" is an important stipulation of M. Gimbutas. That is again an argument in favor of the ProtoTürkic-lingual "Kurganians" who were expanding from east to west, and not vice versa, as did the "Proto-Indo-Europeans" R1a1. That applies without even allusion to the fact that the “Proto-Indo-European” argument of a "mountain landscape" does not work at all in relation to the Dnieper-Volga region, although that did not bother M. Gimbutas a least.

It is clear that the anticipation of some contact continuity and cultural integration associated with the migration of the Proto-Indo-Europeans from the Balkans to the Eastern European Plain and beyond to the Caucasus, Middle Asia, and the Urals, and on to the India and Iran are amply satisfied with respect to the migration of the haplogroup R1a1. It remains unclear why to apply this “contact continuity and cultural integration” only to the "Kurgan Culture". Naturally, this provision (“contact continuity and cultural integration”) worked for all of them, R1a1, R1b1 and many other tribes and haplogroups. This “criterion” is so fuzzy and has almost a universal application, that is it uncear why to use it in the first place (except maybe some special situations of “discontinuity” and “disintegration”).

These postulates and inconsistencies can be analyzed further, but the situation is rather clear. All arguments that support the alleged migration of the "Indo-Europeans" from their "homeland" in the Circumpontic zone, as well as in the Volga-Ural region, or between the Volga and Dnieper, are either erroneous, or do not have specific arguments, and as easily fit the Balkans.

3. The same also applies to the "Anatolian" theory of the "Indo-European homeland" (Gamkrelidze and Ivanov, 1980, 1984, 1989). The linguistic evidence for the landscape, flora and fauna of the "Indo-European homeland" which they analyzed, are perfectly suitable for the Balkans, aside from the fact that they are far from absolute. As is already known, applied formally and indiscriminately, they cause problems with these "arguments" in any territory. However, the Anatolian” theory is fairly applicable to the Proto-IE language some 9-11,000 years ago, however, not to its “homeland”, but to the passing region of the r1a1 migration from the East to the West.

The subject should be not an absolute and unquestionable use of these and similar "arguments", but the optimization of the results of linguistics, archaeology and DNA genealogy. And there, I repeat, the Balkans are optimally suited as an important site for the spread of IE languages around 9-6 thousand years ago. To this we should add the distribution regions and the dating of the "Proto-Indo-European" haplogroup R1a1, considering their migrations to India and Iran (~ 3500 ybp) as a major argument regarding those times, and practically the alikeness of the R1a1 haplotypes in these countries and in the present day Russia, where their proportion in the population reaches 62%. Hence, the “IE

problem" can be held as largely resolved. On the contrary, the territory of the Asia Minor (Anatolia) is categorically not suitable for the epicenter role for the spread from there of the "Proto-Indo-Europeans" around 3600 ybp, and moreover for the spread out to the north, as "developed" by the followers of the "Anatolian" hypothesis. This is incompatible with the DNA genealogy data, according to which the movement was ~ 4500 ybp from the Eastern European Plain and to the south and to the east, to India and Iran.

A summary: if the "Anatolian" theory is applied to "ProtoIndoEuropeans" 11-9 thousand years before present, then it were times indeed for the westward migration of R1a1 from the East across Anatolia and the rest of Asia Minor to Europe. In this case it was not "a homeland" of Proto IndoEuropeans, but their passing point on their migration route.

Again, the time at which T. Gamkrelidze and V. Ivanov, and after them V. Safronov and C. Renfrew placed "Indo-Europeans" in the eastern Anatolia, Southern Caucasus and northern Mesopotamia (Safronov, 1989; Renfrew, 1987; Renfrew, 1998), namely the 5th-4th millennium BC, i.e. about 6,000 years ago, is also incompatible with the arrival there of the R1a1 haplogroup carriers only in the first half of the 2nd millennium BC, that is, two or three thousands years later. Interestingly, to prove the Anatolian hypothesis, extensive materials on the paleogeography, archaeology (in particular, on the development continuity of the local Anatolian cultures), paleozoology, paleobotany, linguistics, were attracted, and in particular the data on borrowing from individual Indo-European languages into the non-Indo-European languages and reverse using comparative historical method, but all these arguments at a closer look work wonderfully in respect to the Balkan homeland.

They also work in regard to the migration of the R1a1 carriers with their "Pra-Indo-European" language, or rather the Aryan language, in the 3rd and 2nd millenniums BC from the Balkans through the Eastern European Plain to the Caucasus and Eastern Anatolia, and in reality adequately explain the linguistic contacts of the R1a1 carriers in these regions.

There is a systemic problem with these linguistic "arguments", because they could very well be simply decoded erroneously, when the authors take the approximate and ambiguous interpretations for the "facts" and then absolutize them. Utterly logical is the observation of O.S. Rubin ("Problems of localization of the Indo-European homeland: a critical review of the modern concepts") that "*the questionable conclusions of Gamkrelidze-Ivanov relating to the chronological framework of the existence and disintegration of the dialect groups raise doubts.*" In fact, this remark is only partial, because not only the chronology of the "IndoEuropean homeland" was incorrect, but also the essence of the hypothesis of the "Indo-European pra-homeland" as being in Asia Minor (see above). The

linguistic constructs of T. Gamkrelidze and V. Ivanov relating to the "Proto-Indo-Europeans" arriving in the Asia Minor in the 2nd millennium BC, on the other hand, do not raise principal doubts. For example, it is quite possible that the first linguistic community which had appeared as the Aryan ("Proto-Indo-European") community was really the Anatolian community in the 2nd millennium BC. Although at the same time the Indo-Iranian branch and the Greek-Armenian-Aryan branch also began appearing, and also that what in the future would become Balto-Slavic branch.

Lately some anthropological evidences have appeared that craniological indicators in the Mediterranean and Asia Minor populations are not compatible with the "Indo-European" indicators in the Middle Asia and South Siberia (Kozintsev, 2008). So the theory of T. Gamkrelidze and V. Ivanov, and also of V.Safronov (1989) and C.Renfrew (1987) failed a test against the new data. More specifically, the cited work of Kozintsev described 245 cranial series of Eurasia from the Neolithic Age to the Early Iron Age, and it has shown that there is no reason to believe that any ancient group from the territory of the Southern Siberia and Kazakhstan are South Caucasoid (Mediterranean), as there is no any reason to attribute migrations to these territories (Siveria and Kazakhstan) from the Middle Asia and Asia Minor, or from the So. Caucasus, at least according to the physical anthropology. The most likely migration source for the Southern Siberia and Kazakhstan, including the Afanasyev and Andronovo cultures, is the population of the Bronze Age N. Pontic steppes, and several Late Neolith and Bronze Age groups from the Western and Central Europe around 4500-4000 ybp, which again the most likely are the "IndoEuropean" R1a1.

A. Kozintsev continues that this similarity can be attributed to the migration of the Indo-Europeans "*from Europe to the east, up to the Central Asia*". He reasonably believes that the "*return of the descendants of one of their groups from the Central Asia to Europe during the Early Iron Age was apparently the cause of the appearance on the historical scene of the Scythians*"(in Europe). About the Scythians, and their relation to the "Indo-Europeans" (I will not apply the word "Iranian" as totally compromised in this context) and the "ProtoTürks" will be addressed below.

4. Regarding the hypotheses of V.A. Safronov and C. Renfrew ("Neolithic Discontinuity Theory"), they are not fundamentally different from those of T. Gamkredidze and V. Ivanov with respect to the "localization of the Indo-European homeland" in both regional and temporal aspects, i.e. they are not correct (references are given above). In the cultural region of the Çatalhöyük 8,000 years ago (6th millennium BC) the "Proto-Indo-Europeans" (R1a1) could have been as late settlers of the R1a1 migration which went westward there 1000-3000 years before that. But it cannot be considered as the "homeland", much like the Amundsen expedition to the North Pole in 1911 did not mean a settling by

the Norwegians of the North Pole, as well as an acceptance of the North Pole as a "homeland" of the Norwegians.

In this connection it is of interest to consider the work of Gray and Atkinson (Gray and Atkinson, 2003). The authors have done a good job, collected a wealth of material, and found that the beginning of the Indo-European languages divergence falls on 7,800-9,800 BC, that is 9,800-11,800 years ago. This, as we now know, coincides with the migration time of the future "Indo-Europeans", the carriers of the haplogroup R1a1, via Anatolia. Gray and Atkinson also concluded that it was Anatolia. On what ground? Because, according to the "Anatolian Theory", the Indo-European language originated there 8,000-9,500 years ago.

Why "originated"? It was just a passing point on the route of R1a1 migration. However, the authors even carried it into the title of the article "*... supports the Anatolian theory of Indo-European language*". What alternatives have been considered in their paper? Why not, for example, the Balkans? None, except mentioning that the "Kurgan Culture" is not suitable, "*because it is dated by the sixth millennium ago.*" The Balkans in their paper are not even mentioned. As we now know, the "Kurgan Culture" had totally no relation to the "Indo-Europeans". The authors, Gray and Atkinson, absolutize the conditional (and far from precise) dating, do not consider alternatives, and there and then absolutize their own, quite questionable conclusions, if to relate them to the "homeland" in Anatolia. There is another, uncritical comment in their paper - "*the formation of the Indo-Iranian family is intriguingly close in time to the possible expansion of the Kurgan Culture*".

In fact, the "formation of the Indo-Iranian family" has nothing to do with "the Kurgan Culture", since the first is R1a1, the second is R1b1, and, as it was repeatedly described above, their migrations were quite different in time and directions. In other words, everything in that phrase is wrong, neither the link of the Indo-Iranian linguistic family with the "Kurgan culture", nor the "intriguingly close" time, which actually differ as much as do the years 6,000 and 3,500 years ago.

The difficulties of matching archaeological evidence and DNA genealogy may also be explained because these disciplines operate with different attributes. In archeology it is a "chain transmission" of the material and cultural traits, which archaeologists often (or even usually) do not associate with migrations, with the movement of people. As noted by Anthony (Anthony, 2007), every archeology student from the 1960s study knows a motto "Pots are not people", and from 1970s-1980s the concept of migration in general, according to Anthony, practically disappeared from the archaeology. In contrast, in the DNA-genealogy the main focus is on migration, their directions, their regions, and their times. Therefore from the standpoint of some Russian archaeologists, the "Eurasian

Indo-European continuum" looks like Catacomb-Timber Grave-Petrov-Andronovo-Sintashta "chain transmission of the cultural traits", together with the language, and not migrations at all. Meanwhile, the same archaeologists note that in the anthropological relation, this chain is practically homogeneous.

However, from the standpoint of DNA genealogy this approach is fundamentally defective (though valid in the paradigm of archaeology). In that particular case the archaeologists have mixed up, have transposed two counterflows of migration of two haplogroups, a ProtoTürkic-lingual R1b tribe from east to west, and an Aryan-speaking, "Proto-Indo-European» R1a tribe from west to east. The anthropology of these two streams is in fact close or almost identical, because they are two kindred haplogroups, both Caucasoids, both formed from the same R1 upstream tribe-haplogroup. And then archeologists suddenly jump from the cultures of one tribe, the ProtoTürkic-lingual R1b from the Khvalyn, Sredny Stog, and ancient Pit Grave and then the Catacomb Cultures, with a general direction to the west, over to the "Proto-Indo-European" Andronov and Sintashta Cultures, formed by the movement of the Aryans (haplogroup R1a1) to the east.

In other words, not some "chain transmission of cultural traits" without migrations had occurred there, but specifically the migrations. That is evidenced by the detection of the haplogroup R1a1 in excavations in Germany dated by 4,600 years ago, and of the same haplogroup R1a1 in excavations in the Andronov culture in the Southern Siberia dated by 3,800 - 3,400 years ago, and the same haplogroup R1a1 (and the same haplotypes) to the west of the Urals, in the Eastern European Plain, dated by 4,800 years ago, and the same haplogroups (and the same haplotypes) in India and Iran, only 800-1,000 years later compared to that at the East European Plain. These were precisely the migrations, rather than simply unembodied "transmission of cultural traits". Admittedly, this is a weak spot of the contemporary archaeology.

DNA genealogy helps to solve, or at least suggest solutions for many questions that archeology and linguistics have not been able to solve. For example, questions of the "*ethnogenesis of the ancient Celts, the time of whose appearance in the Western Europe, like their paths of settlement, the most "traditional" theory can not explain*" (Rubin, "Localization problems of the Indo-European homeland: a critical review of the modern concepts, pp. 84-92), despite the fact that "*migration of Celtic tribes is only recorded in the direction from west to east, not vice versa*" (Alinei, 2004a, b). The DNA genealogy gives an immediate comment and response. First, the Celts are poorly defined from the viewpoint of their origin. Some ancient (the middle of the 1st millennium BC) Celts can be R1b1a2, some can be R1a1. It was already shown that some “Celts” have arrived to the Alps from the Russian steppes, and were the most likely R1a1, with their IndoEuropean language. Some Pra-Celts, of the haplogroup R1b1a2, arrived on the European continent in a

roundabout migrational path, from the Eastern European Plain across the Caucasus, Middle East and North Africa, on to the Iberian Peninsula (4800 ybp), and further into the continental Europe, around 4,000 years ago (see above). Naturally, the movement from the Pyrenees (and from the British Isles, the next phase of R1b1a2 advancement from the Pyrenees) to Europe went from the west to the east. Those Celts were carrying ProtoTürkic languages across the Europe.

In conclusion, a brief pause on the Scythian issue. From the above, it is clear that the Scythian people - in fact, a collective term, were both ProtoTürkic-lingual, and "Iranian-lingual", or more accurately, Aryan-lingual. They were both nomadic pastoralists (which is typical for the Türkic tribes), and farmers (which is often typical for the Aryans). They had both haplogroup R1a1 and R1b1, and maybe Q as well. They lived in felt yurts (many of those who lived in them, were carriers of R1b1 and Q), and also in stationary buildings (many of those were farmers, R1a1). Unfortunately, neither the specialists in Indo-European languages, nor the Turkists are willing to recognize the duality (at least) of the Scythians, Sarmatians, and many other steppe (and not only steppe) tribes of the 1st millennium BC and the beginning of the Common Era. Moreover, these tribes definitely had other haplogroups, such as G, N, C. The carriers of the haplogroup G in the Scythian and Sarmatian times likely were "Iranian-speaking", and lived in the Iranian Plateau much earlier then the Aryan times. Then, of course, they were not "Indo-Europeans". The carriers of the Q, N, and C were most likely Türkic-lingual.

The sooner both sides, the "Iranists" and "Turkists" recognize these facts, or at this point rather considerations, the sooner linguistics would be enriched by new findings and discoveries. Especially, if in addition they would adopt in their research arsenal the DNA genealogy. I dare to hope that this article would facilitate that.

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Современное состояние субкладов и ветвей гаплогруппы R1a1a1

(Краткая справка-комментарий)

И.Л. Рожанский и А.А. Клёсов

В диаграмме ниже мы попытались объединить сведения из трех различных источников информации – дерево гаплогруппы R1a1 (с вышестоящими и нисходящими субкладами,
http://www.isogg.org/tree/ISOGG_HapgrpR.html),
дополнительные сведения о новых снипах (SNP), постоянно поступающие от специалистов в филогении (хотя немалое число новых снипов дезавуируется как ошибочные или частные, обнаруженные у отдельных людей и не находимые у других). Это понятно – любой из нас мог получить снип в Y-хромосоме от своего дедушки или любого другого ближнего прямого предка по мужской линии, и этот снип не найти у других, или он может появиться у других тоже совершенно случайно и не быть «родообразующим» сотни или тысячи лет назад. Третий источник – данные ДНК-генеалогии, согласно которым уже идентифицировано более 20 ветвей в гаплогруппе R1a1, каждая из ветвей имеет свой базовый гаплотип и его датировку (время, отделяющее нас от общего предка ветви).

Большинство ветвей пока не имеет свой специфический снип, хотя он просто обязан быть. Выявление снипов для каждой ветви только дело времени, но число ветвей будет тоже расти, ветви будут дробиться вплоть до отдельных кланов и семей. По некоторым соображениям, снипы в Y хромосоме образуются с частотой один снип на поколение. Ясно, что далеко не все снипы окажутся «ветвеобразующими», но у каждой мужской линии (в понятиях генеалогии) определенно есть свои снипы.

Результат попытки объединения этой информации на сегодняшний день (конец сентября 2011 года) приведен ниже. Обновления этой диаграммы будут регулярно публиковаться в «Вестнике».

В трех случаях ветви идентифицированы характерными аллелями, как в случае «десятников» (DYS388 = 10) северо-западной Европы, башкирской ветви, тоже «десятников» (DYS425=10), и «старой европейской ветви» (DYS392=13). Все три маркера – очень «медленные», и мутации в них происходят в среднем раз в 4,500, 20,000 и 1,900 поколений, соответственно. Вряд ли стоит это переводить как один раз в 112,500 лет, 500,000 лет и 47,500

лет, соответственно, хотя технически это верно. Лучше рассматривать это как одно рождение мальчика с такой мутаций на 4,500, 20,000 и 1,900 рождений. Это – потенциальные ветвеобразующие мутации.

R M207/Page37/UTY2, P224, P227, P229, P232, P280, P285, S4, S9, V45
- **R1** M173/P241/Page29, M306/S1, P225, P231, P233, P234, P236, P238, P242, P245, P286, P294
  - **R1a** L62/M513, L63/M511, L145/M449, L146/M420
    - **R1a1** L120/M516, L122/M448, M459, Page65.2/SRY1532.2/SRY10831.2
      - **R1a1a** L168**,** L449, L457, M17, M198, M512, M514, M515
        - **R1a1a* 392=13** **[Old European branch]**
        - **R1a1a1** M417, L566, Page7, **Z85?**
          - **R1a1a1a** M56
          - **R1a1a1b** M157.1
          - **R1a1a1c** M64.2/Page44.2, M87, M204
          - **R1a1a1d** P98
          - **R1a1a1e** PK5
          - **R1a1a1f** M434
        - **R1a 388=10** **SNP? [North Western branch; the Tenths]**
          - **R1a 388=10** **L664 [North Western-1 branch]**
        - **R1a1a1-Eurasian** **Z280? Position uncertain**
          - **R1a1a1g** M458
            - **R1a1a1g1** M334 Private SNP
            - **R1a1a1g2** L260 **[Western Slavic branch]**
            - **R1a1a1gX** **SNP? [Central European branch]**
          - **R1a1a1-Scandinavian** **SNP? [Old Scandinavian branches]**
            - **R1a1a1-Scandinavian** **L448 [Young Scandinavian branch]**
              - **R1a1a1h** L176.1/S179.1 **[a downstream of L448?]**
                - **R1a1a1h1** L175 **Clan Donald?**
          - **R1a1a1i** L365 **[Northern European branch]**
            - **R1a1a1iX** **L669, L670 [Northern European sub-branch?]**
          - **R1a1a1j** L366 **[Eurasian sub-branch]**
          - **R1a1a1k** P278.2 **[Western Carpathian branch]**
          - **R1a1a1L** Z93, **Z94, Z95**
            - **R1a1a1LX** **Z96**
              - **R1a1a1L1** L342.2
                - **R1a1a1L1AJ** **Ashkenazi Jews branch**
                - **R1a1a1L1SE** **L657? South Eastern branch**
                - **R1a1a1L1K** **Kyrgyz branch**
                - **R1a1a1 425=10** **Bashkir branch**

Об удивительных и неожиданных языковых совпадениях между лакским и аккадским языками

(продолжение; начало см. в Вестнике том 4, № 8, стр. 1584-1592 и обсуждение стр. 1592-1603)

Р.А. Омариева

Вот уже три месяца, как я занимаюсь изучением Чикаго - Ассирийского словаря. События развиваются стремительно - пытаясь найти в словаре определенный пласт лексики, я с удивлением, потрясением обнаруживаю, что практически вся лексика лакского языка сокрыта в этих словарях. То есть вся ныне существующая лексика (как я упоминала ранее, она небольшая по объему, всего-то 13000 слов вместе со всеми заимствованиями, если судить по русско–лакскому словарю Хайдакова, на самом же деле несколько больше, некоторые лакские слова я там не нахожу), также слова-производные от нее, ныне лаками не употребляемые. Реальность превзошла все самые смелые предположения, совпадают слова буква в букву, совпадают междометия, восклицания, совпадает образование форм слов, чисел, падежей. Совпадение топонимики лакских сел и местностей; совпадение практически всех личных имен и родовых имен лаков с таковыми аккадскими; практически одинаковый состав лексики вкупе с теми словами, которые обозначают части тела и процессы размножения, позволяет мне утверждать, что **аккадский язык не является ни семитским, ни ассирийским. Это – архаическая форма лакского языка, именно лакского, из группы дагестанских языков - с незначительными для столь длительного существования языка изменениями.**

Если лингвисты сочтут такое утверждение слишком смелым либо преждевременным, пусть принимают мои слова как предположение - сути дела это не меняет. Далее видно будет. Некоторое количество лексики я предоставляю для анализа лингвистов. Касательно топонимики и личных имен - хотелось бы вынести в отдельную тему, как заслуживающий внимания и особо значимый факт, подтверждающий мое пока пусть предположение. Следующий значимый факт - полное совпадение как названий частей тела, так и слов, обозначающих процесс продолжения рода, размножения. Насколько он, аккадский язык, близок к другим дагестанским языкам, мне трудно судить. Мне кажется маловероятным, что был какой-то «прадагестанский» единый язык. Скорее это могли быть

остатки разных племен - пусть даже с очень отдаленным единым предком, но говорящие на разных языках изначально - ведь все человечество разноязычно, восходя к единым общим предкам Адаму и Еве (*прим. редактора – это положение носит здесь фигуральный характер*).

То, что я называла «удивительным», «неожиданным» - таковым является лишь с моей точки зрения, с точки зрения обывателя, совершенно случайно обнаружившего ранее неизвестные факты. С точки же зрения наук - истории, археологии, генеалогии – все закономерно. Удивительно только то, что лексика лакского языка, являющаяся частью лексики аккадского языка в виде некоего рудимента, сохранила первозданную точность. Позволю себе предположить, почему. Взять латынь, мертвый язык. Прежде чем «умереть», он дал рождение целой группе языков, разошелся в обширной Римской империи по национальным территориям, меняясь в соответствии с субстратом, языком местных аборигенов, и постепенно потерял функции и сошел на «нет». Лаки же, в отличие от имперских римлян, жили традиционалистскими общинами, - такие общины консервативны во всем укладе жизни - в языке, обрядах, ритуалах. И поныне у лаков в каждом селе отличающиеся друг от друга обряды и традиции. Лаки никогда не были воинственным и агрессивным народом, тяготели к наукам, почитали мораль и высокий дух, жизнь в самосовершенствовании. Поэтому всю историю жили, защищаясь, но неуклонно сокращалась территория их расселения и население - законы естественного отбора. Пассионарность лаков всегда была направлена на достижения духовные. Выживают, множатся более агрессивные (но – мироздание так устроено, что агрессивным народам возвращается все по закону бумеранга, как бы напоминая людям, что жить надо по заповедям, и не зря они нам даны).

Судя по лексике, по отрывкам из документов, в древней Месопотамии было четко структурированное общество с очень конкретным укладом жизни. Были классы и слои общества со своим местом в нем: земледельцы и скотоводы; храмовые работники и слуги, купцы и владельцы фабрик по изготовлению тканей из шерсти, утвари, посуды; судьи-законники и военные, лекари и ученые. Судя по тому, что глиняные таблички также хранились в специальных помещениях, в определенном порядке, были своего рода картотеки, строгий учет, толковые словари и списки, - это был очень упорядоченный уклад жизни. Потерянные слова относятся к обозначению представителей общества Месопотамии - их чинов, сфер деятельности, к храмовым ритуалам; к медицинским снадобьям и объяснениям по применению – невозможно установить по названиям, каким современным растениям соответствуют растения или деревья, упоминаемые в рецептах настоев и микстур. Потеряны математические и астрономические термины - народ, который вынужден был из поколения в

поколение воевать, защищаясь от истребления и порабощения, никаких связей с науками – медициной, астрономией, математикой - не сумел сохранить. В какие-то годы численность лаков составляла всего 37000 человек! Не на что опираться для восстановления этой лексики.

Из приведенных в CAD текстов с глиняных табличек мне понятны – иногда фразы, иногда обрывки фраз, также общий смысл - о чем идет речь. Слабое же место CAD- это как раз толкование значений слов и текстов. Это объяснимо - люди, занимавшиеся клинописями, отталкиваясь от нескольких текстов, составленных одновременно на двух-трех языках (Бехистунская надпись, если не ошибаюсь) пытались найти значение текстов огромного количества глиняных табличек. Это можно сравнить с попытками восстановления китайского языка и перевода его на другой язык на основании тысяч китайских иероглифов и двух-трех писем на китайском языке. Если кто-то и взялся бы за такую задачу, заблуждения были бы неизбежны. Не очень нравится мне собственное сравнение, но это – попытка оправдать составителей CAD и толкователей в том числе, которым я бесконечно благодарна - они выполнили колоссальную работу в пределах тех возможностей, которые им были предоставлены.

Их труд позволил мне прояснить вопрос, который неизбежно встает перед любым человеком рано или поздно - «Кто я? И откуда я?» - это очень значимый момент лично для меня, и полагаю - для любого человека. Но, тем не менее, есть некоторая «чрезмерность» в попытках толкования текстов на мой взгляд. Одно дело - когда слово трудно интерпретируется, нет зацепок в тексте и тогда можно оставить в переводе честный пробел. Толкователь же решает задачу перевода с такой невероятной и изобретательной фантазией, что иногда просто поражает и оторопь берет. Например, слово sin- том S-3, звук «щ» в начале, переведено как «урина», моча. В лакском языке «щин» -вода, есть другое слово для обозначения урины - «к1ущалу», помочиться- «к1ущин».Обозначив в словаре воду как мочу, толкователь далее всякие водные настои из текстов рецептур делает настоями на «урине», или же то и дело люди пьют эту самую «урину». Ну не могла цивилизация, где трепанация черепа была рядовой медицинской операцией, применять урину в качестве лекарства или питья! Или слово «lisanu», означающее «знаки», «символы» и повсюду ошибочно трактуемое как язык - в том числе и как физиологический орган, и отсюда масса нелепостей в переводах. Таких моментов очень, очень много. Выбирая слова для статьи в «Вестнике», приходится лавировать с учетом данного обстоятельства - приводить простейшие слова с полным совпадением по написанию и переводу. Но - к сведению лингвистов – позволю себе на этот раз некоторые вольности, вынуждена буду противоречить авторитетам с

их интерпретацией слова или текста, - я имею в виду составителей CAD. То, что я делаю иной, отличный от CAD перевод некоторых слов, находит подтверждение в представленных в словаре текстах из клинописей.

Бедные лаки! Как шотландские пикты свой вересковый мед, пронесли через тысячелетия свой язык. Также насмерть стояли, не желая подчиниться ничьей неволе или культуре! Но – не сохранили. Вернее, сохранили ту малую часть, которая также продолжает «таять», сокращаться с изменением быта, реалий жизни. Те самые «ччинну», плиты из тяжелой древесины с шипами внизу, которые волы с погонщиком, стоящим на них, таскали по кругу, размельчая в солому разложенные по «ттарац1у» снопы зерновых, а мы, дети, катались на этих «ччинну», в моем раннем детстве было обыденностью. Потом пришли сеялки, веялки, комбайны, с их приходом исчез очередной пласт лексики - названия инвентаря, упряжи, процессов очистки зерна, просуществовавшие тысячелетия. Поколения меняются, меняется уклад жизни. Прогресс ли то, в каком русле идет изменение жизни и человека? Лично для меня ответ на этот вопрос не однозначен.

Вернемся к аккадскому и лакскому языкам. Когда я попыталась сказать о связи аккадского и лакского языков некоторым из своих знакомых, живущим в Дагестане, угадайте какая реакция была? Реакцией было отсутствие всякой реакции. Это не впечатляет. Неинтересно. То есть ничего, кроме денег и материальных приобретений, моих дорогих лаков с некоторых пор не волнует - очень серьезный признак нравственного вырождения. Наши предки были другие, мы очень изменились, и не в лучшую сторону, это тоже реалии настоящего времени. Но, несмотря на это, есть во всей этой истории одно очень значимое для меня и для многих представителей лаков обстоятельство: благодаря науке археологии и составителям CAD исчезновение лакскому языку уже не грозит - памятник при жизни ему поставлен. Это - аккадский язык текстов на глиняных табличках, хранящихся в лучших музеях мира, и CAD - Чикаго - Ассирийский словарь. Звучит пафосно, но в следующем продолжении темы собираюсь остановиться на топонимике и личных именах лаков и можно будет простить мне этот пафос: топонимика, имена лаков – особенно моих, кулинских (из села Кули) - просто песня во славу Аккада. На этой весьма оптимистичной ноте перейду к представлению выбранных из словаря слов.

Привожу слова, разделив их на группы:

1. Время, пространство, мир.
2.Человек, части тела, родственные отношения.
3.Животные, растения.
4.Быт, утварь, еда.

Естественно, каждый список представляет лишь малую часть базовой лексики, которая показывает идентичность аккадского и лакского языков. Буквой на латинице я обозначила тома словаря на эту букву, с указанием страницы, где находится слово. Лакские слова даны на латинице и кириллице для представления звукового состава слова. Можно идентифицировать весь словарный состав, делая упор на тексты с применением данных в словаре слов. работа эта кропотливая и на это необходимо время.

Первая группа слов-время, пространство, окружающий мир.

E, стр. 319, ersetu - сущ. 1.земля в космосе. 2. окружающий мир. 3. земля, территория. 4.земля, почва,грунт. Лак.ersi, аьрщи, значения те же.
H, стр. 199, hirru - сущ. -борозда, пахотная земля. Лак. hu, huru- хъу, хъуру - поле, пахотная земля.
H, стр. 252, hurru - сущ. -нора. Лак. huru –хъуру -поля. Hurratu –къурату - с поля.
H, стр. 252, hurruhu (значение не определено). Лак. huruhu – къурухъу - поле под паром.
H, стр. 198, hiritu - сущ. - канава, канал, ров с водой. Лак. hiri – хьхьири-море, hiriatu – хьхьирияту - с моря. (Для обозначения канавы, речки есть ratu-R. стр.219).
H, стр. 100, harharu -сущ. - цепь, горная цепь. Лак. Harhallu-хъархъаллу –гряда, горная цепь.
S, стр. 202, sawu - сущ. - пустыня. Лак. Saw-ссав – небо.
B, стр. 103, baraqu – гл. - излучать свет; стр.110. barihu - сущ. -камень (камень, который сияет подобно barihu - из приведенного текста). Лак. barh-баргъ - солнце.
B, стр. 108, barasu – гл. -сиять. Лак. Bars – барз - луна, месяц, ц1убарз - новолуние.
S-1, стр. 259, salmu-2, -говоря о времени. Лак. Salmu, sal-ssa-ч1алму, ч1алсса - поздний.
S-1, стр. 256, salmu, 1,2 –целый, полностью. Лак. Salumu-salu-ssa, щаллуму –щаллусса - полностью, целый.
H, стр. 231, hulu- сущ.-дорога. Лак. hullu-ххуллу -дорога.

Вторая группа - человек, части тела, родственные отношения.
N, стр.239, ninu (nenu, nini, ninnu) – местоимение «мы».Лак.ninu-нину-мать.
A-2, стр.471, assutu-сущ.-замужество, статус жены. Лак. as dan-аьш дан-ритуал сватовства с подношением подарков родней жениха, после которого девушка считается нареченной.
H, стр. 155, hatnutu-сущ. женитьба.

S-3, стр. 152, su-местоимение-он. Лак.su- чу-мужчина, муж, subaresu-мужчина из Субарту, laqusu- лаккучу-лакец (встречается в приведенных отрывках текстов из клинописей).
H, стр. 149, hatanu (hatnu) –родня через женитьбу. Лак. hati-хъат1и-свадьба, свадебные торжества.
H, стр. 265, huzalu-сущ. значение неизвестно. Лак. huzala-хъузала-работник полей, крестьянин. От «hu»- поле и «zun» – работать.
K, стр. 565, kurru - часть человеческого тела. Лак. ka, karru -ка, кару –рука, руки. Идет еще с пиктографического письма – рисунок развернутой ладони, обозначающий руку и знак «KA».
K, стр. 223. karsu – сущ.- часть тела Лак. Karsi - карч1и – ляжка.
H, стр. 262, husulu - прил. относящееся к описанию тела. Лак. husulu-кьющулу- щиколотка.
H, стр. 95, harrasu- гл.(3) – относящееся к частям человеческого тела. Лак. harasu- haras-alu – хъарац1. хъарац1-алу - подмышки. Там же, стр. 102. haristu – сущ. женщина в заключении. Лак. речь идет о женщине несвободной, замужней.
S-1, стр. 17, sabu – сущ. – значение неизвестно. Лак. sabu- ччабу-влюбленность, любовное желание. Там же, sabu прил.(?) значение не определено. Приведен текст обращения к объекту страсти влюбленного мужчины. Там же, sabu A гл. трепетать, качаться. Лак. sabu –ччабу –быть влюбленным.
S-2, стр. 289, senu, A сущ. сандалии, обувь. Лак. sen, sennu –ччан, ччанну-нога, ноги (ступня).
Q, стр.184, qatu -сущ. рука(кисть). Лак. qata-кат1а-перчатка, hat -хъат-ладонь.

Третья группа - животные, растения.
H, стр. 231, hulu (huliu) сущ. – вид мыши. Лак. Qulu - к1улу-мышь.
H, стр. 244, huqu, hazu сущ. –птица, не определена. Лак. hazi, hazu-къаз - гусь.
D, стр. Dalu - птица, не определена. Лак. dalu-далу- птица из рода куропаток.
H, стр.226, huqqu, hukku- сущ. значение неизвестно. Лак. huqqu- х1юк1у-осленок.
T, стр.488, tuqqu, tukku- сущ. значение неопределено. Лак. tukku –ттукку - осел.
H, halqu-сущ. - потерянное животное. Лак. halqu- ххалку – половозрелый баран.
T, стр. 498, tuttu-сущ. -шелковица, тутовое дерево. Лак. tutu-тут-шелковица, тутовые плоды.
K, стр. 556, kurangu (kuraggu) –из зерновых. Лак. kuragu-кураг- курага, вид абрикосов.

S-3, стр. 4. simmessalu (simissalu, simsalu) сущ. – дерево, возможно, самшит. Лак. simussali –ч1имуч1али- бабочка, род бабочек.
A-2, стр. 206, aqrabu- сущ. - скорпион. Лак. ekrab- экьряб - скорпион.
K, стр. 56, kakkusu, kakkusubi, kakku- мелкое животное. Лак. kakka –къакъа-букашка, насекомое.
M-2, стр. 131, - miteku- значение неизвестно, входит в перечисление синонимов kakku в Malqu. Лак mitekuku-мит1икьукьу-муравей.

Четвертая группа-быт, утварь, еда:
K, стр. 563. kurkuru -сущ. чаша, сосуд, вместилище. Лак. kunkur-к1унк1ур-кастрюля.
K, стр. 83. kallu - сущ. Сосуд из глины или древесины. Лак. kali, kallu-кьали, -лу –бочка, обычно деревянная.
K, стр. 463. kisu-сущ. металлическая чаша. Лак. kisu- к1ич1у- миска.
S-2, стр. 273, siltu, сущ.1 - нож,лезвие. Лак.sila, siltu- ч1ила, ч1илтту-нож, ножи.
M, стр. 438 mazlagu - вилка или крюк (в перечислении посуды) Лак. потерянное слово. «Maz»-язык, «lagan» - ходить, выдвигаться (чтобы брать еду) вилка или подобие вилки.
S-2, стр. 412. sikaru (sikru) 1-сущ. пиво. изготовленное из зерновых. Лак.sekir-чехир-вино, виноградное вино.
S-2, стр. 57, saraqu C 3 гл. - варить или чистить мясо. Лак. salaqu-щалахъу - блюдо мясное.
S, стр. 315 sirqu (sisqu) – ароматическая приправа к еде. Лак. sirqa-ссирка, ссирча – уксус.
L, стр. 110, lasu, A, гл.- месить тесто. Лак. iniqma lasan dan- иник1ма лащан дан- месить тесто; lasu-лащу-кругляш из теста для раскатывания лепешки.
H, стр. 264, huttu - сущ. - банка для хранения чего-нибудь. Лак. huti- къути-банка для хранения чего-нибудь.
H, стр. 263, husuku - сущ. - упряжь или ее часть. Лак. husuku-хъющуку-кочерга для огня.
S, стр. 417. sussulu (sulsullu, sussulkannu) сундук из дерева, реже из металла. Лак. su, su - су – большой деревянный ларь для хранения зерна.
S, siru -сущ. – гипс, штукатурка. Лак. sir, сир - краска для стен, крупных объектов.
K, стр. 569, kursallu (kursullu) – сущ. - корзина, кузов из тростника. Лак. kursullu- к1урч1ул -решето для очистки зерновых.
T, стр. 99, tallu -сущ. балка, поперечина. Лак. tala, tallu - ттала, тталлу-балка, балки.
A, стр. 378, alu, F – сущ. часть упряжи осла. Лак.ali, tukkul ali -али, ттуккул али – попона под седло осла.
S-2, стр. 321, serseru (sisiru) - сущ. - цепь. Лак. serzin - щерзин-цепь.
D, стр.199, dussu - прил.-обильный,изобилующий. Лак. dussu-дуччу -сытый, изобилующий.

Исследование славянских вед «Велесовой книги»

Веда 8.
Первоисток Славянской веры.

Георгий Максименко

"Каково семя, таково и племя".

(Русская народная поговорка)

Предисловие автора

Данная работа является продолжением серии исследований славянских вед «Велесовой книги» с позиции последних изысканий в области ДНК-генеалогии. Её характерным отличием является отсутствие в данной веде каких либо ДНК - генеалогических информационных моментов. Информацию, изложенную в восьмой веде, можно было бы опустить и приступить к обработке следующей, но автор счёл необходимым не пропускать данную информацию, подвергнуть её исследованию и публикации. Одной из причин является желание более полного исследования Славянской культуры и веры в канун проведения в Подмосковье (г. Лотошино) четвёртого Международного Конгресса «Докирилловская славянская письменность и дохристианская славянская культура», проводимого ЛГУ им. А.С.Пушкина, РАЕН и Академией фундаментальных наук. (http://my.mail.ru/community/slavfilosofia/659A54E20AB2973A.html).

Содержание исследуемого первоисточника.

Исходный материал 8-й веды переложенный на кириллицу

11.а-II
Се бо ящете первие Триглаву поклонящетесе яхом. Тому Великоу Слву пьящехом хвалихом и Сварга Дида Божя яко ждете ное се роду Божьску нащельнико. Всенску рдоу студиц вещен яков отец ево лэтэ од кроне сва. В зме николе же не взмерзе. Тоя воде живенце пиуще живихомся до коне не преидехом якожде све ко

нему убендехом до луце гоех Ра истиех. Бгу Перунев и Громверзецу. Бгу пре. Бореня о рцехом живнта Явлны. Не прставате врщате колие. Кои и нои венде стезеоу Правоу до брание. До тризне Влика о вся павщя якове же идоут бе живенте вещние по пэлку Перуноиу. Бгу Свендовидиу Слву рецэхом се бо ста Бг Првие. Явие. Тому пъиема песынема яко свт есе. Чрезъ оне видяхом свиет зрящете. Яве быте. Тои нас о Навие убржешет. Тому хвлу пъиемо пъехом плясаще тем упав зоивахом Бгу нашему якожде тои земе суне нашиу. Звиздя дрезаца свт криепицэ творяцете Слву Свендовидие вску Слва Бгу нашему то бо скрыбеце те сердие нашие. Се смехом одркохом сен одо злоя дэяна нашиа. Добру тецехом сте се бо отрце пущениемо обы и месе. Реще те все утворяще се бо нь виедете оуме ръзтргнещеши. Поцысте се бо те умиемо се бо таина влика есе якожде Сврг Перуно есе. Свендовинд тоие два есьва одържены о Сврзи. Обая Бялбг. Црнъбг сен перуте се тоие Сврг держещете. Бо ие она свенду не быте пъврзещену по тые оба сва Хърс Сывой Вльс Стрыбе держтесе позань Вышень Леле Лиетиц

11.б-II

Радогщ Колендо. Крышень и се о два удрзец Сывой Яр. Дажбо се бо ины суте Биелояре Ладо Коупало; Сэниц Житнец Вэнищ Зрниц Овсэниц Просиц Студец Ледиц. Лютец.

Пота

Птищец Зверенц Милиц Доздец Плдец Ягондец Пшелиц Иръстиц Кленчщ Езеренц Виетриц Сломиц Грибиц Ловищ Биесидц Сниезиц Страниц Свендиц Радиц Свиетиц Крвиц Красиц Травиц Стеблиц.

За се соуте

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Огласовка текста.

11.а-II

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*пр**я**щемо тако **о**трище. Идемо ст**а**д**е** нших вед**о**мы. На тр**а**вие коли бо вестия на ин**ы** ступе идемо эсти по дроузе хв**а**лу Б**о**зем возн**е**сяще Сл**а**ву п**о**яхом. Тако до пол**у**дне. Р**е**щемо Сл**а**ву в**е**лику Х**о**рсу Зл**а**т**о**р**у**ны коло в**о**р**а**тящу. Суряну пиемо. Тажде до в**е**щере. По в**е**щере коли бо ож**и**де огн**и**щи с**и**льжена заждиемо. Сл**а**ву вьщерниу п**о**иемо Дажбу нашы иже реком ес**е** пради нашеи ецимося о чисте быти. Мовлена творяще идемо до сны. Тамо в**е**лика необясь нои.*

Авторский перевод

Этих ищите - первых Триглаву поклоняющихся, мы их имеем. Тому Триглаву Великую Славу поем, хвалим и Сварога – Дида Божьего, так как ждет нас на своём пути. Сварог - роду Божьему основатель и всему роду студиц вечный. Таков отец любого времени от кроны своей. В земле никогда не замерзнет и той водой живящей, пьюще её мы живимся сами, пока к концу не придем и когда сами к нему убудем до лугов его просторов истинных.
Богу перунов и громовержцу, Богу поры – Перуну молвим славления свои:
- Боритесь о сказанном, слова эти жизнью Явлены. Не переставайте вращать колеса, раз ведете нас стезею Прави на брань и к тризне Великой. О всех павших, которые идут без жизни вечной, скажем. Что идут в полку Перуновом.
Богу Свендовиду Славу речем!
Он стал нашим Богом Прави и Яви. Тому поем песни хвалебные, так как Свет имеется. Через него видим мы свет очами видимый. Значит - Яви быть. Той Явью Свендовид нас в Нави убережет. Поэтому ему хвалу поем, запевая пляшущую песню, тем самым обращаемся к Богу нашему:
- Как же ты землю движешь нашу?
Звезды держатся на небе, свет укрепляется, творите Славу Свендовиде всякую, Слава Богу нашему! Тем светом питаются сердца наши. Действия наши самим нам и отзывается все от злых деяний наших. Когда к добру тянемся, есть это отрицание злу противостоящее. Добро и зло шагают вместе.
Говорим вам:
- И добро, и зло, и боги наши, те все сотворены. Понять это и увидеть можно только в уме расторгнутом.
Почувствовать это умеем. В этом тайна Великая есть, когда Сварог перунно выступает. Свендовинд и Перун те оба одержаны нами в Сварге. Оба Белобоги. Чернобог есть противоположность Белобогу. То на них Сварга держится. Сварога она, поэтому свету не быть поврежденному, потому оба боги свои.

Таковы Триглавы наши:
Вышень – Велес и Стрыб, за ними держатся Радогощь – Хорс и Леля. Крышень – это Триглав о двух удерживающих Летице и Колендо. Дажьбо – Сывой и Яр, а это иные ведь Белояры – Ладо и Купало.
Потом следуют Триглавы:
Житнец - Сениц и Веницъ; Страдиц - Зерниц и Просиц; Студец - Ледиц и Лютец.

Милиц - Птичец и Зверенц; Дождец - Плодец и Ягодец; Ирийстиц - Цветич и Пчелиц; Водич - Озеренц и Снежиц; Лович - Рыбиц и Сомищ; Ветриц - Звездиц и

Громич; Весениц - Живиц и Свентиц; Осениц - Соломиц и Листопадич; Зелинц - Травиц и Стеблиц; Листвиц - Березич и Липец.
За этими идут и другие Триглавы:
Беседец - Странниц и Грибиц; Радиц - Родиц и Кровниц; Гостиц - Гориц и Странниц; Мыслиц - Ведиц и Свендиц; Спасиц - Ратиц и Чурц; Маслиениць - Рядиць и Красиц.
Тут будет среди своих и Огнебог Семаргл, общается яро, борзо зарождается и чист. То все Триглавы общие. Своими они идут.
Тужатся отроки в верах, защитой созданы они. А выйдешь вон, то есть прекрасный Ирий. Там Ра река течет, которая отделяет Сваргу от Яви. Числобог учитывает дни наши и называет божьи числа свои, быть дню свершенному, нежели быть ночи. В усечение пустили того, отметив, что это есть Явское. Сон есть в дне божественном. В ночи безликой есть иной же Бог: Дид - Дуб и Сноп наш. Для нас же он Сварог. Слава и Перуну огнекудрому, который стрелы на врагов ворожит, верно предвидя в стезе. По невежеству их есть тем воинам чести суд. Так как Перун златорун, милосердие в справедливости есть и огонь.
Еще мы сурьи сияющей поем хвалу и Богам нашим. Огнищу Перунову славу поём, который есть роком потятич на врагов. Провозглашаем Великую Славу отцам нашим и дедам, которые в Сварге упрятаны так отречённо. После этого ведём стада наши ведомые на пастбища. Если на травы вести, в иные степи, садимся есть по другому, хвалу Богам вознося - Славу поем. Так прощаемся до полудня, провозглашаем Славу Великую Хорсу, златорунное коло вращающему и суряну пьем. Также прощаемся и до вечера. По вечере, если ожидаем огнища сложенного и жаждем огня, славу вечернюю поем Дажьбо нашему. Всё это боги наши, которых провозглашаем и есть это порядки наши, так как заботимся о чистоте бытности своей. Молитвы творяще, идем ко сну. Там великая необъятность нас.

Комментарии.

Уже на начальном пути возникновения Славянской веры уходящей своими корнями в более чем 7000 летнюю историю, человек осмысливал общий закон единства различных явлений и олицетворял их, выражая в различных образах, которые он обожествил, назвав Богами. Но этого было недостаточно для полноты передачи сведений о них. Возникла потребность введения, наряду с обожествленными образами, других понятий – Триглавов.

Вот как описывает понятие о Триглавах президент Академии управления глобального регионального управления, академик **К.П.Петров**, в своей книге «Тайны управления человечеством»:

Уже на начальном этапе зарождения Славянской Веры люди осмысливали различные явления, осознавали их **взаимосвязь и взаимозависимость**. Эту взаимозависимость они связывали с существованием какого-то единого управления всеми явлениями, нашедшего своё выражение в признании людьми Единого Бога, Творца, Создателя – Сварога. То есть надо ясно представлять, что наши предки понимали, что **существует только один Бог**, который управляет всеми процессами во Вселенной. Но перед людьми в разных случаях и ситуациях **Он предстаёт в разных ипостасях**. Проявления же действий (управления) Бога Единого в различных природных и жизненных явлениях, то есть проявления в различных образах, ипостасях, они тоже обожествили, назвав Богами. И вот эти-то **ипостаси** Бога Единого (Сварога), наши предки и называли **Богами**, осознавая при этом их взаимосвязь с Богом Единым и взаимозависимость всех Богов между собой. То есть Славянская Вера Богу не была «многобожеской» и уж тем более «идолопоклонской», как это пытаются сейчас представить русским людям «определённые силы».

Но для полноты описания взаимозависимости и взаимовлияния действий Богов-ипостасей Бога Единого было недостаточно. Так появились Триглавы.

Триглавы выражают **целостность** вполне определённых **процессов**, протекающих как во Вселенной в целом, так и в жизни общества.

Основополагающий Триглав «Правь – Явь – Навь». Через него была выражена наиболее полная мера того, что мы сегодня понимаем под словом Бог, Творец, Род, Абсолют, Создатель и т.п. Этот Триглав даёт ключ к дальнейшему пониманию и правильному восприятию всех составляющих Славянской Веры.

Посмотрите, какой прекрасный символ Триглава «Правь – Явь – Навь» существовал у славян (рис. 9–6).

Как кованое украшение его прикрепляли на ворота, на стены домов. Этот символ применялся и в ювелирных украшениях. А кто из наших

современников видел его где-нибудь в нашей стране? Мы знаем пятиконечную звезду, знаем шестиконечную, знаем «янь» и «инь» … А своего древнего символа не знаем. Его также старательно скрывают от нас.

Рис. 9–6

Скрывают от нас и запутывают также и тем, что славяне – это нация. Славяне – это не нация. **Славяне – это люди, исповедующие Славянскую Веру Богу**. Есть христиане, есть мусульмане, есть буддисты и т.д. И есть славяне. Причём Славянская Вера Богу – самая первая религия человечества. Что касается христианства, то все его основы созданы на базе Славянской Веры. Об этом мы поведём разговор позднее. Основополагающий смысл слова «славяне» самодостаточен – это «славление». «Славление» не предусматривает безсмысленного прошения помощи у Бога о благополучной жизни, которая уже изначально дана человеку Свыше. Славяне – это не национальность, а общность народов, образ жизни, основанный на вероисповедании.

Правь - есть единый и неведомый нам закон развития вселенной и всего сущего. Явь – мир, который мы в состоянии ощутить собственными органами чувств и таким образом проявить его в нашем сознании. Навь – мир, существующий в природе, но недоступный нашему восприятию. Данный Триглав дает понимание, что жизнь вечна, переходит из одного состояния в другое по непостижимому для человека закону.

Понятие "пора" является текущим (временным) понятием и течет Явью, которая творит нашу жизнь. Поэтому имеются круги в нашей жизни, называемые рождением и смертью, потому что Явь нами воспринимается как текущее время, определяемое благодаря движению. Все Творение происходит в Прави. Нави не

бывает по Прави, ибо Навь есть как до того, так и после того. В Прави же есть Явь, в которой мы существуем и приобретаем свой жизненный опыт.

Некоторые Триглавы построены по простому принципу единства противоположностей. Всегда Белобог и Чернобог имеются в них вместе. Следует помнить, что Триглавы имеют такую же значимость в Славянской вере, как и Боги Славян.

Следующий из основополагающих Триглавов **Дид – Дуб и Сноп.** Дидом - Сварогом отражен первоисток, Дубом - род и его ветви, пребывающие в Славянской вере, от корня до ветвей. Снопом - единство и сила неразрывная славянская. Один славянин – колосок, который можно повредить, легко сломав. Колосья, собранные в сноп, разорвать сложнее. Так себе представляли эту веру рода пребывающие в славянской вере и образовавшие на её основе славянский этнос. Сила славянской веры заключена в понимании того, что есть Высший Разум, являющийся Первоистоком, и есть вера народа в то, что он существует.

Когда предаётся вера, разрушается Сноп и теряется Сила рода. Так потеряв Исток, теряются Корни рода. Так, либо примерно так, мыслили предки славян освещая свою веру.

О чём повествуют Триглавы?

Вышень - Велес и Стрыб. Вышень является вершиной двух его составляющих в данном Триглаве. Велес является олицетворением мудрости и знания, а Стриб - его полной противоположностью, т.е. бездарностью и безграмотностью. Следовательно, человек способен постичь вершину мудрости и знания, но может также остаться на всю жизнь безграмотным человеком. Все зависит от него самого.
Радогощь - Хорс и Леля. Радогощь является олицетворением радости жизни. А несет нам эту радость по жизни мужское и женское начало. Этот неразрывный союз двух противоположных начал олицетворяет радость жизни.
Крышень - Летиц и Колендо показывают человеческую возможность введения в обиход времени путем установления в определенных рамках и параметрах летоисчисления и календаря, т.е. годичного коловращения земли вокруг солнца. Отсюда возникло понятие – Сварожье Коло или колендо (календарь). Этот Триглав принято называть удерживающим.
Что касается Триглавов общих, то они со временем расширялись и добавлялись в зависимости от ряда условий развития человека, этноса, исторических событий, быта племени и т.д. Главное, чтобы творились они правильно и не разрушали первооснову Славянской веры.

О чём говорят Триглавы общие?

Страдиц - Зерниц и Просиц (В страду, что необходимо сделать? Своевременно вспахать, засеять, вырастить и собрать урожай зерна и проса, да так, чтобы его хватило и зиму пережить.)

Студец - Ледиц и Лютец (В студеную пору «управляют» лёд, покрывающий водоёмы, и лютый мороз, пронизывающий все живое насквозь, поэтому необходимо утепляться и рубить проруби в водоёмах.)
Весениц - Живиц и Свентиц (С приходом весны все в природе оживает и расцветает).
Милиц - Птичец и Зверенц (Что человеку, живущему в союзе с природой, мило и что он должен оберегать? - Птицу и зверя).
Дождец - Плодец и Ягондец (Что нам дает дождь? Плоды и ягоды).
Ирийстиц - Цветич и Пчелиц (Рай на земле там, где цветут цветы и пчелы собирают мед.)
Водич - Озеренц и Снежиц (Где есть вода? Как в озёрах, так и в снегу.)
Ветриц - Звездиц и Громичь (Что нам приносит ветер? Разогнав тучи, являет взору красоту звёзд. Нагнав тучи, дарит нам грозу).
Осениц - Соломиц и Листопадич (Осенью мы что наблюдаем? Как засыпает природа, оставляя нам солому на полях и красоту листопада.)

А это уже Триглавы, касающиеся других сторон жизни славян:
Радиц - Родиц и Кровниц. (Кому мы больше всего рады в доме? Родичу своему и кровнику своему.)
Мыслиц - Ведиц и Свендиц. (Кем является человек мыслящий? Человеком ведающим и просвещенным.)
Спасиц - Ратиц и Чурц. (Что может спасти человека от подстерегающей его опасности? Ратная сила его и осторожность.)

Изучая природу, человек обретает каждый день всё новые понятия, вытекающие одно из другого, выявляет в природе новое, что, отражаясь в сознании, требует материального выражения, поэтому общих Триглавов исходя их данной веды может быть бесконечное множество.

Ещё раз вернёмся к выдержкам из книги **К.П.Петрова «Тайны управления человечеством»** и посмотрим чем сегодня научно выражены такие понятия как например Триглав: Правь – Явь и Навь, что им соответствует и в какой мере:

Триглав **«Правь – Явь – Навь»** есть ни что иное, как древний аналог современного нам триединства **«Мера-Материя-Информация»**, являющейся первоосновой, своего рода фундаментом Концепции Общественной Безопасности. Дажьбо сумел выразить в предельно обобщённых понятиях первооснову Мирозданья, т.е., говоря современным языком, это был величайший философ своего времени. Однако, кому-то («мировому закулисью») очень надо, чтобы у русских не было своих корней, не было своей письменности, не было своих выдающихся философов древности и т.д., а всё начиналось бы с крещения Руси.

Русские подвижники безусловно наследовали эти древние знания своих предков-славян. И как ни старались исказители истории нашей страны скрыть от нас правду, однако *«нет ничего тайного, что со временем не стало бы явным»*. Правда всё равно прорывается наружу. Так, например, описывая *«Житие преподобнаго Сергия Радонежского»* (издание собственной типографии Свято-Троицкой Сергиевой Лавры, 1904 г.) архимандрит Никон на стр. 172, рассказывая о событиях, предшествующих Куликовой битве, пишет:

«Святой старецъ провиделъ духом нужду еще разъ укрепить мужество Великаго Князя перед самою битвою, и прислать ему въ благословеніе Богородичную просфору и своеручную грамотку, конецъ которой сохранила для потомства одна изъ наших летописей. Грамотка эта, увещевая великаго Князя сражаться мужественно за дело Божіе и пребывать въ несомненномъ упованіи, что Богъ увенчаетъ ихъ дело счастливымъ успехом, оканчивалась следующимъ изреченіемъ: ***«чтобы ты, господине, таки пошелъ, а поможетъ ти Бог и Троица».***

Пытаясь как-то объяснить разделение Сергием Радонежским БОГА и ТРОИЦЫ, в примечании даётся нелепое легкомысленное толкование о том, что под «Троицей» Сергий Радонежский видимо имел «храм Пресвятой Троицы». Сергий Радонежский был не их тех, кто позволял бы себе высказывания, которые можно толковать всякому так, как ему вздумается. В данном случае он даже не сказал, а написал: *«Бог и Троица!»*

Из сказанного видно, что древнему Славянскому Триглаву: Правь – Навь и Явь соответствует современное понятие Триединство: Мера – Материя – Информация, углублятся в детализацию которого не стану, т.к. целью данной работы является показать начальные постулаты первооснов Славянской веры описанных в восьмой веде «Велесовой книги».

Это не первая работа по исследованию дохристианской – славянской веры в данном Вестнике, поэтому имеется возможность более общего ознакомления с

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Максименко Г.З. Исследование славянских вед «Велесовой книги» как дополнительного источника информации, с позиции последних изысканий в области ДНК-генеалогии.
Веда 4. О вере славянской в античный период греческой колонизации Черноморского
побережья (конец VII-IV век до н.э.). Т. 3 №12, 2010. ISSN 1942-7484

Петров К.П. Тайны управления человечеством. Т.1. (с.115-119) М. «Академия управления». 2008. ISSN 978-5-91047-002-0

Исследование славянских вед «Велесовой книги» как дополнительного источника информации, с позиции последних изысканий в области ДНК-генеалогии

Веда 9.
об исходах славян - ариев с Балкан на Карпаты, с Карпат на Днепр, к озеру Ильмень, за Ю.Урал и из Семиречья в Европу. Как и когда это происходило.

Георгий Максименко

«Нет ничего чудесней человеческого мозга,
нет ничего более изумительного,
чем процесс мышления,
ничего более драгоценного чем результаты
Научных исследований»

(А.М.Горький)

Резюме.

Целью данного труда является продолжение серии исследований славяно-арийских вед «Велесовой книги» как дополнительного источника информации, с применением нового научного инструмента в изучении путей миграций человечества – ДНК генеалогии. Проверка данной информации на её соответствие с последними полученными данными в области ДНК-генеалогии.

Несмотря на краткость изложенной в 9-й веде информации она представляет несомненную ценность для исследований. В ней в сжатой форме изложены ряд исходов и путей миграций славяно-арийских племён по разным направлениям и в разные временные периоды. Это позволяет расширить исторический кругозор и получить дополнительное представление о происходящих исторических процессах образования и становления русского народа в его территориальных границах.

Основные направления исследования путей миграций заданы в рамках изложенной в ведах информации. Это исход славян-ариев 6200 лет назад с Карпат на Днепр,

4800 лет назад расселение по Русской равнине, а так же исход за пределы Южного Урала и освоение территории Сибири. Исход в обратном направлении - около 2500 лет назад происходил из Семиречья (от оз. Балхаш) в Европу по маршруту: Загрос – Двуречье (Тигр и Евфрат) – Б.Кавказ – Западное Причерноморье. Каждый из этих этапов расселения и исходов будет рассмотрен поэтапно, с использованием как последних данных в области ДНК-генеалогии, так и с учётом ранее проведённых исследований.

Содержание исследуемого первоисточника

Исходный материал 9-й веды переложенный на кириллицу

15.а -II

Ведя жеривы о Комоние Биеле изыдощьщя одь крае Седьемриецштя о горе Ирштя. Загогря обентьшя виек. Таково по нехщьша иде на Двоериеце ръзбяи о тои комоньством своиемы. Теше до земе Срштие. Тамо ста пождие идьща горыма влкима. Снезиема. Лядоя. Отоще до степны. Тамо стады свои. Скуфе бя се прьва прве одрщена оце наши. Пра…е дрьжящи. О Наве прие влцеие. Сылы дает отрщете врзе не бж…дьши. О прие тие до горя Карпен сте. Тамо ряще о щелы пенты кнзы. Грди и селы ог(н)ь есте. Врзы влкеа. Потеиестнены бя …По нехше идьшя до Илмер езера. Тамо утворяи грд Новь. Тамо пребендиехомь. Ту свергы перве пращуре молихом се рди рожениец Крынь е препросихом. То Дубо крень хлиеб наше Сварг иже твря и свент Бг есе свенту. Бг Праве Яве Наве се бо имяхом о нои во истьву. Се естьва нашие преборящете сылы по тем сесте. Блгу венде якожде пра цы о венде твряи осеме

15.б- II

коя се будеше до заходжна суние. Отуде идь до суне до Непра риеце ясьмо тамо Кые о утверждень грд яке обытваце слвне рди ине. Тамо сен оселещесе огнище твряе Дбу. Снпоу яковь тоя есе Сврг пращоурь нашие. Се крать налиезе на не врг новь о сзесще ижь крве щоурь пяще. Се рате сва устрми Кые на не. Зрящи бе Сврзе вое перуньште вое и жде се врьгоща на не. Потрщяе сылу иее. До ньге рстще покжете заде онь. Се племеное незьва налезе ино на не. Сещя бя влика о пхиждено бя до послдь. Нашие вое зряие то риекста. Бзе нашие жденоуть врзе нашие себь те Вышень грядет на марицех до нои. Рщеть дите гядетсе града ваша напиесте ие аб…бендие Зура. Крипка. То Сварг мене пошлет до вои се б… се бо тьеима тие сылы небесни. Ошиева... . Такожде рциех. Вои… бржещет...

5.б

Ои щасо д щасу сен. Ржданеця среде нои … свия же сьськ бо есь по самыя смьрте … на зазбенжемось мы тако же ильмци якови нас охраниша не идинэ. С нама солсиахусе. Крявь све даяй и намо… дривэ бя на Руси хзарие днесе сва вързи... мы же сьми русищи ни коли не врязи... Оставхом на сурю млекы нашя во травэх за наши утлещемо до нь щалюаи ни травия яко же рэкша пра староци. Даимо сесуритися и апимо тричи во слву Богом пентокрт денеэ… та бо то наишя стара потщина Бозэм длюжна есь потребити … требь та буди повязем мези нои (и Бозе).

Ни Мара ни Морока не смиэмо славити. Ти бо то Дивы соуте наше нещасть. Наше Дидо есь в е Сврзэ.

Авторский перевод.

Принеся жертвы в Коне Белом мы отошли от края Семиречья, что в горах у Иртыша. В Загорье обитали век. От Загорья, по нехоженому, идем на Двуречье. Разделились в том конницей своей. Продвигаемся к земле Сирийской. Там стали числом поменьше идти горами великими, снегами и ледниками. Отошли к степи. Там стада свои встретили. Скуфь была ранее одной из первой одержана отцами нашими. Пращуры наши держали её в Нави порой великой. Скуфь та силы дает. Отречёте врагов от неё, не бежите. В поре той к горам Карпатским шли вместе. Там решение приняли во главе пяти князей. Города и села огонь ест, ветра дуют великие. Потеснены были на другие земли.

По нехоженому шли к Ильмер - озеру. Там создали град Новый и там тоже пребываем. Тут Сибири первых пращуров вспомним, это роды породившие Крынь, ее и переспросим. То Дуба корень, хлеб наш, Сварог, который творит свет и есть Бог этому свету. Бог Прави – Яви и Нави. Это есть наши переборовшие силы по тем сидящие. К благу ведут. Когда была пора отцов, в ведении творили веру всем племенам, которые будут сидеть на Западе. Оттуда идут на Восток к Днепру-реке. Есть там Киев в утверждении, город который обетовали славянские роды иные. Там все оседлые огнищане требу творили Дубу и Снопу, которым является Сварог, пращур наш.

В тот раз налез на них враг новый, который щурясь из сосудов кровь пьет. Тогда рати свои устремил Кий на них. Смотрит, без сибиряков воины перуновы, воинов помощи и ждет, воргоча на врагов и потрачивая силу их. Догола растащит и покажут зады они. Иное племя незваное налезло на них. Сеча была великая, в походе были все до последнего воина. Наши воины, наблюдая врагов своих, говорили так:
- Боги наши поджидают врагов наших. Это ведь наши боги. Вышень грядет на марицех к нам.
Вышень подсказывает нам:
- Идите в поход, гадятся там города ваши. Укрепите их, иначе будет у вас Зороастризм. Зура крепка. Это Сварог посылает меня к вам, так как это темные силы небесные гадят города ваши, завшивленные они.
Также рассуждайте, это воинов наших бережет.

От времени до времени сказано всё.

Рождаются многие среди нас. Своих же сисек, поэтому до самой смерти они свои. Если назад забежать, мы такие же как ильмерцы, которые нас охраняли не единожды. С нами соединялись. Кровь свою давали и нам. Дривь была на Руси, хазары, сегодня свои варяги. Мы же сами русичи, никогда не были варягами.

Выставляем на солнце молоко, наше на травах окисливается. Поэтому наше отличимое от других. На их жалуются, что не травное. О том же говорит и пора нашей старости. Даем молоку осуриться и отопьем трижды его во Славу Богам и так поступаем пятикратно за день. То наша старая традиция, которая Богам есть должная потребность. Треба та будет связью между нами и Богами. Ни Мару, ни Мороку славить не смеем. Те Дивы ведь наши несчастья. Наш Дид есть в ее Сибири.

Тематические исследования.

Рассмотрим исторические процессы, описанные в девятой веде поэтапно и в хронологическом порядке. Это позволит глубже и правильнее понять все происходящие события. Хочу подчеркнуть одно важное, на мой взгляд, обстоятельство. Как уже сообщалось ранее (**Г. Максименко, 2008**), «Велесова книга» представляет собой отдельные веды написанные в разное время и по разным правилам письменности, которые были отобраны из всех имеющихся в наличии на период их объединения в общий свод, который сегодня принято называть «Велесовой Книгой».
Несмотря на сплошное написание, при изучении текста были обнаружены разделители между предложениями выраженные буквой «а», а гласные буквы отсутствуют только в тех местах, где они «читаются» недвусмысленно. Т.е. текст был сознательно скрыт от постороннего прочтения.
По содержанию «Велесовой книги» видно, что это многовековой труд разных авторов. Обнаруживается в ней не только широта лексического разноряда, но также исторические повторения одного и того же события с разных точек зрения.
Что из себя представляет «Велесова книга»? Без ответа на этот вопрос исследование её становится крайне проблематичным и бессмысленным.

«Велесова книга» является сводом 26 славяно-арийских вед. Отобранные Веды были разбиты на две части: веды старых времён и новых, примерно в одинаковой пропорции по объёму информации. Старых вед оказалось восемь, а новых вед - восемнадцать. Все они были переписаны слово в слово на языке своего времени. Данная веда относится к одной из первых вед «новых времён», которую переписчики сочли необходимым поставить в начало второй части свода. Сделано это было очевидно не случайно, т.к. не смотря на то, что она оказалась короткой, в неё вошли ряд исходов и путей миграций славян-ариев на протяжении длительного отрезка времени, длиною около 6000 лет. При этом следует отметить, в данной веде описано преимущественно расселение славян-ариев выбравших Днепровское направление с князем Кием. Те племена, что ушли с его отцом – Ореем в Западном направлении описываются в другой (следующей) веде. Её мы исследуем позже.

1. Исход славян – ариев с Балкан на Карпаты.

Что нам известно об этом исходе из ранее проведённых исследований? Веда информирует нас о следующем:

В поре той (арии) к горам Карпатским шли вместе. Там решение приняли во главе пяти князей. Города и села огонь ест, ветра дуют великие. Потеснены были на другие земли. (ВК-9)

Из ранее проведённых исследований в области ДНК-генеалогии **(А.Клёсов, 2008)** нам известно, что предки ариев прибыли на территорию Балкан. Вот как в материале «Откуда появились славяне и «индоевропейцы»? Ответ даёт ДНК-генеалогия», эти события описывает Анатолий Клёсов, проливая свет на происхождение и прародину славян: «***ДНК наших современников показывают, что самые древние корни ариев, рода R1a1, давностью 12 тысяч лет, находятся на Балканах – в Сербии, Косово, Боснии, Македонии. Через 6 тысяч лет этот род расширится на северо-восток, на Северные Карпаты, образовав праславянскую, трипольскую культуру и положив начало великому переселению народов в четвертом-третьем тысячелетии до нашей эры.»***

Дальнейшие исследования рода ариев гаплогруппы R1a1 показали, что арии появились на Европейской территории 11 200 лет назад. О чём свидетельствует точная датировка указанная в 6-й веде: *Была тайна славная деяний наших от прихода Славянских племён на Руси десять тысяч сто три года назад, либо нагло, грабя, налезли на нас тогда*. (ВК-6) Дата указана на момент написания данной веды. Веда затрагивает широкий пласт исторических событий в жизни ариев с начала их появления в Европе и заканчивает периодом Хазарского каганата и прихода к власти на Киевский престол Аскольда и Дира. Следовательно, веда писалась приблизительно во второй половине IX века, но ещё до смерти Аскольда и Дира, т.е. до 882 года. Получается, предки будущих ариев прибыли в Европу примерно 11200 лет назад. Сверка этих данных была опубликована в **Вестнике РА ДНК-генеалогии Т4. №4 за 2011 г. (С. 905)** По уточнённым данным, полученным **А.Клёсовым (2009 и 2010)**, методом расчётов принятых в ДНК-генеалогии (по результатом выборки данной гаплогруппы), арии появились в Европе около 11000 лет назад. Таким образом, показания, изложенные в ведах, не противоречат данным полученным путём исследования Y-хромосомы.

Первое Европейское продвижение ариев с Балкан на Карпаты состоялось около 6500 лет назад **(Г.Максименко, 2011)** и продлилось по разным сведениям изложенным в ведах от 300 до 500 лет. В ведах эти события описаны следующим образом:

От отца Орея идем. В подробности сказанного защита нам той. К сказанному добавим так; говорим о годах бывших до Дира. За тысяча пятисотыми годами шли парады наши до горы Карпатской. Там осели. Живя укладно роды все

правились отцами родичей. Старейшиной рода был Щеко у ирян, того обучал Паркун, либо нас всех благословлял на то учение. Так все было, жили пятьсот лет. Там (на Балканах) отчизна всем, до самого восходящего солнца. (ВК-6)

На нас погодная пора обрушилась. Русколанью обрушилась, к которой течет. Уселась на земли в той, там же осталась до поры степной варяжской и себе бранится от Дона. Такова была, время это от лета тысяча трёхсотых в Киеве отцов. Из них триста в Карпатской жизни и тысяча в Киев-граде. (ВК-16)

Как можно увидеть из вед, разные племена вышли с Балкан на Карпаты и просуществовали там по разному. Следующий исход пришёлся на тысяча трёхсотые годы по древнему славянскому календарю. Т.е. выход ариев на Карпаты соответствует периоду 6200 лет назад, что гармонично вписывается в трипольскую археологическую культуру распространённую в VI—III тыс. до н. э. **(Wikipedia "Трипольская культура»).**

Следует отметить, вопрос о причастности гаплогруппы R1a1 к данной археологической культуре и причастности к ней «индоевропейцев» вызывает споры. Если украинский исследователь трипольской культуры Института археологии НАНУ **Михайло Видейко** отстаивает причастность и преемственность между населением трипольской культуры и современными украинцами, опираясь на данные генетических экспертиз mtDNA, то директор того же института академик **Пётр Толочко** выражает противоположное мнение, считая данный вопрос не имеющим в современной исторической науке весомых доводов. Примерно таких же взглядов придерживается и доктор исторических наук, профессор, заведующий отделом археологии каменного века Института археологии НАНУ **Леонид Зализняк** утверждающий, что трипольская версия происхождения украинцев является типичным примером исторического мифотворчества, поскольку противоречит научным фактам и якобы порождена чувством искреннего патриотизма и любительства в совокупности с постколониальным комплексом неполноценности.
Однако следует отметить, что в материале Л. Зализняка «О трипольцах, семитах и нардепах – трипольеведах» он отмечает:

Было бы неправильно полностью отрицать роль трипольцев в генезисе украинцев. Как и иные древние народы Украины (скифы, сарматы, готы, фракийцы, балты и т.д.), трипольцы, но в определенной мере, были их предками. По нашему мнению, некоторые элементы традиционной культуры, имеющие ближневосточное происхождение, попали в украинский этнокультурный комплекс как наследие трипольцев. К ним, в частности, относятся реликты культов священного быка, небесного змея и т.д. в украинском фольклоре. Эти же истоки имеет архаическая лексика ближневосточного происхождения в индоевропейских языках, в том числе в украинском, о чем в последнее время пишет Ю.Масенкис. Элементы культур не только трипольцев, но и многих древних народов Украины, стали органическими составными неповторимого украинского этнокультурного комплекса, который, по моему мнению, сложился в V—VII ст., то есть в раннем средневековье. Именно

тогда формировалась этнокультура большинства больших народов средней полосы Европы: французов, англичан, немцев, сербов, хорватов, чехов, словаков, поляков и др. Следовательно, украинцы не лучше, но и не хуже иных народов Европы. Их этногенез — это объективный процесс, обусловленный универсальными законами создания этнокартины континента.

Споры о причастности украинцев к трипольской культуре ведутся постоянно и своего решения не находят даже в рамках одного института. При этом сторонники отрицающие их причастность к данной культуре, руководствуются не столько научно обоснованными аргументами, сколько теми же эмоциями в которых обвиняют своих оппонентов.

Российская Академия ДНК-генеалогии, исследовав данный вопрос и опираясь на результаты протестированной мужской части (Y-DNA) населения Украины (гаплотипы гаплогруппы R1a1) и других славянских народов данной гаплогруппы убедительно показала, что именно данная гаплогруппа, которую имеет большинство жителей Украины, составляет 44% всего населения страны **(«Russian Joumal of Genetics» Т.40 №3, с. 326).** Русские и белорусы в своих государственных образованиях составляют примерно одинаковый – 52% контингент населения, являющийся значительно преобладающим в данных странах. Исследования Российской Академии ДНК-генеалогии при этом показали, что продвижение данной гаплогруппы шло по направлению от Балкан к Днепру с дальнейшим расселением по Русской равнине 4800 лет назад и этому событию соответствуют как ранний так и поздний период трипольской культуры. (А.Клёсов 2008, 2009). Данное продвижение было зафиксировано и при исследовании славянских вед (Г. Максименко, 2008). Как описан исход славян-ариев с Карпат на Днепр в ведах и когда произошло это событие посвящено дальнейшее исследование.

2. Исход славян – ариев с Карпат на Днепр

Рассмотрим дальнейшее продвижение славян-ариев с Карпат на Днепр. Как и когда это происходило.

Это есть наши переборовшие силы по тем сидящие. К благу ведут. Когда была пора отцов, в ведении творили веру всем племенам, которые будут сидеть на Западе. Оттуда идут на Восток к Днепру-реке. Есть там Киев в утверждении, город который обетовали славянские роды иные. Там все оседлые огнищане требу творили Дубу и Снопу, которым является Сварог, пращур наш. (ВК-9)

Из данной выдержки мы видим, что пребывая на Западе (в Карпатах) часть славян-ариев начала своё продвижение в восточном направлении – к Днепру под руководством князя Кия. Из текста видно, что арии продвигались на Днепр уже будучи славянами по вере. Данный вопрос был исследован нами ранее в **Вестнике РА ДНК-генеалогии Т2.№5 за 2009** г. в материале «Как сочетается информация в славянских ведах с последними изысканиями в области ДНК-генеалогии? «Велесова книга» - веды славян. Ч.2 Период и место образования славянской

культуры и веры..» (Георгий Максименко). Согласно данной гипотезе славянская вера была образована родом ариев (гаплогруппа R1a1) на Балканах 7519 лет назад и славянами в тот период времени арии являлись по вере. Само понятие - «славяне» как этнос, было образовано позже, когда данную веру приняли от ариев и другие родовые племена гаплогруппы N1c и I2a. Пояснение это сделано с целью правильной идентификации данных понятий «арии» и «славяне». Это древний арийский род образовавший Славянскую веру, т.е. по родовой принадлежности данный род является ариями, а по вере - славянами. Понимание того позволяет избежать ошибок и путаницы в данных понятиях.

Из девятой веды видно, что исход с Карпат на Днепр частью племён славян-ариев был осуществлён под руководством князя Кия.

Орей отец идет перед нами. Кий ведет за Рушь, Щеко ведет племена свои. Хорев хорват своих. И земля Богранденц на то. Каковы это мы внушаемые, Богов от его деда, Хорев и Щехо у Ини. Сидим в Карпатских горах. И там будем иные города творить. Мину имеем, соплеменников Ини. И Богов своих имеем много, поэтому враги не лезут на нас … (ВК-1)

Идем к Днепру, та река течёт к морю с севера. Всех именовали непрами - припятцами, так как вожди все были там с оседлыми племенами. Пятьсот лет вече у всех там было своё. Так Богами хранились от многого. (ВК-6)

Рядом с ними Русколань. Кий уселся в Киеве. Тому сами племена подлегли. С Кием до целого всем Русь строилась. Так будит у нас иная сила, идет она с Русью. (ВК-7)

Такова была пора эта в тысяча трёхсотом году в Киеве отцов наших. Из них триста лет прожили Карпатской жизнью и тысячу лет прожили в Киев-граде, и начало всей этой жизни идет к Голуни. Там всё и происходило. (ВК-16)

Полагаю этих четырёх выдержек вполне достаточно, чтобы осмыслить данное содержание и понять, исход с Карпат шёл сразу в нескольких направлениях, одно из которых возглавил князь Кий и совершил исход с Карпат на Днепр где и основал город Киев. Календарная дата исхода указывает на 1300-й год по древнеславянскому календарю, из этого следует, что исход и основание г. Киева на Днепре был совершён 6219 лет назад. Как это сочетается с трипольской культурой связанной с неолитическими культурами Балкано-Дунайского региона, относящаяся к периоду раннего энеолита?

Триполье «А» по данным археологии датируется 7500-6500 лет назад. Это соответствует пребыванию ариев на Балканах в районе Дуная с продвижением на Карпаты. Далее, просматривается продвижение к Днепру, что соответствует среднему этапу триполья «В - С1» относящихся к периоду 6500 – 5200 лет назад. И третий, более поздний этап — (Триполье С2) относящийся к периоду 5150 – 4650 лет назад, характерный

расширением территории трипольской культуры за счёт продвижения племён на север и восток, с появлением курганных захоронений. Отмечается миграционная природа трипольцев, наряду с выдвигаемыми гипотезами исследователей (М. Видейко), отмечающими культурную и «генетическую» преемственность между населением трипольской культуры и современными украинцами. Но она подвергается жёсткой критике противниками этой гипотезы. Вероятно это связано и с тем, что **М.Видейко** не указывает дальнейший миграционный путь, а останавливается исключительно на роли украинцев в данном процессе, не показывая полноту всей картины миграционных процессов предков украинского народы гаплогруппы R1a1., тем самым политизируя исключительную роль украинцев в данном вопросе, что не соответствует действительности, т.к. половина населения Украины на самом деле к данной теме не имеет прямого отношения.

С Трипольской культурой, по исследуемому региону, в некоторой степени соприкасается «**Среднестоговская»** археологическая культура эпохи энеолита датируемая 6500-5500 лет назад и распространённая в степях между Днепром и Доном. Развилась, по мнению археологов, на базе днепро-донецкой культуры в ямную. Но это уже следующий этап исхода и продвижения славян-ариев от Днепра через Б.Кавказ к Южному Уралу.

Данная информация хорошо сочетается с проведёнными исследованиями в области ДНК-генеалогии, отмечающими по своим показателям период исхода около 6000 лет назад:

«ДНК наших современников показывают, что самые древние корни ариев, рода R1a1, давностью 12 тысяч лет, находятся на Балканах – в Сербии, Косово, Боснии, Македонии. Через 6 тысяч лет этот род расширится на северо-восток, на Северные Карпаты, образовав праславянскую, трипольскую культуру и положив начало великому переселению народов в четвертом-третьем тысячелетии до нашей эры. (**А.Клёсов, 2008**)

Углублённые исследования проведённые **Анатолием Клёсовым** в соавторстве с **Игорем Рожанским** в развитие этой темы во втором томе № 6 за октябрь 2009 г. Вестника РА ДНК-генеалогии, **«Гаплогруппа R1a: гаплотипы, генеалогические линии, история, география»,** засвидетельствовали разнообразие гаплотипов R1a на Русской равнине укладывающееся на древо с общим предком 4850±500 лет назад. Это является дополнительным свидетельством о направленности расселения данной гаплогруппы с Балкан через Карпаты и Днепр по ряду направлений, включая Ю.Урал и Русскую равнину.

3. Исход славян – ариев к озеру Ильмень и расселение по Русской равнине

По нехоженому шли к Ильмер - озеру. Там создали град Новый и там тоже пребываем. Тут Сибири первых пращуров вспомним, это роды породившие Крынь, ее и переспросим. То Дуба корень, хлеб наш, Сварог, который творит свет и есть Бог этому свету. Бог Прави – Яви и Нави. (ВК-9)

Сопоставление данных ДНК – генеалогии и других научных дисциплин, при исследовании славянских вед показывает достоверность изложенной в них информации, независимо от того, кем и когда они были написаны. Был исход славян-ариев к озеру Ильмень или не был и когда он состоялся. Раз Новгород стоит по сей день, ясно что был, другое дело когда, откуда и как всё это происходило, в этом заключается суть наших исследований.

Придерживаясь изначально заданной темы: «Исследование славянских вед «Велесовой книги» как дополнительного источника информации, с позиции последних изысканий в области ДНК-генеалогии.» продолжим изыскания в развитие и дополнение ранее проведённых исследований по дате образования Новгорода на Волхве - реке, изложенных в **Вестнике РА ДНК-генеалогии, Т. 3 №1 за 2010 г (С.78).** В этой работе удалось всесторонне изучить тему образования Новгорода. Освежим вкратце эту информацию.

Из последних исследований, проведённых **Игорем Рожанским и Анатолием Клёсовым** по гаплогруппе R1a1, с выявлением генеалогических линий гаплотипов, их истории и географии было показало, что разнообразие гаплотипов на Русской равнине укладывается на дерево гаплотипов с общим предком, который жил 4750±500 лет назад (Клёсов, 2008a; Klyosov, 2009b). А общая картина, представленная ими по завершению исследований, выглядит следующим образом:

Итак, углубляется общая картина. 10-12 тысяч лет назад предки гаплогруппы R1a1 прибыли из Азии (видимо, из Южной Сибири) в Европу, сразу же – по историческим меркам – после схода ледников. Относительно небольшое количество их потомков живут и по сей день в Европе, со шлейфом «древних»гаплотипов от Балкан до Британских островов и до Анатолии. Их археологические культуры прослеживаются на Балканах и в Карпатах до 7-8 тысяч лет назад (возможно, совместно с носителями гаплогруппы I). Это, в лингвистических терминах – «протоиндоевропейцы».

В те же времена, или около 6 тысяч лет назад носители гаплогруппы R1a1 стали активно расходиться по Европе, заселенной в то время в ее центральной, атлантической и северной части в основном гаплогруппой I и/или ее подгруппами I1 и I2, и перевалили Карпаты, образовав в итоге широкий фронт заселения

гаплогруппой R1a1 от Балтики до Кавказа. Это – ямная культура, затем полтавкинская, затем срубная культура с экспансией в андроновскую культуру по мере продвижения на восток, в Северный Казахстан, Южный Урал, Среднюю Азию. Именно потому в понятиях лингвистов 6 тысяч лет назад – это время распада праиндоевропейского языка, языка R1a1, и начало образования сатемной группы будущих индоевропейских языков…

Возвращаемся в Европу. Что-то произошло с европейскими R1a1 между 6 и 5 тысяч лет назад, и они почти полностью исчезли, не прошли бутылочное горлышко популяции. Древних европейских гаплотипов почти не осталось, и сейчас они очень редки, составляя доли процентов от популяции R1a1. Примерно 5 тысяч лет назад (по разным данным между 4800 и 5200 лет назад) носители гаплогруппы R1a1 стали возвращаться в Европу, в особенности на территории современных Германии и Польши, создав культуру шнуровой керамики, она же культура боевых топоров, она же культура одиночных могил позднего энеолита и бронзового века Средней и Восточной Европы. Это – основа будущих славян, германцев, балтов, антропологически – кордидов. Их взаимоотношения с культурой шаровых амфор (5400 – 4800 лет назад) и культурой воронковидных кубков (6000 – 4700 лет назад) остаются неясными. Либо эти культуры были культурами носителей гаплогрупп I, либо это R1a1, не прошедшие раньше бутылочное горлышко популяции и почти исчезнувшие из Европы того времени, либо это были культуры смешанных родов I и R1a1 – ответа на этот вопрос пока нет. Но ясно, что возврат R1a1 в Европу был возвратом туда праиндоевропейского языка около 5 тысяч лет назад, в виде уже видоизмененных диалектов и вариантов. Это все – продолжение динамики «распада индоевропейских языков». Видимо, останки представителей шнуровой культуры с гаплогруппой R1a1 в Германии, датированные 4600 лет назад (Haak et al, 2008) – это та самая волна. Их гаплотипы – те же самые, гаплотипы Русской равнины, центральной части Евразии.

Итак, возвращающиеся в Европу R1a1 приносили туда свои гаплотипы с востока, с Русской равнины. Именно поэтому общий предок современных европейских гаплотипов R1a1 – это центральный евразийский предок, Русская равнина. Так произошла интеграция гаплотипов Европы, от Атлантики до Восточной Европы, и Евразии. У подавляющего количества R1a1 на этих территориях – один общий предок, который жил примерно 4800 лет назад. А его дочерние ветви, образовавшиеся при передвижениях основателей ветвей, датируются в основном временами между 2200 и 3200 лет назад, и до 4100 лет назад.

В начале и до середине новой эры, в эпоху Великого переселения народов, произошла очередная миграция носителей гаплогруппы R1a1 с востока Восточной Европы и, возможно, Средней Азии, опять на запад, в Европу. Это были булгары, мадьяры, скифы, сарматы, асы, и много других народностей. Они в очередной раз заселили Европу от Италии и Центральной части Европы до Скандинавии. Тому

свидетельством, например, «молодая» скандинавская ветвь R1a1, прибывшая в Скандинавию во 2-м веке нашей эры плюс-минус четыре века (Таблица 6). Но это было при одиночных «основателях» будущих линий. В большинстве случаев мигранты R1a1 «приносили» гаплотипы со структурой мутаций, опять указывающих на времена общих предков примерно 4500-4700 лет назад. Гаплотипы R1a1 с этой датировкой распространены во всей Европе, и если не разделять их на ветви, как было сделано в настоящей работе, то все они сходятся к тому же базовому гаплотипу Русской равнины с датировкой примерно 4500 лет назад.

Видимо, поэтому значимых субкладов R1a1 практически не обнаружено, кроме тех нескольких древних (R1a1a, R1a1b и R1a1c), расходящихся от общего предка не менее 10 тысяч лет назад. Поскольку более 95% современных носителей гаплогруппы R1a1 произошли от относительно недавнего предка, который жил примерно 4800 лет назад, то и субклады будут относиться к этому относительно небольшому отрезку времени.

Это и есть история гаплогруппы R1a1, история, изобилующая «бутылочными горлышками» популяции, и показывающая, что европейские носители этой гаплогруппы действительно относительно недавние родственники.

Данная информация даёт общее представление об исследуемом периоде и хорошо показывает, что освоение гаплогруппой R1a1 Русской равнины приходится на период 4750±500 лет назад. Эта информация помогла нам понять, насколько верны изыскания по образованию Новгорода на Волхве-реке в разных первоисточниках. Наиболее выпадающими из ряда исследуемых первоисточников, обладающими сведениями о появлении славян-ариев у оз. Ильмень, являются Русские летописи, датирующие это событие периодом 1150 лет назад. Так например, в Повести Временных Лет (ПВЛ) ограничиваются выражением «*Спустя много времени…*». ПВЛ не только не даёт ответа, но ангажирует этот вопрос сокрытием периода образования Киева на Днепре. Сначала упоминается появление полян на Днепре, но о Киеве не упоминается ни слова, а вот при упоминании древлян автор упоминает возведение славянами – древлянами Новгорода: «*Те же славяне, которые сели около озера Ильменя, назывались своим именем - славянами, и построили город, и назвали его Новгородом.*» Очевидно стремление обойти этот вопрос стороной и нежелание показать истинную дату образования Киева и Новгорода. Это так же хорошо видно из описания пребывания апостола Андрея на Днепре и на Волхве - реке. Авторам ПВЛ надо было показать ведущую роль христианства при «творении Руси Великой». С чем они хорошо справились опустив наличие Киева вообще, показав, что он будет стоять в будущем, а по Новгороду пройтись двойным смысловым значением: «*И пришел к славянам, где нынче стоит Новгород, и увидел живущих там людей - каков их обычай и как моются и хлещутся, и удивился им.*»

Перед этим упоминалось, что пришли славяне и построили Новгород, а в связи с появлением там апостола Андрея говориться о встрече со славянами (древлянами) там «*где нынче стоит Новгород*». Т.е. вроде как в 1 веке древляне уже сидят на оз. Ильмень, а Новгорода и не существует вовсе. Ответа на вопрос: когда был основан Новгород, в ПВЛ –нет. Так же как и нет ответа на вопрос: когда был основан Киев.

Все числа и датировки ПВЛ начинаются с 6360 (852) года, с периода царствования Михаила в Царьграде:
«В год 6360 (852), индикта 15, когда начал царствовать Михаил, стала прозываться Русская земля. Узнали мы об этом потому, что при этом царе приходила Русь на Царьград, как пишется об этом в летописании греческом. Вот почему с этой поры начнем и числа положим.»

Из сказанного видно, что не Кий приходил в Царьград, а Русь приходила к Михаилу, а Кий на самом деле жил и правил в Киеве за 5060 лет до этого события.
Вот эта информация отсутствует в ПВЛ, хотя должна была быть известна авторам ПВЛ. Они сочли необходимым данную дату перенести к событиям 852 года. Но и тут не обошлось без конфуза. По некоторым энциклопедическим данным ***"Новгород на Волхве реке один из древнейших русских городов - впервые упоминается в 859 г."*** **Т**ут ПВЛ вступает в противоречие. Если Новгород один из древнейших русских городов, то сличая его с датами указанными в ПВЛ, видно, что 852 году Киев уже стоял, т.к. Кий по летописи возвращался в этом году в город Киев. Следовательно Киев был возведён раньше Новгорода. Это противоречие устранить в ПВЛ так и не удалось. Несколько справедливей обстоят дела в более древних летописных сводах. В **Древнейшем Киевском своде 1039 года в редакции 1037 года** при описании начала земли Русской, **г**ода связанные с образованием Киева и Новгорода не указаны, но видна подмена в более поздней ПВЛ, где говорится, что не при жизни Кия, а **«*По прошествии времени, после смерти братьев этих…*»** стали притесняться поляне и древляне. Позже в ПВЛ уже сказано, что поляне притеснялись и обижались древлянами, т.е. Новгородцами. Всё сведено к внутриродовой междоусобице. Обратимся к **Новгородскому своду 1050 года с продолжениями до 1079 года:**

«Начало земли Русской.
Было три брата … и были ратны с Древлянами и с Угличами.
В эти же времена Новгородские люди, именуемые Словене, и Кривитчи, и Меря, и Чудь дань давали Варягам … и ежели те были у них, насилие творили Словенам и Кривичам и Мери и Чуди. И восстали Словене и Кривичи и Меря и Чудь против Варягов, и изгнали их за море, и начали

владеть сами собой. Словене свою волость имели; и поставили город и нарекли его Новгород...»

Из Новгородского свода явствует, что ни поляне, ни древляне не притесняли друг – друга, а имели ратные отношения друг с другом. Притеснение древлян шло от варягов. Из Новгородской летописи следует, что начало земли Русской и период образования за Киевом. Но дата образования Новгорода в нём так же умалчивается. Не дают ответа и 1-й Печёрский свод, начальный свод 1903 г., и Новгородский свод XI в. В летописях ответа просто нет.

Всё, что удалось выяснить в летописях по Новгороду и Киеву, носит крайне неопределённый характер. Единственное, что более-менее не противоречиво, это то, что Новгород был основан позже Киева. Но насколько позже - по летописям выяснить не удаётся. Самая глубокая привязка может продвинуть нас только к I веку, если сориентироваться по пребыванию апостола Павла на этих землях. Но и в этой летописи имеется неточность, которую без знания даты образования Киева и Новгорода заметить невозможно. Кий (и его братья) основавший Киев не мог при жизни общаться с новгородцами, т.к. Новгорода тогда ещё не существовало и он был образован спустя тысячелетие после смерти Кия, когда его потомки начали расселение по Русской равнине. Из ДНК Y-хромосомы мы знаем, что род гаплогруппы R1a1 славян ариев продвинулся к Днепру около 6000 лет назад, а расселение по Русской равнине началось спустя более чем тысячелетие, т.е. 4800 -5000 лет назад по уточнённым данным (**И.Рожанский, 2011**). Следовательно, князь Кий никоем образом не мог пересечься с новгородцами, которых в природе ещё не существовало. Выйти из этой «тупиковой» ситуации можно было только одним путём, выдвижением гипотезы северной прародины славян и первичности образования Новгорода до образования Киева. Так и появилась на свет ложная «норманнская гипотеза» северной прародины, со ссылкой на индийские веды, где действительно отмечается о приходе ариев с севера (с Ю.Урала). Но гипотеза эта не выдерживала элементарной критики. В конце – концов учённые от неё отказались, изрядно поубавив её сторонников.

Исключение среди русских летописей составляет, пожалуй, только один первоисточник, проливающий свет на дату появления славян-ариев у озера Ильмень, но подлинность которого постоянно подвергается сомнению – **«Сказание о Словене и Русе и городе Словенске»** из Хронографа 1679 года (Опубликована в Полном собрании русских летописей. Т.31. Л., 1977). Эта летопись также подверглась тщательному изучению и была исследована на предмет соответствия изложенной в ней информации в Вестнике Академии ДНК-генеалогии Т.3 № 11 за 2010 г. **(Г.Максименко, Стр. 1943).** Результаты исследований показали достоверность изложенной в ней информации и полное соответствие с информацией изложенной в славянских ведах. Исследования дали

следующие сравнительные результаты.

В ВК-3 сказано:

Это будет князю Славену собрат по ариям - Скивь. Это было во времена событий великих на востоке. Ильмерцы решили:

- Идем от земли Ильмерской.
Как рассказываем, так и ищите. Старшего сына своего Славен оставил старшим Ильмерии и все ильмерцы пошли на север. Там свой город Славен утвердил. Это брат его, скуфе, у моря будет и сам в старые места свои ведёт. По ним сидеть будет внучек Киже - владелец был степью южной. Коров много было у него. Там он и есть.
От того будет время великое в борьбе за Сет. Зуры те распространялись по обе стороны от Дании, до гор Русских и до хопров Карпатских. На Карпатах решили утвердить круг, который будет принимать от имени всех общее решение. Также врагам отпор творили все разом они. От старейшин в родах отказаться решили. Приняли решение Вече созывать единое, сотворя земли наши новые.
Так состояли земли те в объединении пятьсот лет и слово за слово, отворилась между русичами усобица. Враждуя по разным причинам, вновь силу свою утратили, которая имелась между собой. Возрождение свое утратили. Этим воспользовались враги и навалились на отцов наших на юге. Это стряслось с Киевской землей на побережье морском. Киевляне в степи отходят вновь на север. Поссорились там с фряженцами, от того идет помощь врагам. Скуфией это оценится и Скуфь Киевская сразу объединится в единую силу.

Сравним эту информацию с образованием Словенска на Волхве – реке по **Хронографу 1679 года** «Сказание о Словене и Русе и городе Словенске»:

И в лето от сотворения света 3099 Словен и Рус с роды своими отлучишася от Ексинопонта, и идоша от роду своего и от братия своея, и хождаху по странам вселенныя, яко острокрилаты орли прелетаху сквозе пустыня многи, идуще себе на вселение места благопотребна. И во многих местех почиваху, мечтующе, но нигде же тогда обретше все-ления по сердцу своему. 14 лет пустыя страны обхождаху, дондеже дошедше езера некое-го велика, Моикса зовомаго, последи же от Словена Илмер проименовася во имя сестры их Илмеры. И тогда волхвование повеле им быти населником места оного.

И старейший, Словен, с родом своим и со всеми, иже под рукою его, седе на реце, зовомей тогда Мутная, последи ж Волхов проименовася во имя старейшаго сына Словенова, Волхова зовома. Начало Словенску граду, иже последи Новъград Великий проименовася. И поставиша град, и именоваша его по имени князя своего Словенеск Великий, той же ныне Новъград, от устия великаго езера Илмеря вниз по велицей реце, проименованием Волхов, полтора поприща. И от того времени новопришельцы скифстии начаху именоватися словяне, и реку некую, во Илмер впадшую, прозваша во имя жены Словеновы Шелони. Во имя же меньшаго сына Словенова Волховца преименова оборотню протоку, иж течет из великие реки

Волхова и паки обращается в него. Больший же сын оного князя Словена Волхв бесоугодник и чародей и лют в людех тогда бысть, и бесовскими ухищреньми мечты творя многи, и преобразуяся во образ лютаго зверя коркодила, и залегаше в той реце Волхове путь водный, и не поклоняющих же ся ему овых пожираше, овых же испроверзая и утопляя. Сего же ради людие, тогда невегласи, сущим богом окаяннаго того нарицая и Грома его, или Перуна, рекоша, руским бо языком гром перун именуется. Постави же он, окаянный чародей, нощных ради мечтаний и собирания бесовскаго градок мал на месте некоем, зовомо Перыня, иде же и кумир Перунов стояше. И баснословят о сем волхве невегласи, глаголюще, в боги сел окаяннаго претворяюще. Наше же християнское истинное слово с неложным испытанием многоиспытне извести о сем окаяннем чародеи и Волхове, яко зле разбиен бысть и удавлен от бесов в реце Волхове и мечтаньми бесовскими окаянное тело несено бысть вверх по оной реце Волхову и изверженo на брег противу волховнаго его градка, иде же ныне зовется Перыня. И со многим плачем тут от неверных погребен бысть окаянный с великою тризною поганскою, и могилу ссыпаша над ним велми высоку, яко же обычай есть поганым. И по трех убо днех окаяннаго того тризнища проседеся земля и пожре мерзкое тело коркодилово, и могила его просыпася с ним купно во дно адово, иже и доныне, яко ж поведают, знак ямы тоя не наполнися. Другий же сын Словенов малый Волховец живяше со отцем своим во граде своем великом Словенцы. И родися Волховцу сын Жилотуг, и протока проименовася во имя его Жилотуг, в ней же той утопе еще детеск.

Другий же брат Словенов Рус вселися на месте некоем разстояннем Словенска Великаго, яко стадий 50 у соленого студенца, и созда град между двема рекама, и нарече его во имя свое Руса, иж и доныне именуется Руса Старая. Реку же ту сущую едину прозва во имя жены своея Порусии, другую ж реку имянова во имя дщери своея Полиста. И инии градки многи Словен и Рус поставиша. И от того времени по имяном князей своих и градов их начахуся звати людие сии словяне и руси. От создания мира до потопа лет 2242, а от потопа до разделения язык 530 лет, а от разделения язык до начала создания Словенска Великаго, иже ныне Великий Новъград, 327 лет. И всех лет от сотворения света до начала словенскаго 3099 лет. Словен же и Рус живяху между собою в любви велице, и княжиша тамо, и завладеша многими странами тамошних краев. Такоже по них сынове их и внуцы княжаху по коленом своим и налезоша себе славы вечные и богатства многа мечем своим и луком. Обладаша же и северными странами, и по всему Поморию, даже и до предел Ледовитого моря, и окрест Желтовидных вод, и по великим рекам Печере и Выми, и за высокими и непроходимыми каменными горами во стране, рекома Скир, по велицей реце Обве, и до устия Беловодныя реки, ея же вода бела, яко млеко. Тамо бо берущи дорогою скорою звери, рекомаго дынка, сиречь соболь. Хождаху ж и на Египетъския страны воеваху, и многое храбрьство показующе во еллинских и варварских странах, велий страх от сих тогда належаше.

В некоторых источниках информации, таких как летопись Холопьего монастыря на реке Мологе, хронограф академика **М. Н. Тихомирова**, “Записки о Московии” **С. Герберштейна**, записанные многими этнографами, так же отмечается, что

первая столица Руси был – город Словенск, основанный в 2409 г. до н.э. или по старому календарю в3099 г. от сотворения мира., т.е. 4419 лет назад.

Из сказанного в славянских ведах ВК и Хронографе 1679 года видно, что первыми на Волхве реке, в районе оз. Ильмень появились ильмерцы с князем Славеном (Словеном), который образовал город Славенск (Словенск). Вычислить дату их появления на севере (северо-западе) Русской равнины и основания Славенска труда не составило. 7518-3099=4419 лет назад. Т.е. ильмерская ветвь рода ариев R1a1 первая добралась до оз. Ильмень и обосновалась там ещё до появления там второй славяно-арийской волны, которая является основателями Новгорода на Волхве - реке. Из хронографа 1679 г. явствует:

… Первое запустение Словенску. А великий Словенеск и Руса опустеша до конца на многия лета, яко и дивиим зверем обитати и плодитися в них. По некоих же временех па-ки приидоша з Дунава словяне и подъяшаскифи болгар с собою немало, и начаша паки грады оны Словенеск и Русу населяти. И приидоша же на них угры белыя, и повоеваша их до конца, и грады их раскопаша, и положиша Словенскую землю в конечное запустение.

Далее описания событий в славянских ведах и хронографе расходятся. Веды говорят о том, что Новгород был основан в период второй волны появления славян-ариев у ильмерцев, а Хронограф 1679 года утверждает, что во время третьей волны, т.е. за несколько десятилетий до крещения Руси, в период правления Гостомысла (умер около 860 г.) Если мы обратимся к археологии по данному вопросу, то найдём в ней подтверждение изложенной в ведах и Хронографе информации. Археология Новгорода была проанализирована в материале Вестника Российской Академии ДНК-генеалогии, т. 3 №1 за январь 2010 г. «Как сочетается информация в славянских ведах с последними изысканиями в области ДНК-генеалогии? «Велесова книга» - веды славян. Часть четвёртая. Период образования Новгорода на Волхве - реке.» **(Г.Максименко)**

Раскопки на Рюриковом городище произведённые археологом **Н. И. Полянским** показали наличие трёх культурных слоев. На этом городище, расположенном у Новгорода, обнаружены два более ранних слоя, заслуживающие внимания. Обнаружены остатки неолитической стоянки II—III тыс. до н. э. (4000-5000 лет назад) и поселение раннего железного века, относящееся к I тыс. до н. э. (3000 лет назад). Датировка слоёв этого городища, а их всего три, показала следующие периоды:
1-й 4000-5000 лет назад (неолит);
2-й 3000 лет назад (ранний железный век);
3-й 1200 -1100 лет назад (средневековый период).

Первый период соответствует пребыванию племени ильмер из рода ариев на оз. Ильмень и основания там Ильмерии, а 4419 лет назад - города Словенска - по данным Хронографа, либо Славенска - по данным славянских вед ВК. Что же касается образования на его месте Новгорода на втором этапе развития (по данным

славянских вед) либо на третьем этапе (по данным Хронографа), эту тему пока отложим на время, т.к. исследуется период образования Словенска (Славенска), но не Новгорода на Волхве реке. В этом году начались новые раскопки Словенска (Славенска) на Волхве- реке, получено необходимое финансирование и поддержка правительства, премьер-министр Владимир Путин лично побывал на месте раскопок и засвидетельствовал финансовую поддержку данной экспедиции. Но промежуточные сведения и отчёты пока не доступны. Поэтому руководствоваться приходится данными предыдущих экспедиций.

Данные ДНК- генеалогии и проведённые исследования **Игорем Рожанским и Анатолием Клёсовым** по гаплогруппе R1a1, с выявлением генеалогических линий гаплотипов показали, что разнообразие гаплотипов на Русской равнине укладывается на дерево гаплотипов с общим предком, который жил 4750±500 лет назад (Клёсов, 2008a; Klyosov, 2009b). А общая картина, представленная ими по завершению исследований, выглядит следующим образом:

В большинстве случаев мигранты R1a1 «приносили» гаплотипы со структурой мутаций, опять указывающих на времена общих предков примерно 4500-4700 лет назад. Гаплотипы R1a1 с этой датировкой распространены во всей Европе, и если не разделять их на ветви, как было сделано в настоящей работе, то все они сходятся к тому же базовому гаплотипу Русской равнины с датировкой примерно 4500 лет

из чего можно сделать вывод, что их дальний предок мог начать расселение по Русской равнине примерно 4500 лет назад и мог вполне достигнуть оз. Ильмень. Так выглядит последний уровень понимания археологии с позиций ДНК-генеалогии и исследованных первоисточников по данной тематике.

Исследовав информацию, изложенную в ведах «Велесовой книге» (ВК), первое, на что было обращено внимание, изыскиваемая тема по Новгороду содержится в ВК -3,5,6,9 против информации по Киеву изложенной в ВК - 1,6,7,11,16,24. Зная историю вед, это даёт некоторое представление о том, что в первых двух ведах Новгород ещё не существовал в изложении славянской истории, т.е. образован был позже Киева, упоминаемого в самой древней веде.

Из содержания вед было выявлено, что славяне освоили земли ильмерские после того, как уже был утверждён город Киев. И имеется упоминание о князе Славене в этой веде ещё раз: «*род славень передвигался до земли иной, где солнце в ночи спит. Коню травы много. Луга тучные. Речки рыбой полны. Конь никогда и не умрет, годь была еще на зеленом крае. Немного упредили отцов, идущих Ра, река есть велика, отделяет нас от иных людей. Течет до моря Фасисте.*»

Т.е. подтверждается факт передвижения словеней на север к оз. Ильмень от Азовского моря. В этом случае следует отметить и тот факт, что сами ильмеры к этому времени уже пребывали на оз. Ильмер (Ильмень) названному так по наименованию племени.

О том, что они (ильмеры) ушли туда ранее славян, мы увидим из других вед. Пока же отметим, что в данной веде, несмотря на то, что период образования Новгорода не указан, видно, что образован был позднее Киева. На сколько прзднее - не указано в данной веде. Нам не остаётся ничего другого, как только обратиться к более поздним ведам.

*… был народ исчезнувший, ильмерский. Сто корней от восстановления народ наш, так как придет раньше нас к Русской земле. Селились среди ильмерцев, те ведь братья наши, нам, подобие ведь еще, коли были вооружены, нас охраняли, от зла вещи имели, такое же режущее, о вещах «Я» какой и есть. Еще с огня решения не имелось бы…, избирали князя от полюдья до полюдья. Так жили мы же сами, им помощь даем. Таково былое. Зеле либо знали, творили сосуды и запекали в печах. Ведь были гончары доблестные, землепашцы. Тоже скотину водили, понимая и это. Такие отцы наши ведь, придет род злой на них... было понуждение отскочить к Лясию, там живем ловлей. Рыбалим. О былом могли от страсти говорить уклончиво. Так о былом ведём единую тему. Начали города ставить, огнища повсюду раскладывать, по другой теме был холод велик. (*ВК-5)

Из данной веды можно сделать вывод, речь идёт о зарождении ильмер от общего предка на Балканах. В таком случае уже в то время земля именовалась как Русская, о чём свидетельствуют и некоторые другие веды, а Русская равнина была так поименована по Русской земле после начала её освоения 5000-4800 лет назад. Новгорода ещё не видим, но имеем дополнительную информацию, свидетельствующую о прямых родственных связях ильмерцев со славянами в сто корней от рода совместного первопредка, что имеет существенное значение при упоминании отца Ория, в данной веде, жившего 6200 лет назад.

Там пришел варяг. Берет таясь. Она с иного великая Русь, либо творится от полуночи, за это же не имеем может … в лесах ильмерских утвердиться. Там есть дом Киев, которому дана часть малая, там уселись.
… Пятьсот лет вече все правились всеми. Так Богами хранились от многого. Говорили с язенцами, ильмеров было много там оседлыми огнищанами. Так либо скотичи все - венденцы в степях. (ВК6)

Как видим, Русь творилась по ведам с севера, но под севером подразумевался Киев, расположенный севернее от Балкан, а никак не Новгород.

В поре той до гор Карпатских вместе. Там решение во главе пяти князей. Города и села огонь ест. Ветра великие. Потеснены были.
По нехоженному шли до Ильмер-озера. Там создали град Новый. Там пребываем. Тут северги первых пращуров молим, это роды, породившие Крынь, ее переспросим. То Дуба корень, хлеб наш, Сварог, который творит и свет - Бог есть свету. Бог Прави – Яви - Нави, это есть наши, переборовшие силы по тем сидящие. Благу ведут, когда пора отцов, в ведении творили всем … (ВК9)

Если я правильно трактую эти две веды, то можно сделать первую попытку определения времени появления словеней на оз. Ильмень и возведения там Новгорода. Дата исхода славян-ариев с Карпат известна из предыдущих исследований по Киеву - 6217 лет назад. Продвижение к оз. Ильмер (Ильмень) и образование Словенска состоялось 4419 лет назад и заняло, по предварительным данным, около 500 лет, - что вполне вписывается в период освоения Русской равнины 5000-4800 лет назад. Археология показывает второй период пребывания их в интервале одного тысячелетия. Получается, что Словенск образовали арии – ильмеры 4419 лет назад, а Новгород был основан около 3400 лет назад, при второй волне появления там славян – ариев, ещё до появления на Руси христианства. Основание Руси приписанное христианскими летописями Рюрику в 862 году и его потомкам, явление надуманное и политизированное. Русь была образована родом ариев намного ранее указанных в христианских летописях сроков.

Вся правящая церковная верхушка того времени состояла из византийцев. В силу своего менталитета и политических устремлений церковь поступить иначе не могла. Во-первых, свежи были ещё в памяти ранее колонизационные амбиции южных территорий Руси вдоль Черноморского побережья Кавказа и Восточного Причерноморья, которые они потеряли благодаря освободительным войнам славян, во-вторых было велико желание вернуть себе эти южные территории Руси. Истории известно, что ими было собрано и вывезено в Византию множество славянских рукописей для изучения, которые в результате были уничтожены – сгорели.

От времени до времени сказано всё. Рождаются многие среди нас. Своих же сисек, поэтому до самой смерти они свои. Если назад забежать, мы такие же как ильмерцы, которые нас охраняли не единожды. С нами соединялись. Кровь свою давали и нам. Дривь была на Руси, хазары, сегодня свои варяги. Мы же сами русичи, никогда не были варягами. (ВК-9)

Давайте посмотрим к чёму сегодня подводит нас археология по распространению ареала славян:

Расселение племен трипольской культуры в III тысячелетии до н. э., которые жили в огромных поселках и имели развитое для своего земледелие и скотоводство. На рубеже III – II тыс. до н. э. у этих племен наблюдается переход

от неолитических орудий к бронзе и началась борьба за стада и пастбища.

Представители археологической культуры «шнуровой керамики и боевых топоров» расселились на огромной территории от Рейна до Днепра. Их расселение закончилось в XV веке до нашей эры. Если признать прародиной славян широкую полосу Центральной и Восточной Европы, то на востоке эта территория ограничивалась верховьями Днестра,. Южного Буга, Припятью и средним Днепром.

Описанный выше ареал обитания совпадает с границами распространения тшинецко-комаровской археологической культуры (XV – XII вв. до н. э.). Заслуга этой культуры заключается в переходе в начале I тысячелетия до нашей эры к железным орудиям труда.

Чернолесная археологическая культура (X – VII вв. до н. э.) по своей хронологии совпадает с первым взлетом славянского мира. В VIII веке до нашей эры «чернолесцы» вступили в контакт с киммерийцами, в VII веке до нашей эры со скифами.

Милоградская и подольская археологические культуры (геродотовы скифы-пахари или сколоты) являлись как бы восточной группировкой славянского мира, попавшей под сильное культурное влияние скифской цивилизации (V – III вв. до н. э.).

4. Исход славян – ариев за Урал. Расселение по Сибири

Выставляем на солнце молоко, наше на травах окисливается. Поэтому наше отличимое от других. На их жалуются, что не травное. О том же говорит и пора нашей старости. Даем молоку осуриться и отопьем трижды его во Славу Богам и так поступаем пятикратно за день. То наша старая традиция, которая Богам есть должная потребность. Треба та будет связью между нами и Богами. Ни Мару, ни Мороку славить не смеем. Те Дивы ведь наши несчастья. Наш Дид есть в ее Сибири. (ВК-9)

Выше были рассмотрены пути расселения славян-ариев с Балкан на Карпаты, Днепр и расселение по Русской равнине. Но веда не ограничивается в описании только Европейской территории и указывает на переход части племён из Европы в Азию и отмечает пребывание в Сибири. Что нам известно по данному вопросу в совокупности с информацией описанной в других ведах ВК?

В одном из фрагментов **ВК–24** сказано:

Лебедень сидит у града Киева, на горе, который разумен и умён. Правит оды хорян. Самостоятельно терзает илиньское писание. Арабов правит в задоре, так как чин имеет:

- Это которые оды вендов, палка своя от врагов и "Камо" булгары не переносили от новых земель, имеем род свой да ищем, слава ходит что притоки Оби свои были. Там обитали. В годе пора течет и сила людская. Тужатся при написании в порче, и так это земля наша остается от края до края как Русколань в бытность. Земля эта данная нам Богом определена от Евразии. Так ту держим себе.

Веды повествуют о своих землях и территориях. По ранее проводимым исследованиям **(Вестник РА ДНК-генеалогии Т2 №2 за 2009 г. С 200)** было отмечено, что с Днепра часть славян-ариев гаплогруппы R1a1 продвинулась 5200 лет назад на Б.Кавказ и далее с Б.Кавказа перевалила в районе Ю.Урала на Азиатскую территорию. Таким образом, в древние времена гаплогруппа R1a1 оказалась не только на Ю.Урале но и на территории Алтая по притокам Оби: Иртыш (с его притоками ведущими к Южному и среднему Уралу, вплоть до Алтая), Томь, Бия, Каменка, Катунь. О чём собственно и говорится в приведённом фрагменте ВК.

Знакомясь с данными археологии этих районов, стало ясно, что они добрались до этих притоков и осели по ним от Омска до Томска (от Оми до Томи) как повествуют веды в другом месте. Я посетил в этом году Горный Алтай, исследовав археологические объекты на месте. Основное внимание привлекла информация о Каракольской культуре бронзового века (III-II тыс. до н. э.). В ней просматривается связь с носителями Афанасьевской и Майкопской культур, которые, по убеждению, имеют прямое отношение к гаплогруппе R1a1. На месте слияния Бийки с Катунью так же просматривается место древней стоянки и курганные захоронения (местные жители называют их Ороктойской группой захоронений).

Каракольская культура позволяет проследить путь ариев от Б.Кавказа, через Ю.Урал к Горному Алтаю, а курганная группа на р. Бийке свидетельствует об идентичности курганных захоронений на Алтае и Б.Кавказе. И там и там, на территориях, где обитали арии, встречаются захоронения в каменных коробах с уложением тела в позе эмбриона, после чего обкладывался каменный круг и насыпался курган. Всё это помогает предположить и определить движение ариев с Балкан в Азию. Выглядит это примерно так: 6700-6500 лет назад вход ариев с Балкан на Карпаты, 6200 – на Днепр, 5200 – на Б.Кавказ, 5000 – 4800 движение за Урал и расселение по Русской равнине. За Уралом продвижение по территории современного Казахстана (район оз. Балхаша и его предгорий), Алтай, Китай (Туримский район), 3600-3800 уход с Ю.Урала и Б.Кавказа в Индию и Иран.

Характерными чертами захоронений Каракольской культуры являются прямоугольная ограда - кладбище, каменные ящики и полихромные рисунки на плитах ящиков. В этот период состоялся переход от присваивающих форм хозяйства - охоты, собирательства и рыболовства - к производящим формам: земледелию и скотоводству. С этого периода древние алтайцы стали заниматься строительством мелиоративных сооружений и возделыванием пашен, выращиванием таких культур, как просо, ячмень, рожь и других. Следовательно,

племена принесшие культуру земледелия пришли не на пустое место, и данный район был заселён местными племенами. Домашние стада, состоящие из овец, коз, коров, лошадей, летом стали отгоняться в альпийские луга, а к зиме возвращаться в долины. По этой причине в Горах Алтая находится мало племенных стоянок и их количество увеличивается по мере спуска в долины и предгорья Алтая. Курганные захоронения в горах, вдоль рек носят малочисленных характер и увеличивается ближе к низовьям притоков рек. К курганам скифского (арийского) типа относящимся к периоду бронзы археологи Горного Алтая относят памятники объединенные в пазырыкскую археологическую культуру скифского типа: Пазырыкские, Башадарские, Туектинские, Шибинские, Уландрыкские, Укокские курганы, а также тысячи других. Датируют их 1-м тысячелетием до н.э., т.е. определяют их возраст около 3000 лет.

Обратимся к расчётам ДНК-генеалогии проведённым по нашей просьбе **Игорем Рожанским** и посмотрим насколько отличаются большинство алтайских R1a1 по гаплотипам от Русской равнины. В результате были получены следующие данные:

*Если имеется в виду базовый 9-маркерный гаплотип алтайцев из статьи **Андерхилла**, то, похоже, его можно восстановить в более протяженном формате, если привлечь данные еще из 2-х статей, что использовали ту же самую полевую выборку. Вот он в минимальном формате*

13 26 16 11 X X X 12 11 14 11 31 (+ DYS461=11)

Он же из статьи M. Derenko et al. "Contrasting patterns of Y-chromosome variation in South Siberian populations from Baikal and Altai-Sayan regions" Hum Genet (2006) 118: 591–604

13 26 16 11 11 17 X X 11 14 11 31 X X X X X X 14 X X X X X X X X X X X X X X X X 11

*Наконец, в недавней статье **Животовского** и др. те же данные выложены в "полноценном" формате YFiler:*

13 26 16 11 11 17 X X 11 14 11 31 15 X X X X X 14 19 X X X X X X 10 X X 15 X X X X X X 11 (+ DYS635=23)

*Общий предок линии из статьи **Деренко** попадает примерно на 3000 лет назад, но 19-маркерный базовый гаплотип (YFiler + DYS388=12 + DYS461=11) не дает оснований считать, что он относится к древним южносибирским R1a1. К этой ветви в выборке Деренко относится 11-13 гаплотипов из 135-ти, собранных среди народов Сибири. Остальные сходятся к базовому гаплотипу центральной евразийской ветви.*

P.S. В процитированной чуть выше статье "Decreased Rate of Evolution in Y Chromosome STR Loci of Increased Size of the Repeat Unit" приведены 13 гаплотипов,

что сходятся к 17-маркерному базовому - 12 алтайских и 1 из Тувы. Если вырезать из них фрагменты в том формате, что выписан в статье Андерхилла, то эти списки в точности совпадут друг с другом. Почти наверняка, это одни и те же гаплотипы, а, значит, можно рассчитать время до общего предка этой генеалогической линии и европейских R1a1 более аккуратно.

При счете по 17-ти маркерам время до общего предка 13-ти гаплотипов оказывается меньше, чем ранее оценивалось - не 800, а 450+/-175 лет назад. Этот базовый гаплотип расходится с базовым гаплотипом центральной евразийской ветви на восемь мутаций, что соответствует 7625 годам между предками обеих ветвей. В итоге получаем после округления (450 + 4600 + 7625)/2 = 6300 лет назад.

Это в пределах погрешности совпадает с датировкой, что была получена ранее по восьмимаркерным гаплотипам, и попадает во временной интервал, когда начали расходиться европейские ветви R1a1a1-L417. В частности, датировка 6 тыс. лет назад или несколько ранее соответствует выделению северо-западной группы ветвей ("десятников"). Остаются, как минимум, 2 принципиальных вопроса:

1. Как объяснить тот факт, что наиболее далеко разошедшиеся ветви R1a1a1 обнаружены на двух краях ареала гаплогруппы?

2. Почему данные, опубликованные в 2006-м году исследователями из Магадана, оказались лишь частично включены в последующие публикации? Более 100 "обычных" евразийских гаплотипов, найденных у алтайцев, бурятов, эвенков, телеутов, тувинцев, хакасов и шорцев, нигде с тех пор не обсуждались.
(И.Рожанский)

Таким образом, мы видим, в Южной Сибири образовалась «солянка» из гаплотипов с разными датировками, на которую Игорь Рожанский обратил наше внимание при их рассортировке. За комментарием этой ситуации я обратился к президенту РА ДНК-генеалогии **Анатолию Клёсову.** Вот как он прокомментировал эту ситуацию:

Его анализ выше дал датировку 6300 лет по имеющимся в наличии алтайским гаплотипам, что нельзя объяснить походами ариев с Русской равнины в интервале 4500-3000 лет. Потому он и закончил свой анализ вопросом, а не утверждением. Не исключен, строго говоря, и обратный путь, что гаплотипы на Русской равнине 4800 лет назад появились с Южной Сибири, но по совокупности других фактов у нас нет к этому достаточных оснований.

Дело в том, что есть и другие источники R1a1. Это и уйгуры с датировкой 6900 лет назад, и другие гаплотипы Северо-Западного Китая, и гаплотипы Северного Китая, с датировкой 21000 лет назад. Последние - по 5-маркерным гаплотипам, но и по 5-маркерным видно, как они изборождены глубокими мутациями. Далее, то, что Южная Сибирь могла быть местом древних европеоидов, говорят и другие данные антропологов и генетиков. Оттуда в Сибирь ушли носители

гаплогруппы Q, которая образовалась из P, а гаплогруппа P - родительская по отношению R, R1, R1a, R1b.

Надо не забывать и про данные лингвистики, по которым - переводя на язык ДНК-генеалогии - "ностратический язык" был языком сводной гаплогруппы NOP, и сейчас языки этих гаплогрупп "перекликаются" между собой. Что, эта гаплогруппа появилась в Пакистане? А вот Южная Сибирь - тот регион, где NOP могла быть с наибольшей вероятностью, там же и европеоиды.

Так что надо терпеливо анализировать данные, которых пока недостаточно. Никто при этом не запрещает выдвигать гипотезы, и смотреть, как они укладываются в доступные данные других дисциплин, то есть заниматься оптимизацией.

Не менее интересным и заслуживающим внимания является и другая обсуждаемая информация с форума Академии ДНК-генеалогии:

На 1000 км выше Таримского бассейна есть треугольник территории, который зажат между Монголией и Казахстаном. Это - Алтай (на Китайской стороне), в аккурат в середине Саянских гор, там же населенный пункт (город) Алтай. Еще 500 км севернее - Горно-Алтайск. В этом треугольнике - верховья Иртыша. Там живут племена, которые на 32% R1a1, и у которых гаплотипы полностью искажены мутациями, совершенно невиданными в других местах по степени мутации. Возраст общего предка 21000+/-3000 лет. Это - видимо, родина R1a1. R1b в тех племенах нет. Но на 500 км южнее, в районе Урумчи, живут уйгуры, у которых уже есть R1b1 (18%), на втором месте по распространности в тех краях. На первом - все та же R1a1, 22%.

А еще на 500 км южнее - Таримский бассейн, где опять же нашли древние R1a1. При этом почему-то решили, что это ходоки из Европы. Одно из оснований - у них такие же ткани, как у шотландцев, пледы. Но не подумали, что это, напротив, у шотландцев ткани могли появиться от тех древних R1a1. Эту разумную гипотезу высказал И.Рожаниский.

Видимо, та территория от Алтая (Южная Сибирь) и южнее - места R1 и зарождения R1a и R1b. Прямо западнее - Пакистан (где R1a1 имеют 12400 лет до общего предка), Индия (7-8 тысяч лет до общего предка древних R1a1, и 4050 лет до R1a1 с Русской Равнины), и за Гиндукушем - Иран с Афганистаном, где R1a1 - те же 4050 лет, и опять с Русской равнины. Видимо, из-за высоких гор (Памирский узел) древние R1a1 и недавние, с Русской равнины, практически не смешивались. **(А.Клёсов, 2011)**

http://www.rodstvo.ru/forum/index.php?showtopic=1316&st=80&start=80

Можно предположить, что Южная Сибирь, включая Горный Алтай в древности 21 000 лет назад, могла быть первой прародиной гаплогруппы R1a, на которую

вернулась часть ариев спустя многие тысячелетия, будучи уже европейцами, и прошли в Южную Сибирь и на Горный Алтай кратчайшим маршрутом. Обращает на себя внимание и другой факт по Горному Алтаю, это сходство топонимов в ареале обитания ариев в Европе и Азии, описанных в ведах. Приведу один пример. Есть в Горном Алтае река под названием Иня и есть упоминание этого топонима в ВК-7: *Тайна есть, от нее вновь станет былое. Богумиру Боги дают блага земные. Того сами не имеем себе, так как нам была Инь тогда.* Имеется река Инн (приток Дуная) на Балканах, Европейской родине ариев. В ВК она значится как «Инь». Обозначена и территория под названием «Иньская»: *Велеса славьте троекратно, Русь погнутая встанет. Иегунов до целого разделяя, нас от Иньска отречете. Нас нет здесь и некому восстановить имя это украденное.* Это не единственный пример, который можно было привести в качестве сравнения.

Тема освоения Южной Сибири и Алтая активно обсуждалась на форуме Российской Академии ДНК – генеалогии. Куда делись европеоиды R1a проживавшие на Алтае и других районах Южной Сибири? Археологи утверждают, что где-то в 6-м веке н.э. их сменили тюркоязычные монголоиды. Тогда возникает другой вопрос, а куда делись, к примеру, буртасы, мурома, меря, голядь и еще десятки народов, населявших Русскую Равнину вплоть до 12-го века н.э.? **Игорь Рожанский** даёт простой ответ - растворились в среде славян и даёт этому своё обоснование:

С европеоидами Южной Сибири, в принципе, то же самое. Причем по антропологическим данным, насколько известно, процесс метисации был достаточно долгим. В курганах Красноярского края находят и чисто монголоидные черепа с теми же датировками, а порой и в одной компании с андроновцами-европеоидами. Носители таштыкской культуры железного века уже были сильно метисированы, что не исключает существование этносов, в большей мере сохранивших европеоидный фенотип, как те же пазырыкцы.

Далее, данные ДНК-генеалогии говорят о бутылочном горлышке, через которое около 1,5 тыс. лет назад прошли едва ли не все генеалогические линии Южной Сибири, включая C3, N1c1, R1b1a1 и R1a1. Как интерпретировать это наблюдение - отдельный вопрос, но следствием такого горлышка могла быть как резкая по историческим меркам смена популяции, так и "занос" чужой мужской гаплогруппы в среду монголоидного в основе этноса.

Наконец, исход европеоидов с Алтая неплохо вписывается в картину миграций времен гуннов и аваров. Вероятно, к тому времени носители R1a1 уже были тюркоязычны, а значит, их потомков надо искать среди казахов, узбеков, башкир, татар и карачаевцев с балкарцами. Возможно, снип L342.2 можно считать меткой той волны.

В принципе, возможны все 3 сценария (метисация, "занос" и исход), так что в реальности мы имеем, скорее всего, какую-то их комбинацию.

Посетив Горный Алтай, в районе долины реки Катуни и её археологические объекты, ещё раз убедился в том, что эти памятники археологии принадлежат культуре «скифов». Скифов беру в кавычки потому, что на самом деле культуре ариев, той её части к которой можно отнести с таким же успехом и антов, т.е. той части ариев что проделала долгий и не лёгкий путь с Балкан на Карпаты и далее на Днепр – Б.Кавказ – Ю.Урал расселившись за Уралом по всему «скифскому» направлению.

В чём я вижу ошибку археологов? Они пользуются устаревшим понятием о скифах данное Геродотом, который указывает, что основная территория расселения скифов — степи между нижним течением Дуная, Дона, степного Крыма включая районы, прилегающие к Северному Причерноморью. Разделяя их на несколько крупных племен по принципу: царские скифы (восточные живущие в Крыму), скифы-кочевники (западные), скифы-земледельцы (Днепровские), скифы – пахари и т.д. Геродот прав в том, что это действительно место их обитания. Но намного точнее Геродота, ответ кто такие скифы дают славянские веды где сказано, что это арии добравшиеся с Балкан (Дуная) через Карпаты до Днепра и объединившие арийские племена в Скуфь Киевскую.

Далее историки утверждают, что скифы являются группой народов, обитавших в Восточной Европе, Средней Азии и Сибири в эпоху античности. При этом эпоху ранней античности относят к Зарождению царского Рима и Римской Республики VIII в. до н. э. — II в. до н.э., а классическую и позднюю античность к I в. до н.э. — I в. н.э. и II—V н.э. соответственно. И тут начинаются нестыковки, т.к. на территории Южной Сибири (тот же Горный Алтай) их следы обнаруживаются 4700-4500 лет назад, т.е. в доантичный период.

Возникает та же проблема, что и у лингвистов принимающих арийскую группу языков за индоевропейскую и прослеживающих эту группу языков в обратном направлении (из Индии в Европу). На самом деле вся эта история не ираноязычных скифов, а той части ариев, что продвинулась с Балкан (Дуная) за Ю.Урал и дошла до Южной Сибири в промежутке 6200 – 4700 лет назад и осела на всех этих территориях (Балканы – Карпаты – Днепр – Б.Кавказ – Ю.Урал – Тянь-Шань – Алтай). Т.е. на всём протяжении этого пути на самом деле просматриваются следы рода ариев R1a1. Если сравнивать данные по этой гаплогруппе с датировками её пребывания в регионах, тогда всё становится на свои места. Это и есть, на мой взгляд, та самая часть ариев, что некогда образовала свой союз при Киевском княжестве (Скуфь Киевскую) и Антию на Б.Кавказе, но в античный период. О чём это говорит? О том, что на самом деле они не могли попасть за Урал скифами и на самом деле этот путь проделали их предки – арии, следы которых и прослеживает археология под якобы скифами.

Куда же они исчезли с данных территорий? Б.Кавказ и Ю.Урал мы уже рассматривали достаточно полно и обнаружили, что 3800 - 3500 лет назад часть ариев ушла в Индию и Иран. Куда делись остальные арии расселившиеся по Южной Сибири? Довольно подробный ответ на этот вопрос дают славянские веды.

Они совершили обратный исход в Европу по маршруту: Семиречье (оз. Балхаш) – Загорье (Загрос) – Двуречье (Тигр и Евфрат) – Кавказ – Карпаты.

4. Исход славян-ариев из Семиречья в Европу

Принеся жертвы в Коне Белом мы отошли от края Семиречья, что в горах у Иртыша. В Загорье обитали век. От Загорья, по нехоженому, идем на Двуречье. Разделились в том конницей своей. Продвигаемся к земле Сирийской. Там стали числом поменьше идти горами великими, снегами и ледниками. Отошли к степи. Там стада свои встретили. Скуфь была ранее одной из первой одержана отцами нашими. Пращуры наши держали её в Нави порой великой. Скуфь та силы дает. Отречёте врагов от неё, не бежите. В поре той к горам Карпатским шли вместе. Там решение приняли во главе пяти князей. Города и села огонь ест, ветра дуют великие. Потеснены были на другие земли. (ВК-9 таб. 15.а –II).

Попробуем разобраться, о чём говорится в данной выдержке. Речь идёт об обратном исходе рода ариев ветви ЦЕА с Южной Сибири в Европу. Выше мы выяснили, что этим родом были освоены территории Тянь-Шаня, Алтая и ряда других близлежащих территорий Сибири. Возьмём к примеру Иссыкский курган «Золотого человека», он датируется возрастом в 2600-2500 лет, на этот период приходится немало насыпанных курганов в данном регионе. Не исключено, что войны в Малой Азии, Сирии, Персидской державе, поход Александра Македонского в Среднюю Азию и Индию связаны с этим исходом. В ведах дословно сказано: *Принеся жертвы, в Коне Белом отошли от края Семиречья, в горе Иритя.* Речь идёт о жертвоприношении по случаю исхода в горном верховье реки Иртыш. Эта река в своих верховьях располагается вровень по границе Алтайских гор и Тянь-Шаня. Под «конём Белым», описана вечно заснеженная вершина горы Белухи. Т.е. собрались в верховьях Иртыша, под заснеженной Белухой, принесли жертву и договорились всеми племенами, включая алтайцев, тяньшаньцев и возможно таримцев, совершить исход обратно в Европу, на родину своих предков. Местом сбора, как следует из вед, выбрано Семиречье (оз. Балхаш) не случайно. Для общего сбора, с учётом направления движения, это удобное и очевидно «нахоженное» место.

Читаем дальше:
В Загорье обитали век. Таково по нехоженому идем на Двуречье, разделились в том конницей своей. Течем до земли Сириитие.

Под Загорьем упоминается современный Загрос. Следовательно, продвигались по границам пустыни и современных Казахстана, Киргизии, Узбекистана, Таджикистана, Туркменистана, пересекли Пяндж, и через Иран пересеча Загорье (Загрос) вышли к северной части Персидского залива, остановившись среди своих же Иранских племён на век. Напомню, что по ранее проведённым исследованиям в Индию и Иран часть ветви ЦЕА этого рода совершила исход 0коло 3500 лет назад и к периоду исследуемого исхода уже обитали там:

Примерно 4000 лет назад, время ранней андроновской культуры, носители R1a1, будущие индоарии, достигли Южного Урала, основали Аркаим (3800 лет назад) и Страну городов, 3600 лет назад они Аркаим покинули и частью перешли в Индию примерно 3500 лет назад. Примерно в те же времена носители R1a1, уже несколько столетий обитавших в Средней Азии, как об этом повествует Зенд-Авеста, перешли в Иран опять как арии. Не случайно они именовались ариями и в Индии и в Иране - похоже, что это и было самоназвание их рода еще до переселения в Индостан и на Иранское нагорье. **(Клёсов, 2008a; Klyosov, 2009b).**

Спустя век племена вышли на Двуречье (Тигр и Евфрат) разделились на две части и вдоль рек пошли по направлению к Сирии (Сириштие). Дальше, очевидно, разделение это так и сохранилось. Одни пошли через Малый - на Большой Кавказ, а через него к Днепру:

«*Там стали числом поменьше идти горами великими. Снегами. Льдами. Отошли до степи. Там стада свои. Скуфь была это перво-наперво одержана отцами нашими. Пращуры держали. В Нави поры великие. Силы дает, отречете врагов, не бежите. В поре той до гор Карпатских вместе. Там решение во главе пяти князей. Города и села огонь ест. Ветра великие. Потеснены были.»,*

а вторая часть прошла на Балканы через Переднюю Азию, что собственно и вызвало опасение у греков, к тому времени уже колонизировавших Черноморское побережье.

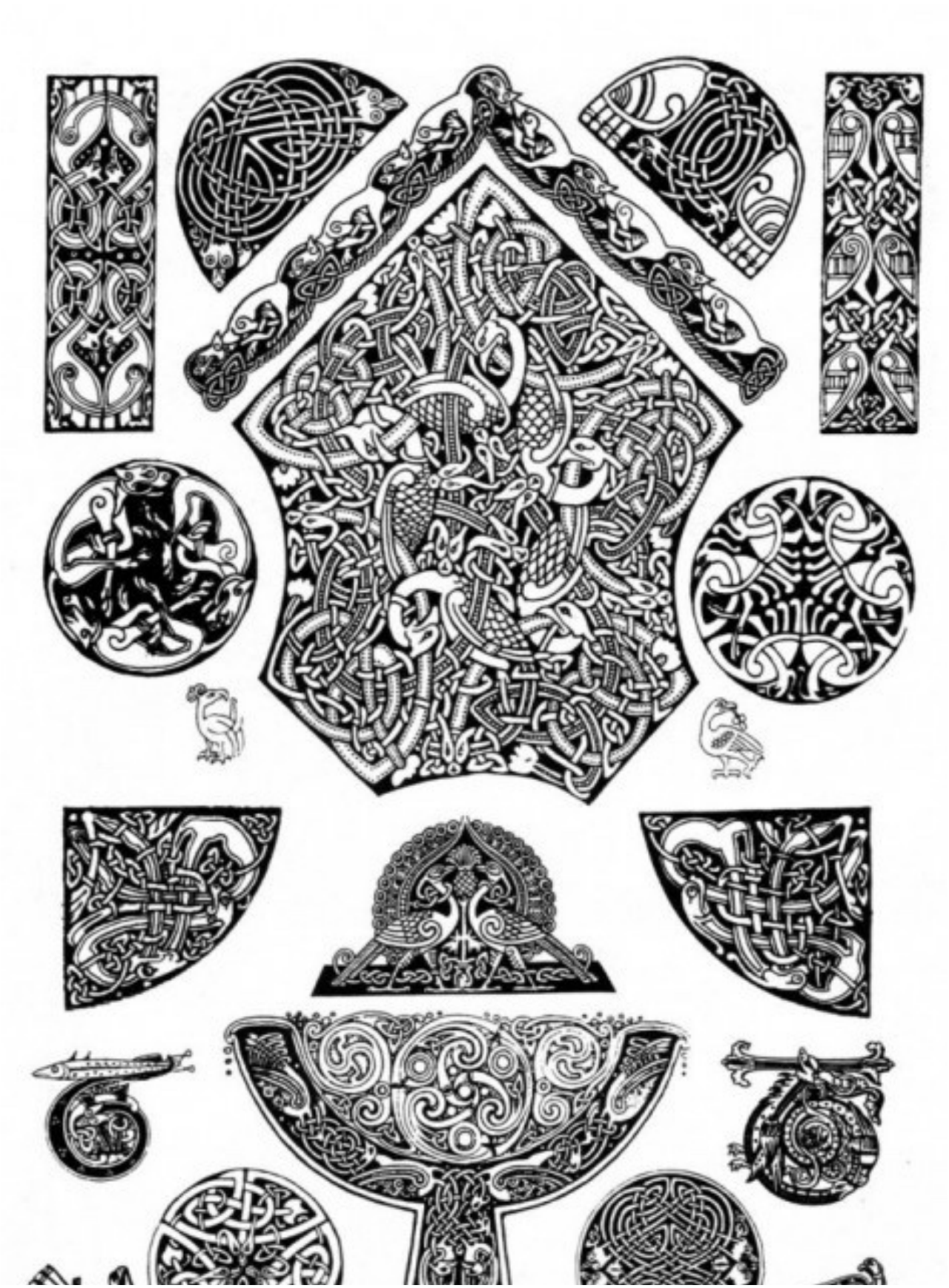
Если говорить о временном коридоре этого исхода из Азии в Европу, то он мог состоятся 2600 - 2300 лет назад. Этот исход из Азии мог быть связан с периодом волны похолодания в районе Алтая и Тянь-Шаня. Из этого не следует, что все покинули этот район в буквальном смысле этого слово. Кто-то остался с надеждой перетерпеть холода, но основная масса ариев сдвинулась с места и так происходило не раз. Благо свои Европейские и Азиатские территории были «застолблены» предками и было куда перемещаться. Давайте посмотрим, не те ли это племена ариев, что в период исхода из Азии в Европу под именем кельтов, набрав достаточно боевого опыта, позволили себе предъявить претензии Риму на Альпы и низовья рек По и Ро (Роны)? Смотрим датировки:

390 (387) — Нашествие галльского (кельтского) племени сенонов во главе с Бренном на Рим. 18 июля — Разгром римлян на реке Алии. 18 июля считалось в Риме несчастливым днём. Опустошение Рима. Гибель Марка Папирия и других старцев-патрициев. Длительная осада Капитолия.
http://ru.wikipedia.org/wiki/%CA%E5%EB%FC%F2%FB (см. ссылку 390 г. до н.э.)
Как видим, стычка Рима с кельтами была 2400 лет назад. Берём верхний коридор исхода ариев с оз. Балхаш 2600 лет назад. Минусуем один век пребывания в Загросе – 2500 и минус время на переход в Европу. Явно меньше одного века. Ещё одно сравнение. Торжественная золотая шляпа кельтского жреца: http://ru.wikipedia.org/wiki/%D0%A4%D0%B0%...ner_Goldhut.jpg и торжественный

головной убор «Золотого человека» найденного в скифском кургане в районе Иссыккуля, недалеко от оз. Балхаш:
http://ru.wikipedia.org/wiki/%D0%A4%D0%B0%..._golden_man.jpg
Находка датируется V – VI веком до н.э. Там же найдена и чаша с рунической надписью явно не тюркского происхождения.

Теперь давайте посмотрим и сравним кельтский орнамент:

1824



1826

Он идентичен орнаменту, принятому в славянской традиции и культуре, что так же может свидетельствовать о тесной связи между ними.

В сведениях представленных по кельтам **И.Рожанским,** говорится о том, что среди коренных жителей Алтая не менее 50 % относятся к гаплогруппе R1a1, причем по большей части к той же ветви, из которой потом выделились киргизы, младшие скандинавы (кимвры), а также какая-то часть индийцев и ханьцев. Вот к какому выводу он приходит в связи с этим:

*Самоназвание южных алтайцев - "алтай кижи", буквально "народ золотых гор". Согласно реконструкциям школы Старостина, общетюркское "кижи" (человек, люди) в рамках ностратической макросемьи имеет родственный корень с тем же значением в индоевропейских языках [ПИЕ *(s)kwel-], тогда как заявленные как когнаты протомонгольское *kulunča и протодравидское *kēl- довольно далеко отклоняются по своей семантике. Их исходные значения - "предок" и "друг/дружба". соответственно. В других ностратических языках этого корня нет, или его наличие логичнее объяснить скрытым заимствованием.*

Таким образом, по строгим критериям мы имеем тюрко-индоевропейскую изоглоссу, ностратическое происхождение которой сомнительно. В индоевропейских языках этот корень представлен весьма широко, а его фонология подчиняется закону регулярных соответствий: рус. "человек" и "челядь", древнеинд. "kulam" (стадо, толпа, род), лит. "kiltis" (род), ирл. "clan", греч. "τελος " (толпа), ст.-англ. "scolu" (толпа), хетт. "kule-" (рядовой общинник <-- толпа). Тот же корень, по-видимому, в этнониме "кельт", известному через посредство греческого.

Очевидно, слово это относится к одному из самых ранних слоев индоевропейской лексики, а его появление в сравнительно молодых тюркских логично вписывается в контакты восточных ариев с предками тюрок в районе Алтая или Саян. Заимствование в противоположном направлении не проходит по фонологии, общий источник в неком третьем языке (не обязательно ностратическом) недоказуем, а, значит, отпадает по принципу Оккама.

Собственно, гаплотипы алтайцев, киргизов и родственных им тюркоязычных народов - сильный аргумент в пользу предложенной этимологии. Более того, есть большая вероятность, что восточные арии, чью Y-ДНК сохранила вечная мерзлота и носят в себе их потомки, называли себя кельтами, или как-либо созвучно. Это слово ведь до сих пор живет в самоназвании алтайцев, и странно, что никто (насколько я знаю) не обратил на это внимание. Все почему-то зациклились на бриттах, гэлах и R1b1b2, а ведь кельтский мир был куда шире, чем эта боковая ветвь, перенявшая свой язык (и уже практически его утратившая) в относительно недавнее время.

Если рассматривать этот вопрос, руководствуясь гаплотипами наших современников, преимущество просматривается у Центральной Евро-Азиатской (ЦЕА) ветви и у тех ветвей, которые близки к нынешним азиатским R1a1, которые по каким-то причинам разошлись в Азии. В пользу этого говорит и религиозный фактор. Во фракийских землях рахманы соответствовали индийским брахманам и изначально носили языческий характер свойственный ариям. Но степень влияния была разной. Если в Индии это течение было основным, то во Фракии носило второстепенный характер. Т.е. эта ветвь разбилась на две части ушедшие с Ю.Урала и на юг и там закрепившаяся окончательно в Индии и Иране, а третья часть с Южной Сибири совершила исход от оз. Балхаш в придунайский регион по указанному в ведах маршруту.

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ДИСКУССИИ

The recent infamous (and failed) attempt to discredit the mutation rate constants. An overview of Busby et al (2011) article in Proc. of the Royal Soc. (B) and Dienekes Pontikos "essay" in his Anthropology Blog

Anatole A. Klyosov
http://aklyosov.home.comcast.net

The article "The peopling of Europe and the cautionary tale of Y chromosome lineage R-M269" by Busby et al came out in August, 2011. It has considered frequency patterns and "diversity" in a large R1b1a2-M269 dataset. Essentially, the authors have described that there is no geographical trend in "diversity" to and across Europe, and that their attempts to calculate timespans to common ancestors of M269 populations in Europe failed.

The reasons why their attempts failed are quite clear for those who study DNA genealogy. The authors failed to subdivide their massive haplotype M269 dataset to branches (in the haplotype tree, which they did not construct anyway) or to proper subclades (see below), and they employed wrong mutation rate constants for their calculations. In other words, they quite brutally violated the principal rules of DNA genealogy. Naturally, they should have obtained confusing and wrong results, and this was exactly what they obtained.

However, instead of blaming their own ignorance, they blamed "*an effect of microsatellite choice on age estimates*". This article explains why the authors (Busby et al, 2011) were totally wrong with their unqualified approaches, and what kind of an unqualified discussion, led by Dienekes Ponticos (http://dienekes.blogspot.com/2011/08/y-str-variance-of-busby-et-al-2011.html) followed after the publication of the Busby's et al paper. A reader can consider this article as an educational material.

Subclades and their base haplotypes

First, a relatively minor issue, regarding a lack of separation of a large haplotype M269 dataset into branches or subclades. It is a minor issue in this context,

because should that separation be carefully made, a wrong choice of the mutation rate constant would nullify results anyway. Still, let us consider how the authors handled the dataset. Let alone that the authors have employed only short, the 10 marker haplotypes (DYS393, 390, 19, 391, X, X, X, X, 439, 389I, 392, 389b – 437 – 438), where X stand for the missing loci 385a, 385b, 426, 388 in the first FTDNA panel, and DYS437 and DYS438 are from the second and the third panel, respectively. It is the 11 marker format employed by Zalloua et all (2008) with the missing DYS388. Its mutation rate constant equals 0.019 per haplotype per the conditional generation (of 25 years), since the individual DYS388 has the mutation rate constant of 0.00022 and its subtraction would not change the mutation rate constant (within 1.1%, that is well within a typical margin of error).

Of course, with such a short haplotype it was hopeless to find any differences between branches or subclades of R1b1a2-M269 and follow their geographic trends and distributions. However, still something could have been found. The following is a list of some M269 subclades in the given haplotype format:

L23	12 24 14 11 – 12 13 13 16 – 15 – 12
L51	13 25 14 11 – 12 13 13 16 – 15 – 12
L11	13 24 14 11 – 12 13 13 16 – 15 – 12
U106	13 23 14 11 – 12 13 13 16 – 15 – 12
P312	13 24 14 11 – 12 13 13 16 – 15 – 12
M65	13 24 14 11 – 12 13 14 16 – 15 – 12
M153	13 24 14 11 – 12 13 13 16 – 14 – 12
U152	13 24 14 11 – 12 13 13 16 – 15 – 12
L2	13 24 14 11 – 12 13 13 16 – 15 – 12
L20	13 24 14 11 – 13 13 13 16 – 15 – 12
L4	13 24 14 11 – 12 13 13 16 – 15 – 12
L21	13 24 14 11 – 12 13 13 16 – 15 – 12
M222	13 25 14 11 – 12 13 14 16 – 15 – 12
L144	13 24 14 10 – 12 13 13 16 – 15 – 12
L159.2	13 24 14 11 – 12 14 13 16 – 15 – 12
L193	13 24 14 11 – 12 13 13 16 – 15 – 12
L226	13 24 14 11 – 11 13 13 16 – 15 – 12
P314.2	13 23 14 11 – 13 13 13 15 – 15 – 12
L176.2	13 24 14 11 – 12 13 13 17 – 15 – 12
SRY2627	13 24 14 11 – 12 13 13 16 – 15 – 12
L165	13 25 14 11 – 12 13 13 16 – 15 – 12
L238	13 24 14 11 – 11 13 13 16 – 15 – 12

Without separation to branches and subclades all that could have been seen was an "overall" base haplotype

13 24 14 11 – 12 13 13 16 – 15 – 12

No wonder it did not show any geographical trend.

In fact, there should be no any geographical trend for R1b1a2 in Europe, since bearers of this haplogroups had entered Europe from different directions, all between 5000 and 4500 ybp. One subclade, apparently L11, entered Iberia from North Africa, over Gibraltar strait, another, apparently L23, entered the Balkans from Asia Minor, and yet the third one moved west from the Pontic steppes, that is from north of the Black Sea. The last route was mistakenly taken by Maria Gimbutas and her followers as the "Indo-European invasion". Those R1b1 had nothing to do with the "Indo-Europeans".

The base haplotype above, albeit short, 10 marker haplotype, can still give us an idea when their common ancestor lived. If we put aside the first three base haplotypes from the list, and leave other 19 which certainly arose in Europe, then those 19 haplotypes have 15 mutations from the base haplotype derived above

13 24 14 11 – 12 13 13 16 – 15 – 12

Therefore, 15/19/0.019 = 42 → 44 "conditional" generations (of 25 years), that is ~ 1100 years from their average "age", which is 2800 years [all the TMRCA values are listed in (Klyosov, 2011a)]. It shows that the "age" of R1b1a2 in Europe equals to 3900±1100 years. The "age" of the first three subclades is (Klyosov, 2011a):

L23 ~ 6,200 ybp
L51 5300±700 ybp
L11 ~ 4,800 ybp (the beginning of the Bell Beakers in Europe).

Back to the cited paper. The authors of the article did some "separation" of subclades. What did they consider?

"M-269", which is a cocktail of all the 22 subclades above, with the cocktail "base" haplotype

13 24 14 11 – 12 13 13 16 – 15 – 12

Then, "M269xL11", which is a mix of L23 and L51.

L23 12 24 14 11 – 12 13 13 16 – 15 – 12
L51 13 25 14 11 – 12 13 13 16 – 15 – 12

They differ by only two base alleles, and – without separation – the predominant subclade will give its base haplotype of the mix.

L11 itself.

L11 13 24 14 11 – 12 13 13 16 – 15 – 12

It is exactly as the whole M269 mix.

U106 itself

U106 13 23 14 11 – 12 13 13 16 – 15 – 12

Only one base allele (DYS390) is different from the above.

L21 itself

L21 13 24 14 11 – 12 13 13 16 – 15 – 12

Again, exactly as the whole M269 mix.

And U152 itself

U152 13 24 14 11 – 12 13 13 16 – 15 – 12

Again, exactly as the whole M269 mix.

So, what the authors were hoping to see when they talk on a "geographical trend", or rather its absence? They saw basically the same haplotypes everywhere. When they followed a separate subclade (a rare case in their work), such as L11 (Fig. 2c in the cited paper), they saw a predominant location (in this case Iberia and France, since L11 as one of the oldest subclades has apparently arrived from Iberia). When they followed a cocktail, such as "M-269", they saw again those downstream subclades.

Overall, this part of the paper is a misnomer.

The mutation rate constants

The situation with the mutation rate constant in the cited paper (Busby et al, 2011) is even worse. It is a striking example of how calculations should NOT be done.

The authors of the cited paper took the "mutation rates" from the Ballantyne et al (2010) paper. That was a bad mistake. It reflects a common misunderstanding

that father-son pairs provide a reliable data for computing the mutation rate constants for individual markers. Nothing can be farther from the truth.

Let me show why it was a bad mistake, and why father-son pairs are practically useless and misleading in computing the rate constants for individual markers, and, therefore, why the Busby et al (2011) paper led to erroneous conclusions regarding the TMRCA calculations.

Let us start with the first two markers, DYS393 and DYS390. Ballantyne et al (2010) have considered 1750 father-son pairs in DYS393 and observed 3 (three!) mutations in all of them. Hence, they concluded, the mutation rate constant equals 3/1750 = 0.00171 mutations per generation. After some numerical manipulations they came to the value of 0.00211 mutations per generation, with some confidence interval from 0.000621 to 0.005000 mutation per generation. Of course, the precisions of 0.00211 and 0.000621 make a reader all smiling, but let be it. It is in a way shocking, but Busby et all took the number of 0.00211 for their calculations. By the way, for three mutations in a dataset the 95% confidence results in the error of margin of 115%, the 68% confidence – in 58% error of margin. However, the authors did not bother with such minor details.

In DYS390 there were 2 (two!) mutations in 1758 father-son pairs. It gives 2/1758 = 0.00114 mutations per generation. Again, some manipulations led them to 0.00152 mutations per generation, with a confidence interval between 0.000352 and 0.004090. Whatever numbers they end up with, DYS390 marker turned out to be slower than DYS393. It was all based on 3 and 2 mutations!

Apparently, the authors did not know that it is all the way around. DYS393 is significantly slower marker compared with DYS390. Everyone who works with haplotypes knows it. For example,

-- 1035 Irish R1b1a2 haplotypes from the Heritage Project show 67 mutations from DYS393=13, and 493 mutations from DYS390=24. From DYS390=25 there were 894 mutations. That is, DYS390 is 7.4 and 13.2 times faster, respectively.

-- 102 Clan Donald R1a1 haplotypes show only 2 mutations from DYS393=13 and 22 mutations from DYS390=25. DYS390 is 11 times faster, than DYS393.

-- 1198 R1a1 haplotypes show 89 mutations from DYS393=13 and 1114 mutations from DYS390=25. DYS390 is 12.5 times faster, than DYS393.

In other words, the "mutation rates" obtained by Ballantyne et al (2010) and employed by Busby et al (2011) were grossly incorrect, and the whole calculations "approach" was doomed. Naturally, when the authors (Busby et al, 2011) have tried to calculate TMRCAs, using different markers ("STR-based

time" as they put is), which were in complete disarray, they "*find evidence for an appreciable effect of microsatellite choice on age estimate*". Hence, "*the cautionary tale*" in the title of their paper. Ironically, it refers directly to the authors themselves.

In the Ballantyne et al (2010) almost 2000 father-son pairs the following number of mutations have been observed in the first 12 markers (in the FTDNA format): 3, 2, 7, 5, 3, 6, 0, 0, 6, 9, 1, 6. Clearly, it was absolutely insufficient for any meaningful statistics. Here is the 95%-confidence based margins of errors for these numbers of mutations in the 12 markers: ±115%, 141%, 76%, 89%, 115%, 82%, n/a, n/a, 82%, 67%, 200%, 82%. Obviously, the Ballantyne et al (2010) "mutation rates" are not usable in DNA genealogy. They are undoubtedly useful in some qualitative or semiquantitative considerations, in maybe forensic studies, but not in TMRCA calculations.

Here is a comparative list of the Ballantyne et al (2010) "mutation rates" and John Chandler list of mutation rates, which I can testify is the most accurate one for the first 12 markers. For the more extended marker panels it is not that accurate and largely not usable as well (Klyosov, 2009), however, we are discussing here the 10 markers wrongly employed by Busby et al (2011) [Table 1, Supplement]:

Y-STR	Chandler (2006)	Ballantyne (2010)
DYS393	**0.00076**	**0.00211**
DY390	**0.00311**	**0.00152**
DYS19	**0.00151**	**0.00437**
DYS391	0.00265	0.00323
DYS439	0.00477	0.00384
DYS389I	**0.00186**	**0.00551**
DYS392	0.00052	0.00097
DYS389II	0.00242	0.00383
DYS437	0.00099	0.00153
DYS448	**0.00135**	**0.00039**
DYS456	0.00735	0.00494
DYS438	**0.00055**	**0.00014**

Marked are the markers which differ between 2.0 and 3.9 times (200% and 390%) between the Ballantyne and widely accepted Chandler lists.

Last but not the least – in order the father-son pairs to produce statistically accepted mutation rate constants for the individual markers, there should be at least 400 mutations in each locus (this would give a 10% margin of error with the 95% confidence). For this, the study should employ at least 800,000 father-son pairs in one experimental setup, and still some "slowest" markers will have only a few mutations in each. Until this experiment is conducted, "mutation rates" obtained from father-son pairs will be statistically insufficient. Furthermore, even

in that case those "mutation rates" will be measured per generation, though historical studies consider years, centuries and millennia. It means that the obtained "mutation rates" should be calibrated anyway, by converting "generations" to average year spans. This work is already done with respect to the average mutation rate constants for more than 30 marker panels (Klyosov, 2009; Klyosov and Tunayev, 2010; Klyosov, 2011d). The most widely used values are (in mutations per the haplotype panel per a conditional generation of 25 years):

12 marker haplotypes	0.022
17 marker	0.034
25 marker	0.046
37 marker	0.090
67 marker	0.120
111 marker	0.198

An extended comment by Dienekes Ponticos in his Anthropology blog (http://dienekes.blogspot.com/2011/08/y-str-variance-of-busby-et-al-2011.html)

A FOREWORD BY ANATOLE KLYOSOV:

The Busby et al (2011) paper met an enthusiastic response among people who had only a slight knowledge (rather, lack of it) in DNA genealogy, in consideration of mutations in the DNA, calculations of timespans to common ancestors, confidence intervals/margins of error, etc. Since they had little knowledge in the area, they, of course, have never realized that Busby et al employed wrong mutation rates and used a wrong approach. Apparently, they did not even think where the "mutation rates" were taken from by the authors. There were delighted that "*different microsatellites produce different data*", and it was enough for them to celebrate.

Ignorance loves to celebrate when it sees an apparent mishap by others (false one in this case), who know much more then them. It is a sort of "revenge by ignorance".

Here is what Mr. Ponticos triumphantly wrote in his blog (here it is in a slightly shortened form, in which irrelevant passages are removed):
(http://dienekes.blogspot.com/2011/08/y-str-variance-of-busby-et-al-2011.html)

August 27, 2011

Dienekes Ponticos:

Y-STR variance of Busby et al. (2011) dataset

I calculated the Y-STR variance of the Busby et al. (2011) dataset, for both the 10 and 15 Y-STR sets, as well as 4- and 5-most "linear" subsets thereof. Generation length of 31.5 years is used for the calendar year estimates.

My position that Y-STRs are effectively dead for age estimation stands, but I thought it'd be a good exercise to do this, as my personal adieu to more than a decade of Y-STRs: they didn't live up to their promise, but, indirectly, they helped create an entire field of "genetic prehistory" that will live on after their demise.

The greatest contribution of the Busby et al. (2011) paper is that it has cured the naivete of some who bought into the "more STRs = more accuracy" scheme. After this paper all Y-STR based estimates (including my own, above) are suspect.

The non-linearity of the Y-STR mutation model is only one of the problems of Y-STRs…

… From now on I am going on a Y-STR boycott on this blog…

Thankfully, it will only be a few years more until we can move past the Y-STR swamp… One way or another, we're bound to know more in the future, and destroying the Y-STR behemoth is the first step toward making some real progress in genetic prehistory.

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MY COMMENT:

The irony here is that the author of the above uses “generation length of 31.5 years” without any justification, calibration or whatsoever. Why not 30 years? Not 25? Not 20 years? 18? 36 years?

The thing is that all calculations using mutations in haplotype result in “kt” value as the final parameter; “k” here is the mutation rate constants, and “t” is a number of generations, whatever “generation” is. By setting – absolutely arbitrarily – 31.5 years as the generation length, and leaving the “k” value as is, whichever way it was obtained, is to demonstrate, again, a complete ignorance in the subject. In my works, for example, the kt value was determined from a

average number of mutations per haplotype (or marker) bound to a certain timespan (known genealogy or a known historical event), it was set as 25 years per generation, which is now a strictly mathematical value, and k was calculated from it (see above for 12, 17, 25, 27, 67, 111 marker haplotypes).

Then, by studying dozens and hundreds haplotype datasets the "k" value for each haplotype panel was examined, verified and cross-verified, and that is how the mutation rate constants were calculated. The work continues, however, by applying the mutation rate constants and the respective calculations to various historical events, chronology of haplogroups and subclades, etc. The work with STRs, mutations and mutation rate constants is basically done. That is why it was amusing to read a hymn of aggressive ignorance and arrogance as it is cited above.

Discussion in the Dienekes Ponticos blog

After that ridiculously triumphant "essay" by Mr. Ponticos that "*Y-STRs are effectively dead for age estimation stands*" and "*from now on I am going on a Y-STR boycott on this blog*" was published, a lengthy discussion broke loose at his site. I will reproduce here only the most relevant pieces, and some of the pieces are edited here. Mainly, I have removed some lengthy and totally wrong passages, and condenced them to their main points. Also, I have inserted my comments after some incorrect statements and calculations, in order to show how things should be calculated.

(http://dienekes.blogspot.com/2011/08/y-str-variance-of-busby-et-al-2011.html)

Anatole Klyosov:
Excellent, Dienekes. I truly appreciate your boycott. It means that one more person who understands nothing in the area, is out.

Until you and other realize that DNA genealogy takes the chemical kinetics approach, and it has nothing to do with "population genetics", you fail to obtain meaningful data.

Here are a few rules of DNA genealogy:

(1) Separate a haplotype dataset into DNA-lineages. Typically, there is a mix of them in almost any dataset. In those cases a "common ancestor" is a phantom.

(2) Employ the mutation rate constant which is calibrated and which is different

for ANY haplotype format. There are more than 30 haplotype formats in current use. Hence, there are more than 30 mutation rate constants which should be in use.

(3) Employ well-defined criteria to prove that every separate DNA-lineage in a dataset has one and only one common ancestor. There are several criteria, and two principal ones are (a) consider only separate branches on a haplotype tree, and (b) observe a fit between the "linear" and the "logarithmic" calculation procedures. In other words, time-dependent dynamics of mutations for each lineage should obey the first-order kinetics.

The way how you have "calculated" data based on mutations across a dataset is exactly the same as Zhivotovsky did. Threw everything into a blend, got some meaningless cocktail, and voila. The problem with Zhivotovsky and yours "calculations" is not only a wrong mutation rate, but lack of separation of DNA-lineages. In those cases all "calculations" are doomed.

You better listen to a professional in chemical and biological kinetics, rather then follow you unqualified and primitive way of consideration of pretty complex haplotype datasets, which, nevertheless, obey very clear rules of kinetics. If you believe that anthropologists understand physical chemistry in general, and chemical kinetics in particular without studying it, you are completely wrong.

Dienekes:
Anatole, I've simulated your method and it doesn't work; the logarithmic method in particular is crap and has incredibly huge confidence intervals.

Your lineage sorting is also crap, since haplotype clusters are not lineages, ancestral haplotypes can't be inferred (hence the need for "base" haplotypes). You go one step further and infer a number of phantom ancestors, reifying haplotype trees as phylogenies.

In particular, erroneously reconstructed ancestral haplotypes lead to a systematic underestimation of ages.

Your method overlooks all important sources of uncertainty to come up with artificially low confidence intervals…

MY COMMENT (more comments follow below):

Aggressive ignorance always amuses me. The “critic” has no idea that the logarithmic method is in fact a well-known description of first-order kinetics,

and mutations in the DNA follow the first order kinetics. He also has no idea that confidence intervals depend on a number of experimental points in the dataset, that is a number of mutations in the dataset (when the linear method is employed) and/or a number of base haplotypes in the dataset (when the logarithmic method is employed).

In other words, the "critic", if he knows the field, should have said – "if there are only a few mutations in the dataset, or there are only a few base haplotypes in the dataset, confidence intervals are wide". However, it is a common thing in chemical kinetics, that only a few experimental points lead to relatively large margins of error. The large number of experimental points, the narrower the confidence interval, the smaller the margin of error.

Here are a few actual examples with mutations and haplotypes:

1. The first is an introductory "theoretical" example, to show the principle of the approach. A dataset containing ten of 12 marker haplotypes contains only one mutation. It means that the dataset contains 9 base haplotypes. The linear method gives 1/10/0.022 = 4.5 generations (which is rounded to 5), and the logarithmic method gives [ln(10/9)]/0.022 = 4.8 generations (rounded to 5). Clearly, the logarithmic method here is MORE accurate compared to the linear method, since the first one is supported by only one "experimental point" and the second one is supported by 9 experimental points. The respective confidence interval of 68% (95% is unrealistic in this particular example) gives 0 to 9 generations to a common ancestor in the first case (calculations by the linear method) and 3 to 6 generations in the second case (calculated by the logarithmic method).
2. The Donald Clan currently has 143 haplotypes in its R1a1 "Red Subgroup", and their first 12 markers contain 81 mutations from the base haplotype, and those 143 haplotypes contain 86 base haplotypes in the series. It gives 81/143/0.022 = 25.7 generations to the common ancestor (by the linear method) and [ln(143/86)]/0.022 = 23.1 generations (by the logarithmic method). The Clan claims that their common ancestor, John, first Lord of the Isles, died in 1386, that is 625 years ago, or 25 "conditional" generations ago. The both methods showed 25.7 and 23.1 generations (I intentionally do not round up the numbers). The margin of error in this particular case is ±14.95% and ±14.71% for the linear and the logarithmic method, respectively.

NOTE: let me quote again an ignorant "critic": "*your method … doesn't work; the logarithmic method in particular is crap and has incredibly huge confidence intervals.*"

The following list provides a few examples out of dozens published in Proceedings of the Russian Academy of DNA Genealogy since June, 2008.

1. A series of 2299 of 67 marker haplotypes of R1b1a2-P312
http://www.familytreedna.com/public/R-L21/default.aspx?section=yresults
was considered in (Proceedings, vol. 4, No. 6, p. 1141). It had too many mutations to count, hence, the logarithmic method was employed to 12 and 25 marker panels. They contained 154 and 7 base haplotypes, respectively. It gave [ln(2299/154)]/0.022 = 123 → **141 generations** to a common ancestor for the 12 marker panel, and [ln(2299/7)]/0.046 = 126 → **145 generations** for the 25 marker panel (the arrow shows a correction for back mutations, as described in [Klyosov, 2009]). The difference between these two results is only 2%, and provides a timespan to a common ancestor of 3525-3625 years. It turned out to be a quite reasonable dating for the P312 subclade. In an earlier paper (Klyosov, 2009) I have shown that 750 of 19 marker haplotypes published by Adams et (2008) contain 2796 mutations and 16 base haplotypes. It gives 2796/750/0.0285 = 131 → 150 generations (3750 years to a common ancestor) by the linear method, and [ln(750/16)]/0.0285 = 135 → 156 generations by the logarithmic method (0.0285 is the mutation rate constant for the 19 marker panel [Klyosov, 2009]). It should be noted that those 750 Iberian haplotypes contained those from several R1b1a2 subclades, which would slightly distort the pattern, however, as we see, all the data are within a margin of error which is around ±400 years for those results.

The same is applicable to the 2299 of P312 haplotypes, which contain a number of subclades. Nevertheless, the data show that even in that case the obtained results quite fairly fit each other. For more accurate dating the subclades should be resolved and calculations made within of each subclade, as described in (Klyosov, 2011a).

2. Let us compare the linear and the logarithmic method for R1b1a2-L21 dataset of 1024 of 67 marker haplotypes (Proceedings, vol. 4, No. 6, p. 1144). The list of haplotypes is provided in
http://www.familytreedna.com/public/R-L21/default.aspx?section=yresults
It contains 16056 mutations in all 67 markers, which gives 16056/1024/0.12 = 131 → **150 generations**, that is 3750±380 years to a common ancestor (0.12 is the mutation rate constant for the 67 marker panel). Those 1024 haplotypes contain 4 base 25 marker haplotypes, which gives [ln(1024/4)]/0.046 = 121 → **138 generations**, that is approximately 3450 years to a common ancestor (0.046 is the mutation rate constant for the 25 marker panel). One can see that the results obtained with the logarithmic method are within the margin of error with those obtained with the linear method.

3. A dataset of 808 of R1b1a2-P312 haplotypes, which is a subset of those 2099 haplotypes considered above, and taken from the same project: http://www.familytreedna.com/public/R-L21/default.aspx?section=yresults The first 25 markers contain 5252 mutations, which gives 5252/808/0.046 = 141 → **164 generations**, that is 4100±415 ybp (years before present) for the linear method. In the 12 marker panel the set contains 39 base haplotypes, which gives [ln(808/39)/0.022 = 138 → **161 generations**, that is 4025 ybp for the logarithmic method (Proceedings, vol. 4, No. 6, p. 1152-1153).

4. 312 haplotypes of R1b1a2-M222 dataset (the same FTDNA Project cited above) contain 98 and 25 base haplotypes in their first 12 and 25 markers, which gives [ln(312/98)]/0.022 = 53 → **56 generations**, that is 1400 years to a common ancestor, and [ln(312/25)]/0.046 = 55 → **58 generations**, that is 1450 years to a common ancestor. These figures are practically identical. The linear method gave 1450±150 ybp. The same figure was obtained earlier (Proceedings, vol. 3, No. 2, p. 288) for 266 of 25 marker haplotypes, which contained 667 mutations, which gave 667/266/0.046 = 55 → **58 generations**, that is 1450±160 ybp. Again, the linear and the logarithmic methods give the same results.

5. 337 haplotypes of R1b1a2-P312* dataset (the same FTDNA Project cited above) contain 4956 mutations in the 67 marker panel, which gives 4956/337/0.12 = 123 → **141 generations**, that is 3525±360 ybp. The first 37 markers of the same dataset contain 3663 mutations, which gives 3663/337/0.09 = 121 → **138 generations**, that is 3450±350 ybp, and the first 25 markers of the same dataset contain 1981 mutations, which gives 1981/337/0.046 = 128 → **147 generations**, that is 3675±380 ybp (Proceedings, vol. 4, No. 6, p. 1164). This example shows that all the three panels give the TMRCA values within the margin of error, which are practically the same as those obtained by the logarithmic method (see above). Again, the linear and the logarithmic methods give the same results.

6. 312 haplotypes of R1b1a2-U152 dataset (the same FTDNA Project cited above) contain 4950 mutations in the 67 marker panel, which gives 4950/312/0.12 = 132 → **152 generations**, that is 3800±380 ybp. The first 12 markers of the same dataset contain 17 base haplotypes, which gives [ln(312/17)]/0.022 = 132 → **152 generations**, that is 3800 ybp by the logarithmic method, exactly as with the linear method (Proceedings, vol. 4, No. 6, p. 1168).

7. In case of recent datasets, that is derived from recent common ancestors, the logarithmic method can be also very useful. It shows that the dataset is "uniform", that is all the haplotypes descended indeed from one common ancestor, when the linear and the logarithmic methods give the same TMRCA. This can be exemplified with the "Pale Green" R1b12a group in the Clan Donald series. The group contains 8 of 37 marker haplotypes and 10 of 25 marker

haplotypes. The first set contains 11 mutations, which give 11/8/0.09 = **15 generations**, that is 375±120 ybp. The second set contains 5 base haplotypes, which gives [ln(10/5)]/0.046 = **15 generations**, which is the same timespan to the common ancestor (Proceedings, vol. 4, No. 6, p. 1212).

8. Here is an example of a relatively recent common ancestor of a branch (with DYS392=15) of haplogroup N1c1 (the South-Baltic branch), which was analyzed using a very "slow" panel of 22 markers (Klyosov, 2011b, 2011c), with the mutation rate constant of 0.006 mutations per haplotype per the "conditional" generation of 25 years. The branch contained 24 haplotypes, which contained only 9 mutations and 16 base haplotypes, which gives 9/24/0.006 = **64 generations** (no back mutations with such slow markers for this timespan), that is 1600 ybp, and [ln(24/16)]/0.006 = **68 generations**, that is 1700 ybp (Proceedings, vol. 4, No. 8, p. 1611). Again, the linear and the logarithmic methods give pretty much the same results.

9. The same slow 22 marker panel was employed in the analysis of 67 haplotypes of G2c2 subclade, which contained 14 mutations and 54 base haplotypes. It gave 14/67/0.006 = **35 generations**, that is 875 ybp, and [ln(67/54)]/0.006 = **36 generations** (Proceedings, vol. 4, No. 7, p. 1402).

10. 911 of 12 marker haplotypes of R1a1 dataset contain 25 base haplotypes, which gives [ln(911/25)]/0.022 = 163 → 195 generations, that is 4875 ybp by the logarithmic method. The linear method of analysis of multiple datasets gave similar dates, in the range of 4475 – 4825 ybp (Klyosov, 2009; 2011). Again, the linear and the logarithmic methods give pretty much the same results.

11. Here is an example of a significantly more ancient common ancestor, in haplogroup G, of which 180 of "slow" 22 marker haplotypes have been considered. They had 504 mutations and 10 base haplotypes, which gave 504/180/0.006 = 467 → 496 generations, that is 12400±1400 ybp, and [ln(180/10)]/0.006 = 482 → 518 generations, that is 12950 ybp. As one can see, the linear and the logarithmic methods give pretty much the same results, within 5% difference, which is well within a typical margin of error.

12. A private communication from Stephen Goodrich, who has employed the linear and the logarithmic methods to calculate the TMRCA for 205 haplotypes of E-V13 subclade. The haplotypes had 549 mutations and 16 base haplotypes in the 12 marker format. He obtained 549/205/0.022 = 122 → 140 generations, that is 3500±380 ybp and [ln(205/16)]/0.022 = 116 → 132 generations, that is 3300 ybp, only 6% difference, which is within the margin of error. Besides, 25, 37 and 67 marker haplotypes had 1270, 2342 and 3191 mutations in those 205 haplotypes. It gave 135, 127 and 130 generations, respectively (131±4 generations, that is within 3% variation between their principal values), which after the correction for back

mutations gave 3900±405, 3650±370, and 3725±380 ybp, respectively. The last figure (obtained from 205 of 67 marker haplotypes) is the most reliable one since it includes all 25 and 37 markers from other parts of the same dataset. It is also within the margin of error with the data obtained with the logarithmic method for 205 of 12 marker haplotypes (3300±600 ybp).

13. Another private communication from Stephen Goodrich. He has "cleaned" the dataset, removed identical haplotypes of individuals with the same last names, and finally obtained a dataset with 165 haplotypes of E-V13 subclade. The haplotypes had 417 mutations and 13 base haplotypes. He obtained 417/165/0.022 = 115 → **130 generations**, that is 3250±360 ybp and [ln(165/13)]/0.022 = 115 → **130 generations**, which is the same thing for the linear and the logarithmic methods.

The list of examples can go on and on, however, it seems, it is enough to appreciate again the ignorant "critic"s comment: "*your method … doesn't work; the logarithmic method in particular is crap and has incredibly huge confidence intervals.*"

Now, back to the discussion. It gives a good and educational illustration what happens when unqualified people believe that they can criticize and dismiss established approaches and methods of DNA genealogy. Typical mistakes which they make are based on (a) lack of knowledge in margins of error of individual "mutation rates" of separate markers (obtained, for example, from father-son pairs, as it was explained above), (b) lack of knowledge in that haplotype datasets typically represent a mix (a superposition) of various populations deriving from different common ancestors, (c) lack of knowledge that datasets can be calculated (aiming at TMRCAs) only when it is proven that they are derived from one common ancestor (in terms of DNA genealogy), (d) lack of knowledge that various "rate constants" publish on various websites were not calibrated using known genealogies and/or known historical events, and that they are typically unreliable.

The discussion gives a number of good examples of said lack of knowledge. What is really striking is that how people with such a meager knowledge in the field can be so aggressive in attacking others. Though, ignorance and arrogance is a common thing among many people.

BACK TO DISCUSSION (after several days of silence after the Dienekes negative remarks, quoted above):

Anatole Klyosov:
O.K., since the readers are silent, let me explain why the Fig. 4 from the Busby et al paper ("*Here is a figure from the paper, showing age estimates of sub-haplogroups R-S21 vs. R-S116*") is not adequate, mildly speaking.

First, they took totally wrong mutation rates - from Ballantyne et al (2010) [father-son transmission]. The data are based on just a few mutations, and awfully unreliable. Let me show it.

Everyone who worked with haplotypes and their mutations, knows that DYS393 is a very slow marker, and DYS390 is a fairly fast one. Indeed, Chandler's table, the most reliable one for the first 12 markers, shows the respective mutation rate constants as 0.00076 and 0.00311 (mutations per marker per generation), a 4-time difference.

What do we see in the Ballantyne's data? 0.00211 and 0.00152 (!) DYS393 is FASTER than DYS390 (!!). An utter nonsense. How did it happen? Very simple: Among 1758 father-son pairs Ballantyne et al observed just 3 mutations in DYS393, and 2 mutations in DYS390, and they took it (!) as a solid base for their absurd mutation rate constants.

This is applicable to all their "mutation rates". The reason is that among those almost 2000 father-son pairs, there were 3, 2, 7, 5, 3, 6, 0, 0, 6, 9, 1, 6 mutations in the first 12 markers. It just cannot be used for mutation rate estimates.

Enough? Not quite. Just a minor thing in this context. When one works with "fast" markers, a correction for back mutations is MUCH higher. Otherwise one obtains a systematic deviation in TMRCA's from slow to fast markers.

So, the conclusion number one: forget about Fig. 4 and the "principal conclusions" of the Busby et al paper. They are all wrong.

Now, I can present here data on "*age estimates of sub-haplogroups R-S21 vs. R-S116*", based on a much better approach. This is an important question, because it likely sets a good DNA-related time estimate for Bell Beaker movements from Iberia up North to the continental Europe.

I think, Dienekes, that since you presented here negative "side of the coin" you with your fairness would like to see its positive side. Aren't you?

Mike:
Oh, well. I suppose Mark Twain would have the appropriate words.... "Reports of my death have been greatly exaggerated."

Anatole Klyosov:
O.K., good. Now, let's move to HOW TMRCAs from U106 (S21) and P312 (S116) haplotype datasets should by properly calculated.

For U106 I will use an old (2008) collection of 284 haplotypes, from the U106 FTDNA Project. For those who want to know, I can give a reference to the published haplotype tree of all 284 haplotypes. It is nice and symmetrical, showing that it all derived from one (in terms of DNA genealogy) common ancestor.

The 25 marker base haplotype of the tree is as follows:

13 23 14 11 11 14 12 12 12 13 13 29 -- 17 9 10 11 11 25 15 19 29 15 15 17 17

All 284 of the 25 marker haplotypes contain collectively 1853 mutations from the above base haplotype. It gives 1853/284/0.046 = 142 → 166 "conditional" generations (25 years each), that is 4150±430 years to a common ancestor.

Here 0.046 is the mutation rate constant for 25-marker haplotypes, 142 → 166 is the correction for back mutations, as both described in (Klyosov, J. Genet.Geneal., 2009).

In order to verify the calculation procedure, just for fun, one can look at the Donald Clan dataset for the main, the Red Group R1a1 haplotypes. A while ago (2007) the list contained 68 of 12 marker haplotypes, in which there were 17 mutations in the first 6 markers, and 44 mutations in the first 12 markers. It gives:

17/68/0.0088 = 28±7 generations to a common ancestor
44/68/0.022 = 29±5 generations

The 68 haplotypes contained 53 base 6 marker haplotypes, that is

[ln(68/53)]/0.0088 = 28±5 generations

and 41 base 12 marker haplotypes, that is

[ln(68/41)]/0.022 = 23±4 generations

In 2007 the list contained 60 of 25 marker haplotypes, with 69 mutations and 18 base haplotypes. It gives:

69/60/0.046 = 25±4 generations to a common ancestor
[ln(60/18)]/0.046 = 26±7 generations

By the end of 2008 the Donald Clan list contained 84 haplotypes, with 44 mutations in the first 12 markers and 52 base haplotypes. It gives:

44/84/0.022 = 24±4 generations to a common ancestor
[ln(84/52)]/0.022 = 22±4 generations

Among those 84 haplotypes in the 25 marker format there were 109 mutations and 21 base haplotypes. It gives:

109/84/0.046 = 28±4 generations to a common ancestor
[ln(84/21)]/0.046 = 30±7 generations

In 2011 the list contains 143 haplotypes, and the formulas became as follows:

81/143/0.022 = 26±4 generations to a common ancestor
[ln(143/86)]/0.022 = 23±3 generations

214/143/0.046 = 32 generations to a common ancestor
[ln(143/36)]/0.046 = 30 generations

One can see that the number of mutations climbs up over four years, and a number of the base haplotypes decreases with time. The reason is simple: the Clan opens its doors wider and begins to accept people who actually not descendants of John, Lord of the Isles. I am writing about it here to show how sensitive is the main method of DNA genealogy. One can see that the numbers shift but they shift both for the linear and the logarithmic methods.

The Clan's common ancestor, John, first Lord of the Isles, died in 1386, that is 625 years ago, or 25 "conditional" generations ago. The both methods for the last 12 marker series showed 25.7 and 23.1 generations (I intentionally do not round up here the numbers). The margin of error in this particular case is ±14.95% and ±14.71% for the linear and the logarithmic method. That is, it is about the same.

O.K., back to R1b1a2. U106 subclade has 4150±430 years to its common ancestor, calculated from 25 marker haplotypes. Anyone can go to the U106 Project, get 25, 37 and 67 marker haplotypes, and calculate each series the same way. The mutation rate constant for 67 markers is 0.12, for 37 markers it is 0.09. I bet you will get the same figure within the margin of error or much better for each series.

The same procedure for P312 can be applied for 337 of P312 haplotypes in Mike Walsh FTDNA "L21" Project. They contain 1981 mutations in 25 marker format, 3663 mutations in 37 marker format, and 4956 mutations in 67 marker format.

Therefore,

1981/337/0.046 = 128 →147±15 generations,

3663/337/0.09 = 121 → 138±14 generations,

4956/337/0.12 = 123 → 141±14 generations

It all gives 3675, 3450, and 3525 years, plus-minus as indicated.

As you see, all complaints about "meaninglessly wide margins of error" are false. In fact, 147, 138, and 141 generations on average give 142±5 generations (within 3.5% consistency), which is much narrover compared to formally calculated margins of error listed above.

In the 67 marker format the U106 and P312 base haplotypes differ from each other by 6 mutations. This places THEIR common ancestor, presumably L11, at 4800 years bp. I can explain how it was calculated, if someone cares to know it.

NOTE_1 added two week later: No one of the discussants showed any interest to the last offer.

NOTE_2 shows a "knowledge level" of discussants who have decided to continue – see the follow-up comments.

Jeanlohizun:
Firstly I would like to say that unlike Chandler's et al (2006) publication in the Journal of Genetic Genealogy, at least the Ballantyne et al (2010) paper actually studied fathers-son pairs, so in that sense is far more reliable and descriptive than panels of 12, 25 or 37 markers from amateur Projects as FTDNA.

AK: >What do we see in the Ballantyne's data? 0.00211 and 0.00152 (!) DYS393 is FASTER than DYS390 (!!). An utter nonsense.....

So what if the sample size of mutations was small, at least this was an actual generation (father-son) mutational measurement, not some calculated mutations based on the assumed descendants of a man who live 650 years ago, which can lead to large confidence intervals in terms of errors, especially when assuming a constant generation time of 25 years regardless of the place of origin or history of each of the lineages.

AK: >So, the conclusion number one: forget about Fig. 4 and the "principal conclusions" of the Busby et al paper. They are all wrong

As much as you wish this paper was wrong, the essence of what this paper has brought over cannot be overturned by your rants about mutation rates in experimentally obtained data.

Anatole Klyosov:
As always in the commentator's remarks, there is no substance.

Comment 1: negative and irrelevant.

Comment 2: empty-worded and incorrect.

Comment 3: off target, highly questionable, and irrelevant to the subject of this discussion.

jeanlohizun:
Now the question is how you came up with the 26 generations number for the Clan Donald; you mentioned that John Lord of the Isles died in 1386, so it seems to me you simply took the year when the paper was written (2008) subtracted the year of death of John Lord 1386, and divided the result by 25 years per generation. This yields 24.88 generations; likely you added 1 or 2 generations assuming he was a father or a grandfather when he died, and voila 26 generations. Did I get that right? Now here is a major issue with your calculation, not every generation is of 25 years, often times, especially during the middle ages, people had children even when they were 50. For example I know this person, who was born in 1983, and he has a distant ancestor born in 1560 in Lekeitio, Vizcaya, by assuming a generation time of 25 years, they must be 16-17 generations apart from each other. In reality they are only 12 generations apart from one another, and I know people younger than him who are once removed from the same ancestor, meaning they are 11 generations apart from that common ancestor. Thus assuming a generation time of 25 years can sometimes lead to erroneous mutation rates per generation. Which is why is far better to do what Ballantyne et al (2010) did of actually measuring the mutations in a sample of fathers and sons.

Summary:

- How did you calculate standard deviations, margins of error, confidence intervals.

- How did you come up with the correction formula, was there any experiment, or was it just that it would fit your data?

- How do you account for irregular generations (i.e. more than 25 years, less than 25 years, adoptions, etc) when calculating average mutation rate per generation using this ancestry clan projects from FTDNA?

Anatole Klyosov:
I have published answers and explanations to all those questions you asked. And to dozebs of other questions which you have not asked.

NOTE: My "critic" still did not get that 25 years per a "conditional" generation is a mathematical figure and has nothing to do with a "common generation" which is a floating number.

jeanlohizun:
Yes I'm in Academia.

How do you make sure the following doesn't happen: We have a DNA Project for R1b-M269 bearers, and they were tested using say 10 STRs. Then on that sample we have Murcians (n=23) and Catalans (n=200). It just so happens that the Murcians have 150 mutations from the base haplotype, on the other hand the Catalans have 400 mutations from the base haplotype. Thus if we analyze the sample indiscriminately without separating the two subgroups, it yields that there are a total of 550 mutations, which translates into an average mutation rate per marker of 550/(223*10) = 0.2466. Then using a constant mutation rate of 0.0025 (this is a hypothetical number), it yields 98 generations, which of course is then multiplied by a constant for back mutations. Now if instead of using the whole sample we take just the Murcians (n=23) it turns out that it yields a total of 150 mutations which translates into an average mutation rate per marker of 150/(23*10)=0.6521, again using the 0.0025 (hypothetical) gives out 261 generations, which translates into a TMRCA 2.66 times older than that of the combined sample.

Again I did not get the impression from your analysis of Adams et al (2008) that you looked at each single Iberian population independently, nor did I get the impression that you broke down haplogroups R1b-M153 or R1b-M167 from the R1b (xM65,M153 or M167) to do the STR diversity analysis.

Anatole Klyosov:

1. Standard deviations, margins of error, confidence intervals.

They are determined by a number of mutations in a properly handled haplotype dataset, by an assumed margin of error in the mutation rate constant, by a choice

of sigma confidence level, and by actual fit to actual data (actual genealogy and actual known historical events).

After calculations of hundreds and probably thousands of haplotype datasets, I came to a formula which makes the best (it seems) and reasonable fit with actual data. I have demonstrated the result above in this thread (with the example of 337 haplotypes using 25, 37 and 67 marker haplotypes; explanations are given above):

1981/337/0.046 = 128 → 147±15 generations,

3663/337/0.09 = 121→ 138±14 generations,

4956/337/0.12 = 123 → 141±14 generations.

It all gives 3675, 3450, and 3525 years, plus-minus as indicated.

As you see, 25, 37 and 67 marker haplotypes fit quite well with each other. This is for one particular dataset, for R-L21. An average number of generations is 142, and the principal numbers are within 3.3% margin. For a much more massive dataset the number is 150±15 generations (3750±380 years) from a common ancestor, which is pretty much the same. As you remember, L21 is under M269, under L23, under L51, under L11, under P312.

A whole ladder for 30 subclades of R1b1a2-M269 with dates and confidence intervals is given in Proceedings, June 2011 (vol. 4, No. 6, p. 1127), http://aklyosov.home.comcast.net

2. Corrections for reverse (back) mutations.

When you look at the formula you have quoted above (taken from my paper in J. Genet. Geneal., 2009) [I did not like the title of the journal, that is why I set a new journal, on DNA genealogy, and it is very different indeed), you immediately recognize that it is the Poisson distribution. The way how this particular formula was derived is described in the Proceedings, October 2008, pp. 631-641. You need to use an e-translator, because the article is in Russian. It contains a few pages of mathematics, which I cannot reproduce here due to limited space. It does not need any experimental confirmation since it is based on Poisson distribution (PD), as hundreds and thousands of other applications in the world. In fact, all calculations of mutation rates, as well as practically all chemical kinetics approaches are based on the PD. This is also illustrated in cited J. Genet. Geneal.

3. 25 years per "conditional" generation.

It has nothing to do with a common "generation". It is a mathematical value. Common generations is a floating timespan. It depends on many factors - culture, lifestyle, climate, wars, famine, etc. It cannot be used in calculations, therefore, all those endless discussions which value to take - 16, 18, 20, 25, 27, 30, 31.5, etc. years are practically senseless. None of them would be right for different peoples and different times.

In fact, it is not needed. When you work with haplotypes and mutations, you get "kt", a product of the mutation rate constant and a number of generations. Therefore you can chose whatever t (the length of generation) you like, and you get the mutation rate constant from it. They bound to each other. I chose 25 years, and the mutation rate constant came out of it as 0.022 for 12 marker haplotypes, 0.046 for 25 market ones, 0.090 for 37 marker ones, 0.12 for 67 marker haplotypes, and 0.198 for 111 marker haplotypes (Klyosov, 2011d). The last value should be verified, but it would not be changed much. If one does not like 25 years per generation, he/she can take, say, 31 years, and the mutation rate constants will shift proportionally. The final result (in years) will be exactly the same.

I hope it helps.

Now, to your question of "*How do you make sure the following doesn't happen: We have a DNA Project for R1b-M269 bearers, and they were tested using say 10 STRs...*" (see above)

This is a kindergarten "problem". It is "Rule No. 1" with which I have started this thread - do not mix different lineages (branches, populations). In that example Murcians have 150/23/0.025 = 261 generations to a common ancestor (w/out a correction), Catalans have 400/200/0.025 = 80 generations. If you mix the two, you get a phantom "common ancestor" somewhere in between. It is a no-no. In that particular case if you mix them you get 550/223/0.025 = 99 generations, almost three times lower than the oldest, 261 generations. In fact, after correction for back mutations you get 99-->110 generations and 261-->350 generations, that is the error equals 320%. That is exactly how "Zhivotovsky method" works (rather, it does not work): they mix all branches, get much lower TMRCA, and multiply it by 3 (by using 3 times lower "population mutation rate"). The problem is that they multiply by 3 everything, right and wrong TMRCAs, and as a result you never know what you got. Often a result is 300% higher than it should be.

Dienekes:
Anatole, do you really believe that R1a1 folk built both Gobekli Tepe _and_ Stonehenge?

MY COMMENT:
Dienekes clearly undestood that his case is lost, and he is trying to change the subject. I decided to leave here his questions and comments as a good illustration of his "methodology" in considering scientific issues which are not quite understood as yet. Instead of encouraging a brainstorming attempt, as a scientist is normally trained to do, Mr. Ponticos prefers to play a role of a policemen in science. He pretends that he KNOWS the truth, and demonstrates an utter intolerance to those who dare to advance new hypotheses.

Anatole Klyosov:
The question is not what I "believe" or "not believe". "Believe" belongs to religion, not science. By the way, I have never wrote what you have mentioned in any scientific edition, such as I know or I believe. However, a legitimately scientific question would be whether we have any data (or indications) of R1a1 (possible) presence in the regions of Gobekli Tepe and Stonehenge and in the respective time periods? Next question would be whether the two mentioned sites have something certain in common, say, from architectural viewpoint? Design?

Agree, that when we start to lay out DATA and their thoughtful consideration, we gain knowledge regardless the (current) answer would be "yes" or "no". I said "current", because some new data might appear and a current answer might go from yes to no, or in the opposite direction.

Agree, this is the way science works.

So I suggest you to ask me a different question - such as "Do you have ANY indications that R1a1 were in Anatolia some 11-9 thousand years before present and in Europe 5-4 thousand years bp?"

From my side, I would ask you a reciprocal question: Do you know for fact that there is no ANY indication that R1a1 were in Anatolia some 11-9 thousand years before present and in Europe 5-4 thousand years bp?"

This is how a constructive discussion takes place, rather then throwing questions with an accusatory connotation.

Mike:
Dienekes, I think many readers are interested in the objective arguments related to the methods and tools used. In that regards, can the concerns about Anatole's methods be explained more explicitly?

Dienekes:

My own experiments on Y-STRs can be found in the Y-STR Series label of this blog. People are free to evaluate his arguments and data for themselves, but I don't plan to devote any more time on them and on Y-STRs in general, unless some convincing new development takes place that will make me change my opinion on them.

Anatole Klyosov:
Dienekes, your "answer" is again off target. The question was: *can the concerns about Anatole's methods be explained more explicitly?*

My answer to the question is that NOBODY has ever shown that the method is incorrect or based on incorrect assumptions, or that the mutation rate constants are incorrect, or the results are incorrect. Nobody. In fact, nobody has even tried to consider it, using any specific examples. Your quotation above is a good example. You just have said on passing that the method is bad. I gave above a specific example, with R-L21. Where are the critique? Take any L21 dataset (or any dataset on that matter), show me that my methodology is incorrect, that the results should be noticeably different, that the margin of error makes the data meaningless, etc.

I have seen in my life in science very many people who have no idea what they are talking about, or who criticize without offering anything positive on the subject. So, you are not alone. We have the same situation here. Not the first time, not the last one.

DP: >My own experiments on Y-STRs can be found in the Y-STR Series label of this blog.

You forgot to mention my response to it, which completely nullified your "*own experiments on the Y-STR*".

Anatole Klyosov:
Back to Gobekli Tepe. In fact, the whole discussion was based on a recent paper in National Geographic (June 2011, p. 39-59), which said, I quote - "Known as Gobekli Tepe, the site is vaguely reminiscent of Stonehenge, except that Gobekli Tepe was built much earlier... some 11,600 years ago". The "vague" resemblance with Stonehenge was explained on a picture showing Gobekle Tepe as vertical pillars (16 tons of weight) arranged in a circle, with horizontally placed huge stone blocks on top of each one (T-shaped pillars).

But the main question here is - since when hypotheses (brain storming) are met with such hostility? Do you know who built Stonehenge? Which "haplogroup"? Do you know who built Gobekli Tepe? Which "haplogroup"? O.K., you do not

know. In fact, nobody knows. Again, why such hostility to ideas, which - in principle - can be examined and verified?

However, there are indications that R1a1 were in Central Asia some 20,000 years ago, that they might have been moving through Anatolia westward some 12-10,000 year ago (where some proto-IE language could have been left), and that they have been in Europe thousands of years before 4600 ybp (the last date from Haak et al, 2008). Stonehenge was built between 4500 and 3500 ybp (radiolabeling data are summarized in Johnson, Solving Stonehenge, 2008, 288 pp).

Please, Dienekes, try sometimes be positive in considering someone else's ideas, which CANNOT be overthrown, as least yet, by contemporary science. Do not try to control things when you can just listen. Peacefully. Open-mindedness is a good thing in science. It is probably not a good thing for police officers and prison guards, and, apparently, in this blog.

First, please lay out here, for example, a couple of those proposals of mine you disagree with, and JUSTIFY (based on clear and commonly accepted scientific evidences) what is wrong with them. I bet that you fail.

ALL my hypotheses are based on actual data that cannot be just dismissed. People generally base their attitude on "conventional wisdom", not on scientific data.

Please keep in mind that I am a professional scientist, and I have been trained to advance hypotheses in a brain storming manner. After I offer them, the next step is a careful consideration what they support, what they contradict, and what is a balance between the two. And by "support" and "contradict" I mean DATA, not "opinions", and not "conventional wisdom". This is what science is about.

It is in a way disconcerning, how so many folks are far away - mentally - from this truly scientific methodology. They curse, "dismiss", aggressively attack, as it is something that intrudes their privacy, their family life, their wellbeing, a loyalty of their spouses. Sometimes I want to scream - folks, it is just a HYPOTHESIS! It just my attempt to explain things that contemporary science cannot explain. Why such hostility? Do YOU have anything to offer in that regard?

A mystery, truly.

Here are some relevant data and observations regarding the quoted.

1. R1b1 arose in Central Asia around 16,000 ybp. There are a number of

indications to it, such as a pattern of mutations in R1b1 haplotypes in Central Asia (Uigurs, Kazachs, Tuvans, Bashkirs, etc.), which dramatically differs from that in R1b1 in Europe, and the respective dating. Then, a trek of archaic Turkic languages which well coincides with the R1b1 migration route. Then, similar elements which might belong to a proto-Turkic language which only remotely reminds current Turkic languages along this R1b1 migration trek. Linguists cannot read that proto-Turkic language, it has practically disappeared. On the other hand, there are common elements in the Basque, Northern Caucasian languages, Sumer language, some Dene-Caucasian languages and other agglutinative languages, compared to flexive IE languages. So my suggestion was that an ancient language of R1b1 was that agglutinative language which can be called Dene-Caucasian, or Proto-Turkic, or whatever, it does not make any difference how to call their non-IE language, since there is no name for it as yet. I can call it "Erbin" to reflect that it was the R1b1 tribe who spoke it. On the other hand, it is known that there was/were many non-IE languages across Europe before 1,000 BC (and some of them were carried into the 1st millennium AD).

In short, R1b1 arose ~16,000 ybp in Central Asia, they spoke a non-IE language (Erbin), they made their way to Europe and arrived ~4800 ybp by several routes. They brought their non-IE language to Europe that time, and only 500 BC a first IE language was found in Celts/Kelts, who are often referred to be R1b1. Still, it is not clear, they might have been R1a1. After it, and along with disappearance of the Etruscans, Europe started switching to IE languages back again. "Back" - because IE languages are much older, and probably they were in Europe, or even dominating in Europe some 10-6 thousand years before present.

As you see, this is a very interesting and vaguely understood story or migrations of people and languages in Europe.

A similar story was with R1a1. Clearly, they did not appear in Europe out of the blue. Clearly, it is a brother subclade of R1b1. Clearly, they also came from Asia very long time ago. Apparently, it was them, who spoke IE languages 10-6 thousand years before present, and clearly it was them who brought IE language to India and Iran ~3500 ybp.

Indeed, it was shown that the most ancient R1a arose in Central Asia, either in the Altai region or in North China region (some of the local Chinese populations are up to 25-30% R1a1), where there are dated - by different haplotype datasets - between 17 and 21 thousand years ago. From there they have migrated to Europe by the "Southern Route" (unlike the "Northern Route" of R1b1) - via Tibet, Indostan, Iran, Anatolia to the Balkans, where some "oldest" R1a haplotypes are found (with DYS393=13, not 11 as among other R1a1). This branch is coined "R1a Old European branch" among total 22 branches of the R1a1 clade, and it is dated between 11 and 8 thousand years back.

From there R1a1 appeared ~4800-4600 ybp on the Russian Plain, and moved eastward as a chain of archaeological cultures now shows, up to Andronovo and Afanasievo cultures (it is unclear for the last one, are they from Europe, via Andronovo, or they are the original R1a from 20,000 ybp). R1a1 are excavated in South Siberia and in Tarim basin.

Again, this pattern explains and put together many historical and linguistic puzzles, including those of the "Nostratic concept". Again, here I laid out only a small fraction of facts and observations. They are described in more details in my publications.

Jeanlohizun:
In your study "*all 750 haplotypes showed 2796 mutations with respect to the above base haplotype, with a degree of asymmetry of 0.56. Therefore, the mutations are fairly symmetrical, and a correction for the asymmetry would be a minimal one. The whole haplotype set contains 16 base haplotypes. An average mutation rate for the 19-marker haplotypes is not available in the literature, as far as I am aware of, and cannot be calculated using the Chandler's, Kerchner's, or other similar data. However, the Donald Clan latest edition of 88 haplotypes contains 63 mutations in the above 19 markers. Taking into account the 26 generations to the Clan founder (see above), this results in the mutation rate of 0.0015 mut/marker/gen and 0.0285 mut/haplotype/gen, listed in Table 1.*

The logarithmic method gives ln(750/16)/0.0285 = 135 generations, and a correction for reverse mutations results in 156 generations (Table A), that is 3900 years to a common ancestor of all the 750 Iberian 19-marker haplotypes. It corresponds well with 3500±480 ybp value, obtained above for 12- and 25-marker Basque haplotype series. The "mutation count" method gives 2796/750/19 = 0.196±0.004 mutations per marker (without a correction for back mutations, that is obs = 0.196±0.004), or after the correction it is 0.218 ± 0.004 mutations per marker, or 0.218/0.0015 = 145±15 generations, that is 3625±370 years to a common ancestor of all 750 Iberian R1b1 haplotypes."

So why did you not separate the lineages of the different Iberian populations and instead used the bulk of lineages? By not separating the lineages and mutations into the different populations you have completely missed any possible internal population that can have a much higher diversity value. Because as I showed before it is possible for two populations to have a lower TMRCA when they are combined together than one of them can have separately.

****
NOTE (by Anatole Klyosov): My "opponent", being a novice in DNA genealogy (actually, he is not there as yet) missed an important rule of this discipline: a haplotype dataset has one common ancestor (in terms of DNA genealogy) if the

linear and the logarithmic methods gave the same or a similar results. For the 750 Iberian haplotypes the linear method gave 145±15 generations, and the logarithmic method gave ~156 generations to a common ancestor, that is within 8% and well within the margin of error. It means that those 750 haplotypes descended from one common ancestor, who lived within 3625-3900 ybp, and other (downstream) subclades do not distort this TMRCA, at least significantly.

In fact, the objection of my "opponent" is seriously flawed because EVERY dataset contains "a bulk of downstream lineages". The question is whether that "bulk of lineages" has descended from one common ancestor. In that case the calculations provide a timespan to THAT, the oldest common ancestor for the dataset.

A different situation is that when there are two or more different common ancestors of the haplotypes in the dataset. In that case the linear and the logarithmic methods will give quite different TMRCAs, because mutations in the dataset would not follow the first-order process.

For example, those Murcians (with 261 generations to a common ancestor) and Catalans (with 80 generations to their common ancestor) being combined in one dataset would give quite different TMRCA's by the linear (99 generations) and the logarithmic methods (likely around 40 generations). It is a typical mistake made by a novice who does not have any experience in those matters.

I have reprinted the following quite lengthy and totally incorrect passage by my "opponent" as a lesson of how NOT to analyze data. He was doing some acrobatics with numbers taking them as a rabbit from the hat, without even thinking that some Chandler's "mutation rates" are inaccurate or plain incorrect (some of them are), that individual marker's "mutation rates" often have huge margins of error, etc. As a reader has probably noticed, I have never employ individual markers mutation rate constants, only those by whole panels (12, 25, 37, 67, 111 markers) in their entirety, and always use the calibrated data. My "opponent" does not have such a feeling and take those often erroneous numbers for granted, as if they are proven, verified, calibrated. Overall, comment of my "opponent" is truly a bad joke. It is sad that he does not realize it.

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Jeanlohizun (cont.):
As for your estimation of the mutation rate of 0.0015 mut/marker/gen, I have to say, the results are not reproduced when using the average measured mutation rates of 14 of the 19 STR markers Adams et al (2008) used. Also certain STR have been shown to mutate faster in one haplogroup than in others (i.e. DYS392 in Haplogroup N and Q, or DYS388 in Haplogroup J). You used estimated data

from one R1a1 project, and extrapolated that data to R1b1b2 bearers, yet there are indeed differences between the mutation rates of different haplogroups.

MY COMMENT: the last two sentences are totally incorrect. The mutation rate constants are the same in different haplogroups, as it was shown many times.

Jeanlohizun (cont.):
For example out of the 19 STR used by Adams et al (2008) 14 have mutation rates readily available on the Web, I used the old estimated mutation rates by Chandler et al (2006) which have a 15-20% error for the mean of each mutation rate, and differ from empirically measured mutation rates found in the YHRD.org.

These 14 STR are DYS19 (0.00151), DYS388 (0.00022), DYS389i (0.00186), DYS389ii (0.00242), DYS390 (0.00311), DYS391 (0.00265), DYS392 (0.00052), DYS393 (0.00076), DYS437 (0.00099), DYS438 (0.00055), DYS439 (0.00477), DYS460 (0.00402), DYS385a (0.00226), and DYS385b (0.00226). There aren't estimated or measured values for DYS434, DYS435, DYS436, DYS461 or DYS462 respectively.

Then we have that the mean mut/marker/gen is 0.0020. The problem is that the standard deviation of that average is 0.0014, which leads to huge margins of errors. Anatole mentioned that there were 2796 mutations present in the 19 STR, thus subtracting the mutations found in DYS434 (16 mutations), DYS435 (4 mutations), DYS436 (5 mutations), DYS461 (127 mutations) and DYS462 (45 mutations) which are a total of 197±20 mutations. Thus the total number of mutations in the remaining sample would be:

2599/750/14 = 0.2475±0.0019 mutations per marker.

Now an assumption taken when taking the average of markers with very different mut/marker/gen rates is that one should expect faster markers to have the same ratio of mutations to the slow markers as they have in mutation rates (i.e there should be 2.9 times more mutations on DYS19 than in DYS392), in order to overcompensate for the mean mut/marker/gen. However as we would see, that is not the case. For example dropping the slowest STR markers and their mutations from sample should have no effect on the generations to MRCA because we assume they behave linearly. In the Adams et al (2008) the slowest STRs are: DYS388 (0.00022), DYS393 (0.00076), DYS392 (0.00052), DYS437 (0.00099) and DYS438 (0.00055).

If we drop this 5 STR then the mean mut/marker/gen turns into 0.0028 and the standard deviation drops to 0.0010.

Let's now explore what is effect of dropping the 5 slowest STR on the overall

variance of the Adams et al (2008) sample. Thus far there are a total of 2599±20 mutations on the sample, subtracting the mutations found in DYS388 (17 mutations), DYS392 (67 mutations), DYS393 (103 mutations), DYS437 (223 mutations) and DYS438 (54 mutations) which are a total of 464 mutations±40 mutations. The total number of mutations in the remaining sample would:

2135/750/9=0.3163±0.0089 mutations per marker.

Doing the same thing for the 5 slowest STRs, which have a mean mut/marker/gen of $6.08*10^{-4}$ and a standard deviation of $2.8752*10^{-4}$

464/750/5= 0.1237±0.0106 mutations per marker.

Now doing the correction for back mutations assuming a symmetric tree yields:

14 STR—Corrected Mutation rate per marker: 0.2823±0.0025
14 STR --- Mean mut/marker/gen: 0.0020
14 STR--- TMRCA (25 years/gen): 3529±31.25 ybp

9 STR (Fastest) --- Corrected Mutation rate per marker: 0.3751±0.0125
9 STR (Fastest) --- Mean mut/marker/gen: 0.0028
9 STR (Fastest)--- TMRCA (25 years/gen): 3349±112 ybp

5 STR (Slowest) --- Corrected Mutation rate per marker: 0.1318±0.0121
5 STR (Slowest)--- Mean mut/marker/gen: $6.08*10^{-4}$
5 STR (Slowest) ---TMRCA (25 years/gen): 5412±495 ybp

So which one are we going to choose as the right TMRCA, in the ideal case all STRs should yield a very close TMRCA regardless of their mutation rate, and thus why Dr. Klyosov uses an average mut/marker/gen, but as I just showed above, the choice of STR is very important in the calculations of TMRCA. Fast mutating STR tend to overshadow slow mutating STR in big samples, whereas slow mutating STRs tend to overshadow fast mutating STR in small samples. The thing is that given that we cannot control the direction (back or forth) of the mutations, over long spans of time slow STR are better are predicting TMRCA. However because they are slow, a small sample size would tend to undermine its presence. On the other hand the method of averaging mutation rates regardless of their values is very unreliable because it tends to undermine the values of slow STR in big samples. Thus I agree with Busby et al (2011) conclusion that is not the amount of STR but the sets of STRs what matters when determining TMRCA.

NOTE (Anatole Klyosov): I have decided to place this gibberish above with an educational purpose only, though I doubt that anyone would take it seriously.

Some more comments, and those more specific, are made below.

Anatole Klyosov:
Unfortunately, you are too quick with the word "failed" directed to others, which know MUCH more than you in the area you dare to criticize. You had to write - "I seem failed to understand...". This would have been a fair and a correct statement.

>*So why did you not separate the lineages of the different Iberian populations and instead used the bulk of lineages?*

Because there was no need in it back in 2009. I could have done it, and the fit between the linear and logarithmic methods would have been even better. But it was good enough: 145±15 and 156 generations, respectively. As you see, they are the same within the margin of error. The difference between their principal values is less than 8%, which is well within typical margins of error in DNA genealogy.

Remember, in the above example which you gave earlier, the difference was 4 times, or 400%. Can you see the difference between 400% and 8%?

The second reason why I did not separate the lineages back in 2009 is that that time I was not looking for recent lineages. I have done the separation in a recent paper, in June 2011 (Proceedings, 2011). In the latest paper I have isolated 30 subclades and determined the TMRCA for each one. Please notice that the Iberian major R1b1a2-P312 subclade had the TMRCA of 3900±400 ybp (page 1133) and 3525±360 ybp (pp 1162-1163, different datasets). As you see, they are all the same thing.

One more advice to you: please look at the core data, not on some "side dishes". It is like checkers on a cab. They are not that important compared to the ride itself.

So, we are done with the first part.

The second part, in which you have manipulated with those five markers, is totally flawed. In fact, you got huge margins of errors, and you did not realize it. Instead, you wrote truly absurd things. Look what have you done:

14 STR--- TMRCA (25 years/gen): 3529±31.25 ybp

Can you imagine? Margin of error of 31.25 years! 0.9% (!!) What is 31.25 years, where came it from (!?)

Next:

9 STR—TMRCA (25 years/gen): 3349±112 ybp

Margin of error of 3% (!!) Where those 112 years came from, again?

Next:

5 STR --- TMRCA (25 years/gen): 5412±495 ybp.

Margin of error of 9% (?)

It is all grossly incorrect. The way how you have been doing it would give you margins of error no less than 60-80%.

Result: all you calculations are based on an incorrect platform. You should have re-calibrated your "estimated" 4, 5, and 9-marker "haplotypes", using some known genealogy, to make sure how they work. In fact, all "dating" which you have obtained - 3529, 3349, and 5412 are around ~ 4100±1140 ybp, within 30% margin of error. That is what you have actually obtained.

You have made many additional errors in your "explanations", but it is not worthwhile go over them. The thing is that your main conclusion -

>*Thus I agree with Busby et al(2011) conclusion that is not the amount of STR but the sets of STRs what matters when determining TMRCA*

is applicable to you personally (meaning you are free to agree with whomever you want), but not to the field itself. You need just learn how to treat data correctly.

jeanlohizun:
If you think I manipulated something then why don't you go back and count the amount of mutations present in the Adams et al (2008) sample of 750 haplotypes for the markers DYS388 (0.00022) [17 mutations], DYS393 (0.00076) 103 mutations], DYS392 (0.00052) [67 mutations], DYS437 (0.00099) [223 mutations] and DYS438 (0.00055) [54 mutations]. You would see that there are 464±40 mutations. You are the one that doesn't realize that once you mix together slow STRs such as DYS388, DYS393, DYS392, DYS437, DYS438 with fast STR such as the other 9 you undermine the value of the slow STRs.

MY COMMENT:

It is grossly incorrect. A "minor" thing is that my "opponent" cannot count mutations. For example, in DYS388 in the Adams et al (2008) dataset there are not 17 mutations, but 17 mutated alleles, of which 14 alleles 12→13, and 3 alleles 12→14, altogether 20 mutations, not 17. Similarly, in DYS393 there are 114 mutations, not 103; in DYS392 63 mutations, not 67; in DYS437 222 mutations, not 223, and in DYS438 65 mutations, not 54. My "opponent" does not know that two-step mutations are counted as two mutations, not one.

However, the miscalculated 20 mutations is a relatively minor thing in this context. What is much worse, many of those "excessive" mutations are not random, and they cannot be subtracted individually and used as a basis for calculations of the mutations rate constants. Those mutations specifically belong to certain subclades of the Iberian R1b1a2. For example, many of DYS393=12 belong to the L23 subclade (in most other R1b1a2 subclades DYS393=13). Many of DYS437=14 belong to the M153 subclade (in most other R1b1a2 subclades DYS437=15) [Klyosov, 2011a], and so on. Therefore, many of the 114 mutations in the slow DYS393 marker are not random mutations, they are differences between L23 and P312, L21, U152 and other subclades. That is why there are so many of them (114), though only ~ 72 mutations in DYS393 should be truly random. Overall, since the TMRCA for the M153 subclade is ~ 3640 ybp, practically the same as that for the P312 subclade, the distortion is not (or only slightly) noticeable in the difference between the TMRCA obtained with the linear and the logarithmic methods, and the overall TMRCA, largely related to R1b1a2-P312, is acceptable.

On the same reason, only ~ 94 mutations in DYS437 from the observed 222 mutations are random. The rest, 58% of the mutations, belong to differences between subclades. However, when almost 3000 of mutations are considered altogether, a hundred of non-random mutations make only 3% of the total count, which is within the margin of error. That is why only total counts should be considered, across the whole dataset (if it satisfies the criteria of the linear method and the logarithmic method resulting in the same TMRCA) or within the subclades. To calculate the "mutation rate constant" from those distorted "mutations" of the individual markers – it is a complete disaster. That was exactly what my inexperienced "opponent" did.

And after such a dramatic failure he rhetorically states:

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jeanlohizun (cont.):

You can't truly explain why when only the slowest 5 STRs are used the sample produces a TMRCA older by at least 1500 ybp than that of the combined sample

or the fastest 9 STRs. I'm simply showing to you that the mean mut/marker/gen method is flawed; because for it to work you would have to have a direct proportionality between mutation rate and number of mutations present in each STR, and such proportionality does not exists, at least not in the Adams et al sample.

MY COMMENT:

That is exactly what I mean. The person has no idea how much he does violate the rules of DNA genealogy. He mixes different branches/subclades with each other, while they involve different base alleles values, and he tries to calculate "the mutation rate constant" for those phantom mixes.

Here is the most important conclusion which I do not get tired to repeat: **DO NOT EMPLOY INDIVIDUAL MARKERS FOR CALCULATIONS. Employ only the whole haplotype panels.**

That is why my "opponent" is falling to that trap deeper and deeper. I quote:
>I was simply trying to show the readers that while in your ideal world slow STRs, fast STRs and the combined sample should all produce a somewhat close result, the reality is that they don't. There is no way around it, using the 5 slowest STRs in the Adams et al sample produces 464 mutations, which divided by the average mutation rate of those 5 slowest produces 209 generations to TMRCA without the correction for back mutations.

It is not in my "ideal world", but in the real world different markers must all produce the same or close results, however, when they are related to ONE COMMON ANCESTOR and when there are many of haplotypes in the dataset, in order to satisfy statistical criteria. When my "opponent" keep overcounting "mutations" (by mixing random mutations and mutations between subclades), he overcounts the TMRCA, and instead of 126 → 145 generations, that is 3625 ybp, he obtains 209 → 264 generations, that is 6600 ybp.

The case is closed.

However, my "opponent" continues in a blind rage:

jeanlohizun (cont.):

AK:> *It is all grossly incorrect. The way how you have been doing it would give you margins of error no less than 60-80%.*

All you calculations are based on an incorrect platform. You should have re-calibrated your "estimated" 4, 5, and 9-marker "haplotypes", using some known genealogy, to make sure how they work. In fact, all "dating" which you have obtained - 3529, 3349, and

5412 are around ~ 4100±1140 ybp, within 30% margin of error. That is what you have actually obtained.

I used the same data you used, and anyone can use here, and count the mutations in the slowest STRs and they would see what I'm saying. Whether you are ready to admit that your methodology might have overlooked at the possibility of the STRs not behaving linearly is another story. Again I could explain it to you in more details if you want, but basically STRs do not behave as nicely and predictable as you want to portray them.

MY COMMENT:

What can I say? Just shrug. That is what I call the aggressive ignorance.

Anatole Klyosov:
You have just written many words on a subject you are not knowledgeable in. Your manipulations are all based on an indiscriminate extraction of Chandler's numbers without their verification. Without even thinking that they (or just one of them) might be incorrect. Have it occurred to you that some numbers might be incorrect indeed?

You have overlooked my comment above in this thread:
AK: >>Indeed, Chandler's table, the most reliable one for the first 12 markers...

Why do you think I mentioned only the first 12 markers as the most reliable? Because I know all of them, and examined and cross-examined each one of them. This reflects the principal difference between a professional (in kinetics of time-related processes) and you with your ignorance in the subject. You just grab numbers without thinking how reliable those numbers are.

You do not look at the core of the problem. You do not want to pay any attention at the fact, that those Iberian R1b1a2 haplotypes produce essentially the same TMRCA whether they are calculated using 19 marker haplotypes, 25 marker, 37 marker, or 67 marker haplotypes, using either linear or logarithmic methods. All those results are within margins of error. In spite of this obvious result, you grab something indiscriminately, manipulated mindlessly with them, and voila. In a way, you have repeated the same flawed "approach" as the paper (Busby et al, 2011) beloved by you. They also grabbed something (wrong "mutation rates" from father-son pairs) without thinking, and voila.

Another serious mistake made by you (even if the all the Chandler's mutation rates are correct) is that you mix the lineages/subclades/branches and count mutations in the <u>individual</u> loci. As a result, you take 750 alleles of, say, DYS437, in which DYS437=15 in the P312 subclade and DYS437=14 in the M153 subclade

(Klyosov, 2011a). It is a slow marker, and in P312 it rarely mutates as 14 ← 15 → 16, and in M153 it rarely (with the same mutation rate constant) it mutates as 13 ← 14 → 15. As a result, you see a cocktail (superimposition) of alleles – a little or none of 13 and 16 (which are truly random mutations of M153 and P312, respectively, and plenty of 14 and 15, which is a mix of M153 and P312. And you "calculate" the "mutation rate" from that cocktail!

Indeed, among those 750 alleles of DYS437 we see none of "13" (that reflect a very slow mutation of the allele "14" in the M153 subclade), little of "16" (only 9 of them out of 750, which shows a very slow mutation of the allele "15" in the P312 subclade and maybe some other relatively minor subclades there, such as U152 and U106), and plenty of "14" (213 of them) and "15" (528 of them). Overall you see 222 mutations (213 + 9), but they are not random mutations, they are the inherited alleles of the M513 and P312/U152/U106 subclades, respectively.

Should you separate these subclades, you would see just a few (on none) mutations in DYS437 within those subclades. That is how the mutation rate constants should be calculated.

As a result, you grossly overcounting a number of mutations, you artificially elevate the "mutation rate" for DYS437, and when you divide the overcounting by elevation, you wrongly inflate the TMRCA (you have obtained 6600 ybp instead of ~ 3625 ybp). And after such an acrobatics you attack the mutation rate constants that they are wrong, and different markers give you different TMRCA! Of course they do, since you cannot count mutations properly.

Now, suppose those 750 Iberian haplotypes contain 37 haplotypes of M153 (having DYS437=14) [Klyosov, 2010] and 713 of "other" R1b1a2 subclades having DYS347=15. If the mutation rate constant by Chandler for DYS437 is correct and equal to 0.00099 mutations per marker per generation (25 years), and if there are 130 generations to a common ancestor of all of the named subclades (I am simplifying, but not much, since all of the TMRCAs are around 3600-4000 ybp, and 130 generations after the correction for back mutations gives 3725 ybp), than we get – theoretically – 37x0.00099x130 = 5 mutations (13 ← 14 → 15) in that marker in the M153 subclade, 713x0.00099x130 = 92 mutations (14 ← 15 → 16) in that marker in the P312 (and others with the base "15" allele), and the rest, 32 alleles (in M153) will be unchanged "14", and 621 alleles (in P312) will be unchanged"15". With some minor assumptions on symmetry or non-symmetry of the mutations, and by comparing with the observed figures, we see no "13" alleles in M153 (instead of 2-3 of them at the symmetrical mutations), all five 14 →15 from M153, nine alleles "16" from P312, 83 of 15 →14 mutations from P312, plus their own 32 of "14" (M153) and 621 of "15" (P312).

In summary, that is what we can see in alleles of DYS437:

13 zero
14 32 + 83 = 115
15 5 + 621 = 626
16 9

Total of “14” and “15” should be 115+626 = 741

In reality, we see

14 213
15 528

Total of “14” and “15” is 741. The exact fit is, of course, a coincidence, however, it shows that the mutation rate constant for DYS437 by Chandler (0.00099) is generally correct. We observe more alleles “14” and less “15” among those 750 DYS437 alleles, however, it might be cause by a number of factors, among them unknown subclades in the dataset and a series of small branches-lineages in the dataset. Overall, it is all compensated in the mutation pattern, since the see the first order of mutation accumulation pattern, as is proven by the comparison of the linear and the logarithmic methods.

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MY COMMENT:

After it the discussion moved from the mutation rates to history of haplogroups and languages. This was prompted by a negative comment of one of the discussants that we cannot follow the spread of languages and haplogroups as I have outlined earlier, with respect to Proto-Turkic languages and haplogroup R1b1.

Anatole Klyosov:
It is rather senseless to discuss the matter after I laid out here the background of the concept point by point, and you did not bother to respond with DATA. Hence, the way you choose to respond cannot be accepted.

>*Turkic languages are now accepted as a branch of the Altaic language family by most linguists.*

WHICH Turkic languages? Do you know dating of origin/split of those languages which are considered by "most linguists"? Do you realize that I am talking about a time period for R1b1 and their language between 16 and 5 thousand ybp?

>*...both the homeland of the Turkic language family and the homeland of the Altaic family are commonly thought to be somewhere in Greater Mongolia and/or eastern part of Siberia... So your R1b1-Proto-Turkic connection isn't plausible (whatever R1b1 Central Asian Turkic people now carry seems to be entirely from the pre-Turkic inhabitants of Central Asia).*

You gave a very confusing and self-conflicting statement (rather, a mix of conflicting statements), in which the first one is disconnected from the last one. You do not argue that R1b1 arose in Central Asia, and likely in the Altai region, which I have demonstrated many times. You do not argue that R1b1 had their language, which I call "Erbin" (due to lack of other names) and which linguists have not even considered (if they did, a reference please). Then, I suggested that considering their (R1b1) possible route this Erbin might have been a Proto-Turkic language. How much linguists know on Proto-Turkic languages? How much do YOU know about Proto-Turkic language? Have you ever read anything on Proto-Turkic languages? I have.

I have argued many times that the term Proto-Turkic was brought by me only because the apparent R1b1 migration route across the Eastern part of Eurasia coincides with the area of the present Turkic language, some of the very archaic. If one does not like the work “Proto-Turkic”, call the R1b1 language (thousands ybp) Dene-Caucasian, Sino-Caucasian, or any other name one likes. I call it “Erbin”. What is wrong with it?

How you would respond to a paper featured in the current Dienekes selection, which concluded that (modern) Turkic language in the present day Turkey was not brought from the East, as many other Turkic languages in the world?

I would not bet on that conclusion, however, it does not conflict with what I am taking about. Maybe there is something in it. If the present Turkic language in Turkey was not brought (in the common era) from the East, so who brought it and when?

You probably have not heard on a concept of "brain storming", when you first express various scenarios, and then look at available data and see what potentially confirms and what clearly contradicts. Where is that balance in your "critique"?

Dienekes:
Turkic languages belong to the Altaic language family. Altaic languages (Mongolic, Turkic, and Tungusic, and more distantly Korean and Japanese) are primarily located in central-east Eurasia and spoken by Mongoloids and admixed Mongoloids. We also have good evidence now that there is a common

autosomal component to Altaic speakers (see one of the links in the post), and this component is also aligned with East Eurasians (Mongoloids).

Every single piece of evidence points to the fact that Turkic languages were first spoken by Mongoloids. So, even if Anatole was right about R1b in the Altai a very long time ago - which he isn't… there is no reason to associate that R1b with any sort of Turks. Actually the time depth he is talking about precedes the formation of the Turkic languages anyway.

MY COMMENT:

Those people still cannot get that they talk on the contemporary "Turkic languages", which linguists date by the first millennium AD, and I talk on Proto-Turkic languages of ancient R1b1 many thousand years ago.

Dienekes:

AK: >How you would respond to a paper featured in the current Dienekes selection, which concluded that Turkic language in the present day Turkey was not brought from the East, as many other Turkic languages in the world?

Turkic languages were brought to Anatolia from the east; we are fortunate that this event happened in full light of history, so there is no argument to be had here.

What the current paper has concluded is that the arrival of Turkic languages in Anatolia was not the result of massive migrations from the East, which is a reasonable conclusion that has been confirmed time and again.

MY COMMENTS ON THE FOLLOWING.
My "opponent" continues his gibberish. It was clearly shown above that (a) the "mutation rates" from farther-son pairs are largely incorrect because they are based on only few mutations and statistically insufficient, (b) the individual markers cannot be considered for calculations because their alleles are either mixed from different subclades, branches, lineages, or there are only few of them, (c) haplotype datasets should be separated to branches/subclades/principal lineages, having one common ancestor, (d) both the linear and the logarithmic methods should be applied and the respective TMRCAs should be compared; only if they are very similar (approximately equal to each other or are within the margin of error) the dataset can be calculated according to the rules of DNA genealogy.

However, my "opponent" ignores all the said above and continues to "attack" in his fruitless attempts to "prove" that calculations based on mutations are meaningless. I place his hopeless "comments" here just to show how ignorant "critics" of DNA genealogy can possibly be.

Jeanlohizun:
So you think that you estimated mean mutation rate from the Donald clan project is far more reliable than using empirically measured mutation data from Father-sons pairs? Well I got news for you: certain STRs such as DYS388 mutate differently in different haplogroups, so there goes the first strike in using the data from R1a1 to R1b1a2.

MY COMMENT:
Our novice again is totally confused. The mutation rate constants are the same for different haplogroups, branches and lineages. I have already explained what might be a "mechanism" of that wrong belief that "*certain STRs such as DYS388 mutate differently in different haplogroups*", and I explained it taking DYS437 as an example. When a set of alleles in a certain marker, be it DYS437 or DYS388 or whatever, is a mix of different subclades and lineages with different base DYS388 (or whichever marker), it views by novices as a "faster mutation" in that marker. It is particularly pronounced in ancient haplogroups. For example, in different populations alleles in DYS388 can vary between 7 and 18, however, it is largely stable in each one of them when one separates subclades and lineages. In haplogroups J1 and J2 alleles in DYS388 in different lineages vary between 13 and 18. When those lineages are mixed in the same dataset, a novice sees it as "wow! They are fast mutating alleles!".

Wrong.

Jeanlohizun (cont.):
Second strikes goes in that as I showed above, and unfortunately for you, I'll show again using different data sets, the usage of a combined STR set tends to results in disastrous TMRCA estimations. I bet you didn't even bother to check the standard deviation of the combined STR set. You seem to have forgotten that when the standard deviation of a set of mutation rates is almost the same as their mean, then you are in trouble. Something you don't realize is that doing the mutation counting method on the Donald clan assumes that in the slowest markers the R1a1 people of the Donald clan would have the same number of mutations relative to their sample size and to their TMRCA as the Iberian set from Adams et al (2008).

MY COMMENT:

Gibberish continues. Again that "*the usage of a combined STR set tends to results in disastrous TMRCA estimations*" after all my explanations above. All those rhetorical "*second strike*", "*you did not even bother to check*", "*you seem to have forgotten*", "*you do not realize*" are supposed to replace actual data and arguments based on actual data. All examples which I have shown include standard deviations, margins of error, confidence intervals. The mutation rate constants which I employ are not based only on Donald Clan data, I use them largely for illustrative purpose. The constants have been examined and verified and cross-verified using very many actual genealogies and actual historical data.

Jeanlohizun (cont.):
In order for you calibrated mutations to work (even if used independently and not in the disastrous mean mut/marker/gen method) that would mean that if the people from the Donald Clan project had say for example 14 mutations in the DYS388, DYS392, DYS393, DYS437, and DYS438 of their 88 haplotypes, the people from the Adams et al (2008) would have a similar number proportional to their sample size and TMRCA. Whereas you don't take into account the effect of random chance, and the fact that a complete different set can have more or less mutations in those five positions. Did you know that the mutation rate forward and backward can be different for several STRs.

MY COMMENT:
Gibberish continues non-stop. The novice apparently got an impression that I base the mutation rate constants only on Clan Donald data. In fact, said five markers have only 11 mutations in the recent 143 haplotypes in the Clan Donald dataset. However, as I have said repeatedly, I do not use the individual mutation rate constants due to their inaccuracy. I use only "whole panel" mutation rate constants, such as in 12, 17, 25, 37, 67, 111 marker haplotypes, and many other panels, more than 30 of them (they have been published in Klyosov, 2009; Klyosov & Tunyaev, 2010; and in various issues of this Proceedings). The last sentence in my "opponent" quotation above does not make sense. The mutation rate "forward" and "backward" are the same by definition in each marker. The reason is simple: the copying enzyme does not know if it is making a copying error from an allele "17" as 17→18 or 17→16.

Furthermore, the following statement is totally incorrect:
…if the people from the Donald Clan project had say for example 14 mutations in the DYS388, DYS392, DYS393, DYS437, and DYS438 of their 88 haplotypes, the people from the Adams et al (2008) would have a similar number proportional to their sample size and TMRCA.

In fact, the Donald Clan R1a1 (Red Subgroup) have 11 mutations in said five loci in the recent 143 haplotypes, as follows:

DYS	mut	the mutation rate constant (Chandler, 2006)
393	2	0.00076
388	0	0.00022
392	0	0.00052
437	1	0.00099
438	8	0.00055

As one can see, the number of mutations is small, statistically insufficient, hence, not "proportional" to the respective mutation rate constant. On the same reason it would not be "proportional" to the number of mutations in the 750 Iberian haplotypes, which, besides it, represent a mix of various subclades. My "opponent" again and again makes the same double mistake. He neglects – (a) statistics, and (b) subclades, branches, lineages in datasets, which must be resolved as much as possible before to count mutations in them in order to make any meaningful conclusions.

Jeanlohizun (cont.):
So in this hypothetical example of the people from the Donald Clan having 14 mutations in their 5 positions above mentioned, what if one were to test a different set of people who had a known common ancestor also 26 generations ago, and they turned out to have only 4 mutations in those 5 positions.

MY COMMENT:

This can easily happen. However, it would not change a thing in our understanding of DNA genealogy, because we understand a power of statistics.

Since my "opponent" does not understand some elementary things, let me explain in more detail. If the Chandler's mutation rate constants for said individual five markers (DYS 393, 388, 392, 437 and 438) are correct, then for all five collectively the mutation rate constant is 0.00304 mutations per the 5 marker haplotype panel. For 650 years (25→26 conditional generations, 25 years in each) those 5 markers should produce – theoretically – 11 mutations, because 11/143/0.00304 = 25 → 26 generations from the common ancestor. In fact, in reality there were exactly 11 mutations in those 143 haplotypes. So, a combination of those 5 individual mutation rate constants gave quite reasonable the collective mutation rate constant of 0.00304. The exact number of 11 mutations is, of course, a pure coincidence, since these 11 mutations with a confidence interval of 95% (two sigma) is 11±7 mutations, and that with a confidence interval of 68% (one sigma) is 11±3 mutations.

Therefore, if another group of people having a common ancestor of 26 generation ago produces only 5 mutations in that 5 markers, it would mean that their number of mutations is 5±4 with the 95% confidence, and 5±2 with the 68%

confidence. As one can see, 11±7 is overlapping with 5±4, hence, within 95% confidence the two group of people can easily have a common ancestor the same 26 generation ago.

Jeanlohizun (cont.):
The only way to truly calibrate the data using the genealogy calibration instead of actual measured empirical data, would be to test multiple datasets with a known common ancestor and average the mutation rate of each STR independently, and check that the standard deviation is somewhat reasonable. Nonetheless I would keep bringing forth data that shows that the usage of a combined STR sample is flawed because fast STRs undermine slow STRs in large datasets.

MY COMMENT:

The first statement is technically correct but presently unreal. In order to make it real we have to have huge ("multiple"!) datasets with known common ancestors and having at least 100 mutations in each individual marker. Those ("multiple"!) datasets do not exist as yes, and will not exist in foreseen future. Such an unreal "suggestion" only a novice can make, who does not have a "reality check".

For example, to have a "known common ancestor" the genealogy should be not deeper than 500 years ago (20 conditional generations). In order to have 100 mutations in DYS388 over 20 generations, we need 100/0.00022/20 = 22,727 haplotypes in the dataset, and – remember – with one common ancestor of all those almost 23 thousand people after only 20 generations. Even in this case those 100 mutations will be in fact 100±20 with 95% confidence, and 100±10 with 68% confidence. This will be an accuracy of the obtained mutation rate constant for DYS388. And this is not the slowest marker among the 67 marker panel. There are 11 more markers which are slower compared to DYS388 (Klyosov, 2011).

Onur:
The only thing I could add is that Proto-Altaic and all of its Proto-branches (Proto-Turkic, Proto-Mongolic, Proto-Tungusic, Proto-Korean and Proto-Japonic) were most probably all spoken in a region comprising what is now Greater Mongolia, northeast of what is now China and/or the eastern parts of Siberia, thus by full or almost full Mongoloids. Also, the Altai region isn't fully in Central Asia but in the intersection between Central Asia, Greater Mongolia and eastern Siberia. Central Asia proper is the region comprising the former Soviet republics that end with "-stan", and, unlike the regions that are the most likely homelands of the Proto-Altaic and Proto-Turkic languages, which are both east of Central Asia and are Mongoloid regions from time immemorial, Central Asia proper was

originally inhabited by non-Altaic-speaking full or almost full Caucasoids until the migrations of Altaic-speaking Mongoloids to there from the east beginning from the 1st millennium BCE at the earliest.

MY COMMENT:
I do not know why the above comment was made and what was its purpose. The commentator noticed that Proto-Turkic languages were spoken in the eastern part of Central Asia, and that Central Asia was inhabited with "full Caucasoids". In fact, nobody knows the exact borderlines of the "Proto-Turkic" regions and "Caucasoid" regions in Central Asia 16-10 thousand years ago. Since R1b1 were moving from Central Asia and spoke Proto-Turkic languages (or Dene-Caucasian, or Sino-Caucasian, or some of "Nostratic languages", or "Erbin" language, whatever linguists want to call it), I do not see any counter argument here.

Anatole Klyosov:

DP: >Turkic languages belong to the Altaic language family... Every single piece of evidence points to the fact that Turkic languages were first spoken by Mongoloids. So, even if Anatole was right about R1b in the Altai a very long time ago - which he isn't… there is no reason to associate that R1b with any sort of Turks. Actually the time depth he is talking about precedes the formation of the Turkic languages anyway.

The last sentence in the above quotation dismisses the first one. There more inconsistencies in the quotation, however, I got used to it.

The discussion is pointless unless you, Dienekes, describe which language the earlier R1b1 spoke, between, say, 16 and 6 thousand years ago (or in any time period within that range). Because why to argue if you do not know? You cannot dismiss what you do not know, and when you do not have an answer.

This is a fundamental part of a scientific paradigm: if you do not know, and cannot even suggest, do not argue.

Science is not based on dismissals and denials, it is based on advancing of hypotheses and on their examinations and verifications.

What you do, is neither examination nor verification. It is an attempt of vague discrediting without offering a counterhypothesis.

Anatole Klyosov:

Jean: >So you think that you estimated mean mutation rate from the Donald clan project

is far more reliable than using empirically measured mutation data from Father-sons pairs?

No doubt. However, you forgot to mention that the Donald Clan was just the first step, and after it the data obtained were cross-examined and cross-verified on dozens of genealogies, historical events and other evaluations, and some adjustments were made and again examined and verified.

If you care, in the Proceedings, December 2010, p. 2039-2058, the first paper has the title "Reconsideration of the average mutation rate constant for 67 marker haplotypes from 0.145 to 0.120 mutations per haplotype per generation", by Klyosov and Rozhanskii. Dozens of 67 marker datasets are considered there, to make the reconsideration. Can you see how serious people are who work in the area?

I have explained why the father-son pairs are not there yet, and why they often give misleading and incorrect data due to poor statistics. Furthermore, I gave above concrete examples of those incorrect and inconsistent data from multiple father-son pairs. It is not my fault that you cannot understand it.

Jean: >Well I got news for you: certain STRs such as DYS388 mutate differently in different haplogroups, so there goes the first strike in using the data from R1a1 to R1b1a2.

Here your ignorance goes again. It is not "news", I have researched into it for years. The verdict: DYS388 as well as ALL mutation rate constants are the same for ALL haplogroups. In short - the copying enzyme (in fact, the whole copying machinery) does not know what haplogroup is picked by us for that particular individual or a population.

DYS388 seems to be "jumpy" in J2 haplogroup only because one does not separate branches on a haplotype tree. Because the haplogroup is ancient one, it contains many branches with different DYS388 values. When one mixes them, the dataset contains DYS388 alleles in a rather wide range. When one separates branches, DYS388 is the same in each one of them. The best mutation rate constant for DYS388 is 0.00022 per the conditional generation of 25 years. It is THE SAME for all haplogroups and their subclades.

Examples for father-son transmissions in DYS388:

-- in the Ballantyne series: 0 mutations in 1636 pairs, that is the mutation rate constant is <0.0006 per generation,
-- in the Burgarella collection: 0.00042 per generation.

Do you see how jumpy and inconsistent data are in father-son pairs, even for as many as about 2000 of them?

In the R1b1a2-P312 series of 2299 haplotypes (that is, 2299 DYS388 values) - 82 mutations. Since the calculations gave 4000 ybp for the dataset (to a common ancestor), that is 160 "conditional generations" of 25 years, the mutation rate constant for DYS388 is equal to 82/2299/160 = 0.00022 per generation.

In the R1a1 series of 1198 haplotypes (that is, 1198 DYS388 values) - 48 mutations (including 17 mutations with DYS388=10 counting them as one mutation each). Since the calculations gave 4600 ybp for the dataset, that is 184 "conditional generations" of 25 years, the mutation rate constant for DYS388 is equal to 48/1198/184 = 0.000217 per generation, that is practically 0.00022.

In the Chandler table it is the same 0.00022 per generation.

As one can see, the two haplogroups (R1b1a2 and R1a1) as well as a multi-haplogroup study by Chandler all give the same mutation rate constant for DYS388.

Dienekes:
I _did_ advance a hypothesis about the origin of Turkic languages: that they came from Siberia/Central Asia and were associated with Mongoloids initially.

MY COMMENT:

It seems that Dienekes barks at a wrong tree. I have never talked about the "origin of Turkic languages". They might have originated from the Mongoloids, or from Australoids or from Denisovans or from the Neanderthals – I could not care less at the moment. I was talking about bearers of R1b1 haplogroups, that when they were migrating westward 16-10 thousand years ago and later, they spoke Proto-Turkic languages, or however we call them. It seems that the word "Turkic" for some is like a red towel for a bull. I have suggested many times – let call them "Erbin", it would have the same meaning as the Proto-Turkic in this context.

Onur:

DP: >I _did_ advance a hypothesis about the origin of Turkic languages: that they came from Siberia/Central Asia and were associated with Mongoloids initially.

It is very unlikely that Proto-Turkic or any other Altaic main branch or Altaic itself developed in Central Asia proper. From the early Chinese records we know that Altaic speaking tribes (including Turkic speaking ones) primarily lived in a

region north of, not west of, where Chinese speakers lived in early Chinese historical times (well into the Imperial Chinese times). Central Asia proper, on the other hand, was home to various Indo-European speakers before the Turkic and other Altaic expansions, which began during the 1st millennium BCE at the earliest (for most of the southern regions of Central Asia proper, as late as the 2nd millennium CE), thus well after the formation of the main branches of the Altaic language family. I also think the term "Altaic" is a misnomer, as the Altaic main branches are concentrated in a region east of the Altai mountains, so the Altaic homeland is probably east of the Altai region.

MY COMMENT: The commentator continues to speak on relatively recent times, of "Chinese records", "Imperial Chinese times", "the 1st millennium BCE at the earliest", "the 2nd millennium CE", etc. It is irrelevant to the "Erbins", their times and their language some 16-10 thousand years before present.

Jeanlohizun:
I can see that you stubbornly keep using the average of combined sets of STRs (Slow+Fast), even though anyone with access to any data set can see by running a quick experiment that often times the data from one data set cannot be extrapolated to another one, even more so, that in big data sets fast STRs undermine the TMRCA compared to slow STRs. So what if you analyzed hundreds of 67 marker datasets, none of them were actual datasets of father-son pairs, where one can truly see the true mutation rate of several markers across a generation.

MY COMMENT:

I understand that the reader probably gets tired from that parade of non-competence of my "opponent". However, I still continue to consider it as an educational material. It shows how hard for some people "in academia", as my opponent introduced himself (see above), to get simple principles and conclusions from experimental data. He still talks about "*the true mutation rate of several markers across a generation*" from father-son pairs, after all my explanations and illustrations with actual data from father-son study, in which almost 2000 pairs produce 0, 1, 2, or 3 mutations in "slow markers". One just cannot obtain "the true mutation rate" from those data. Hence, wrong dating, wrong interpretations of data, wrong "historical conclusions". Individual "mutations rates" are available only for a few markers, and for "slow" markers most of them are unreliable, except those from the first 12 marker panel. Even with them we know that their combinations do work with actual haplotype datasets, but individually they are practically not applicable. There are too few of mutations in slow markers in datasets.

Jeanlohizun cont.:

All of them (calculations) were based on the assumption of a single common ancestor who live in x time ago, and who you assume is the common ancestor of all branches of that tree, and all branches are x generations from it. Again all these assumptions carry a lot of built in errors with it them that you keep dismissing. If you were a serious member who works in the area, you would have had a grant, you would have gone into the field and collected data yourself, and your results would have been in one of the major Genetic Journals. Instead you scavenge onto others collected data (i.e. Adams et al.2008) or use data collected from projects from FTDNA, that no single serious person would consider using because it lacks the quality control required for it to be consider a randomly collected representation of a population… The thing is that there might be no such thing as mutation rate constants.

MY COMMENT:
Those are several quite popular statements among population geneticists who do work in DNA genealogy. One is the claim that "these assumptions carry a lot of built in errors with it them that you keep dismissing". When you ask those "critics" to name those "assumptions", specifically, they start to list items long ago proven to be assumed correctly. They "claim" that mutations in markers are not random, that one cannot take 25 years as a generation length, that mutation rate constants are different in different haplogroups, that mutations in haplogroups are induced by radiation, etc. They do not like "*the assumption of a single common ancestor who live in x time ago, and who you assume is the common ancestor of all branches of that tree, and all branches are x generations from it*."

As it is show above, all those negative comments are rejected by actual studies in DNA genealogy.

Jeanlohizun cont.:

AK: >I have explained why the father-son pairs are not there yet, and why they often give misleading and incorrect data due to poor statistics. Furthermore, I gave above concrete examples of those incorrect and inconsistent data from multiple father-son pairs. It is not my fault that you cannot understand it.

The fact that the sample size (in father-son pairs - AK) might be small doesn't invalidate it at all, at least is still the far best empirically collected data we got of mutational rates across a generation. So they are often "misleading" because they contrast your estimated mutations rates. Well your data is subject to tons of errors, and I tell you what: For the 25 marker, find the average mutation rate in each one of those 25 positions, then tell me what the mean mutation rate is, and what the standard deviation for that mean is. So your methodology is misleading and incorrect because of poor statistics (i.e. the mean mut/marker/gen for 25

markers is in the same range~0.002 that the standard deviation).

MY COMMENT:
It is an interesting psychological problem: One tosses a coin three times, gets two heads and one tail, and insists that the probability to get the head is 66% and that for the tall is 33%, because "*the sample size might be small doesn't invalidate it at all, at least is still the far best empirically collected data*". Wonderful. If you call it misleading and say that in fact if is on average 50:50, you get a response that "*they are "misleading" because they contrast your estimated*" data.

Wonderful. Some smart folks work in academia…

Jeanlohizun cont.:

AK: >Examples for father-son transmissions in DYS388:
-- in the Ballantyne series: 0 mutations in 1636 pairs, that is the mutation rate constant is <0.0006 per generation,
-- in the Burgarella collection: 0.00042 per generation.

Do you see how jumpy and inconsistent data are in father-son pairs, even for as many as about 2000 of them?

The data is neither jumpy nor inconsistent, it is randomly collected data, so it comes as no surprise that DYS388 being a slow markers had no mutations present in one of the samples, it is still far better than some estimated mutational rate with a trillion assumptions. Estimates are never better than empirical data.

AK:> In the R1b1a2-P312 series of 2299 haplotypes (that is, 2299 DYS388 values) - 82 mutations. Since the calculations gave 4000 ybp for the dataset (to a common ancestor), that is 160 "conditional generations" of 25 years, the mutation rate constant for DYS388 is equal to 82/2299/160 = 0.00022 per generation.

How did you know their common ancestor was 160 "conditional generations" ago? Well you had to use estimated numbers from another data set. So you seem to forget that if there is an intrinsic error carried from the other calculations (which I'm pretty sure by now, there is), this mutation rate constant would also carry that intrinsic error. Again it seems we are going in circles.

MY COMMENT:
I understand that the situation is hopeless, but still continue. The mutation rate constant 0.00022 for DYS388 was obtained by John Chandler (2006) after considering mutations in DYS388 in various datasets in various haplogroups. If I have used in my example that mutation rate constant in a reverse task, I would have received 160 generations for that specific example. The number "160

generations" of 25 years each, that is 4,000 years, came from a multitude of datasets for R1b1a2-P312, which give TMRCAs varying between 3625 and 4200 ybp. In other words, all those pieces of knowledge form a consistent picture.

Anatole Klyosov:
To Dienekes and Onur.

All right, now you are talking on some interesting things, minus confusions, unrelated to the subject of R1b1 appearance, migrations, and their language.

For example, known Turkic languages which appear in the 1st millennium AD, are irrelevant here, since we are talking on R1b1 between, say, 16 and 6 thousand ybp. So why constantly bring in contemporary Turkic languages?

If you folks did not catch it, my " R1b-Proto-Turkic theory" can be equally called "R1b-Sino-Caucasian theory", or "R1b-Dene-Caucasian theory", or "R1b-Erbin theory", or whatever, since linguists do not have a name for that language. They apparently see some remnants of it, however, do not know where to assign it. Hence, "Eniseian", "Proto-Turkic", "Dene-Caucasian", "Sino-Caucasian", "Sumer", "North-Caucasian", "Basque" languages, which are, apparently, all tips of one and the same iceberg, which was an ancient R1b language. Erbin.

Here is what I am talking about. All said languages are agglutinative languages, all belong to different time periods, all are found on the migration route of R1b1. That is why they do not look alike. They reflect different millennia, hence, differ from each other but all have similar elements. That is why Sumer language was considered as Manjurian, Tunguscan, Siberian, having Turkic elements, etc. by various linguists, and all, of course, are in disagreement with each other. Sounds familiar? That is why Basque language was considered as being related to North-Caucasian languages, or Sino-Caucasian, and some linguists support it and some deny it. It is normal, since all those are ancient languages.

Regarding "Mongoloids", both Q and R are sister haplogroups, both are from Central Asia, and, maybe, both are from the same Altai region. So why R1b1 and Q could not interacted some 16,000 years ago and much later?

Unless we all agree that what is written above makes sense, there is no point to argue.

Do we all agree? If not, why not?

Dienekes:

AK: >Hence, "Eniseian", "Proto-Turkic", "Sino-Caucasian", "Sumer", "North-Caucasian", "Basque" languages, which are, apparently, all tips of one and the same iceberg, which was an ancient R1b language. Erbin.

Linking these various languages is a very controversial, albeit valid hypothesis.

The link, however, of the proposed macro-family with R1b is completely arbitrary. What is the evidence that "Sumer" was R1b or that Sino-Tibetan (which is part of Sino-Caucasian) was R1b?

AK: >*Regarding "Mongoloids", both Q and R are sister haplogroups, both are from Central Asia, and, maybe, both are from the same Altai region. So why R1b1 and Q could not interacted some 16,000 years ago and much later?*

First of all, R1b1 is not from the Altai even if R is from Central Asia (something that is uncertain in itself).

Second, R1b1 is not the same as R, and R1b1 is absent in a great many Altaic speaking populations. The fact that R1b1 is found in some Turkic populations does not mean that it goes up to the Proto-Altaic population; indeed the largely Mongoloid character of that population and the absence of R1b1 in most of its extant branches argue strongly against it. So, you have trouble getting R1b1 to Proto-Altaic, let alone whatever hypothetical "Erbin" might have been spoken in even more ancient times in inner Asia.

Jeanlohizun:
Here is something folks so you can see how the approach taken by Klyosov in calculating TMRCA by calibrating the mutations rates per generation using family clan projects interacts with reality. Given that he has completely dismissed any empirically measured data from father-son pairs because of what he calls “poor statistics”, mainly fluctuations on the mutation rate per generation when two different samples are tested. He claims such is not the case with his calculations; this is what he said about it:

AK: >*In the R1b1a2-P312 series of 2299 haplotypes (that is, 2299 DYS388 values) - 82 mutations. Since the calculations gave 4000 ybp for the dataset (to a common ancestor), that is 160 "conditional generations" of 25 years, the mutation rate constant for DYS388 is equal to 82/2299/160 = 0.00022 per generation.*

In the R1a1 series of 1198 haplotypes (that is, 1198 DYS388 values) - 48 mutations (including 17 mutations with DYS388=10 counting them as one mutation each). Since the calculations gave 4600 ybp for the dataset, that is 184 "conditional generations" of 25 years, the mutation rate constant for DYS388 is equal to 48/1198/184 = 0.000217 per generation, that is practically 0.00022.

In the Chandler table it is the same 0.00022 per generation.

Of course because the TMRCA is not a known one, but an estimated one using the same methodology, this is going in circles.

MY COMMENT:
A gross misunderstanding again. There are no "circles" here. There are two different datasets, R1b1a2 and R1a1, one has 2299 alleles of DYS388, another 1198 alleles of the same marker. One has 82 mutations in this marker, another 48 mutations. One was independently found to have a common ancestor of 160 generations ago, another of 184 generations ago. The figures were found to be proportional, 82/2299/160 = 48/1198/184, and both of them equal to the Chandler's mutation rate constant for DYS388 = 0.00022.

Where is a "circle" here? On the contrary, the example shows that all basic relevant assumptions here were correct, and the given examples are consistent with each other and with the independent data.

Jeanlohizun cont.:
The mean mutation rate methodology was known for underestimating TMRCA, using an underestimated TMRCA would likely result in the mutation being faster than it truly is. Nonetheless I have argued that one cannot extrapolate estimated data from one set to another, instead it is better to use the empirically measured data in father-son pairs.

My COMMENT:
It is hopeless indeed. The first statement is just empty words, the second was explained many times above, but to no avail.

Jeanlohizun cont.:
But let's assume for a second that Anatole Klyosov is correct, and as he showed above we should expect DYS388 to yield an average mutation rate around 0.00022, let see what happens when we use a different sample.

The Iberian sample from Adams et al (2008) was used in the first paper published by Anatole Klyosov to show as a practical example of his methodology. He put the base haplotype of DYS388 as 12. The Iberian sample has 19 mutations (17 mutations up, 2 down) found in the position DYS388 amongst the 750 R1b-M269 haplotypes. Anyone can do the analysis which is found in the supplementary information section:
http://download.cell.com/AJHG/mmcs/journals/0002-9297/PIIS0002929708005922.mmc1.pdf

Now Anatole Klyosov in his study used the mean mut/marker/gen of 0.0015 mut/marker/gen obtained from measuring the amount of mutations in the same 19 STRs used by Adams et al (2008) on the members of the Donald Clan project, which all descend from a punative ancestor John Lord of the Isle who was an R1a1 bearer and lived 26 generations ago. With this mean mutation Anatole Klyosov dated the TMRCA of Iberians to 3625±370 ybp.

Here is his results:

" The "mutation count" method gives 2796/750/19 = 0.196±0.004 mutations per marker (without a correction for back mutations, that is λobs =0.196±0.004), or after the correction it is 0.218 ± 0.004 mutations per marker, or 0.218/0.0015 = 145±15 generations, that is 3625±370 years to a common ancestor of all 750 Iberian R1b1 haplotypes."
http://www.jogg.info/52/files/Klyosov1.pdf

Now let try to see if the readily available mutation rate for DYS388 which was shown to yield similar results in two different datasets according to Klyosov produces the TMRCA in this different sample. There are 19 mutations in the DYS388, with 17 up and 2 down, this has a degree of asymmetry of 0.8947, thus a=0.6233, a1=0.3149.

The observed mutation rate per marker is:

19/750 = 0.02533 mutations per marker.

Applying the correction factor yields 0.02543.

Now 0.02543/0.00022 mut/marker/gen = 116 generations (2890 ybp) clearly outside of the range of error of 3625±370 ybp. Now does this mean that all Iberians descend from a common ancestor who lived 2890 years ago, likely not. What this means if we assume the TMRCA of Iberians to be 3625 ybp (145 generations) as Anatole Klyosov claimed, then the estimated mut/marker/gen that would produce such TMRCA would be $1.754*10^{-4}$. Thus proving what I said above that using an underestimated TMRCA (i.e. 4000 ybp for R1b-P312) would likely result in the mutation being faster than it truly is (i.e. 0.00022>0.000175).

MY COMMENT:

Most of the above considerations are incorrect. Again, let us consider it for an educational purpose.

The first and the most important comment: I have analyzed 2796 mutations in 750 of 19 marker haplotype dataset. This provided a reasonably good statistics,

even when we knew that those 750 haplotypes include a number of subclades, such as M153, P312, U152, U106. However, the majority of the haplotypes were of P312 (for example, there were only 37 haplotypes of the M153 subclade [Adams et al, 2008; Klyosov, 2010], less than 5% of the total), and most of them are of the same "age", between 3600 and 4200 ybp (Klyosov, 2011a).

Now, my "opponent" considers 19 mutations in only one marker, DYS388, "*17 up and 2 down, this has a degree of asymmetry of 0.8947, thus a=0.6233, a1=0.3149"*.

In fact, there are 20 mutations there, 18 up (12 of "13" and 3 of "14", the latter are two-step mutations and count as two mutations each) and 2 down ("11"). However, it would not change much. What is worse, my "opponent" calculates "degree of symmetry" of those mutations, which he learnt about from my publication (Klyosov, 2009). And, being not a good student, he applies this concept literally, without thinking. Since my "opponent" likes to use the 95% confidence interval, then 20 mutations are in fact 20±9 mutations, since for 20 mutations the confidence interval is ±45%. That is how those 20 mutations should be treated. To consider here "*degree of asymmetry of 0.8947, thus a=0.6233, a1=0.3149"* is absolutely senseless, particularly with four digits (!) of precision.

In fact, 20±9 mutations can be considered as from almost totally symmetrical to almost totally asymmetrical, so it would be better to disregard a degree of symmetry in this case altogether. Otherwise it would be a pure speculation.

So, follow the "logic" of my "opponents" we continue:

(20±9)/750 = 0.027±0.012 mutations per marker.

Now, the correction factor (for back mutations) is negligibly small in this particular case. Let me show it.

Generally the correction factor is derived from the right-hand side of the following equation (Adamov & Klyosov, 2008; Klyosov, 2009)

$$\lambda = \frac{\lambda_{obs}}{2}(1 + \exp(\lambda_{obs}))$$

where:

λ_{obs} = observed average number of mutations per marker in a dataset (or in a branch, if the dataset contains several branches/lineages),

λ = average number of mutations per marker corrected for back mutations.

Since in this case λ_{obs} = 0.027±0.012, the correction factor equals to 1.014±0.006, that is around 1.4%. It is within any reasonable margin of error, and clearly why: the marker DYS388 is very "slow", and does not produce any back mutations for a VERY long time, namely for tens and hundreds thousands of years. If to apply it in this particular case, it would "correct" the value of 0.027±0.012 mutations per marker to 0.0274±0.0122, which is a negligent "correction.

Jean: >Now 0.02543/0.00022 mut/marker/gen = 116 generations (2890 ybp) clearly outside of the range of error of 3625±370 ybp.

Wrong statement. What in fact we have, is (0.027±0.012)/0.00022 = 123±55 generations, that is 3075±1375 ybp. It is well within the margin of error with the value of 3625±370 ybp, obtained earlier.

The reason for that wrong statement by my "opponent" is simple: he keeps forgetting about statistics, relies on a few scattered mutations, exaggerates "precision" of his calculations, and fails miserably with his conclusions.

Jean: >Thus proving what I said above that using an underestimated TMRCA (i.e. 4000 ybp for R1b-P312) would likely result in the mutation being faster than it truly is (i.e. 0.00022>0.000175).

A wrong statement again. In reality the last line should be:

20±9 mutations in 750 alleles of DYS388 during a timespan of 3625 years, or 145 generations, results in the mutation rate constant for DYS388 equal to (20±9)/750/145 = 0.00018±0.00008, which is within the confidence interval with the value of 0.00022, obtained earlier by Chandler (2006) and confirmed by Klyosov (2011b).

Jeanlohizun cont.:

Now if we look at DYS392 which has 71 mutations (35 mutations up, 36 down) from the base haplotype. This has a factor of symmetry of 0.5070, thus $a=1.983*10^{-4}$, and a1=0.9989. The observed mutation rate per marker is:

71/750=0.09466

Applying the correction factor yields 0.09935.

Now using estimated mean mut/marker/gen of Chandler et al (2006) of 0.00052 yields:

0.09935/0.00052 mut/marker/gen = 191 generations (4776 ybp).

Using empirically measured mutation rates for DYS392 which were estimated to have a mean mut/marker/gen of 4.123×10^{-4} (95% CI: 1.513×10^{-4} to 8.972×10^{-4}) we get 0.09935/0.0004123 = 241 generations (6024 ybp).

MY COMMENT:

It is the same story as the preceding one.

In fact, there are 63 mutations in the 750 DYS392 alleles, 35 up (31 of "14" and 2 of "15", the latter are two-step mutations and count as two mutations each) and 28 down (24 of "12" and 2 of "11"). However, it would not change the outcome much. The mutations are reasonably symmetrical, though some excess of DYS393=14 might be caused by an admixture of the M222 subclade, which has DYS392=14 as its base allele. So, it might be some excessive number of mutations here in DYS392. At any rate, 63 mutations with the 95% confidence (25% margin of error) are in fact 63±16 mutations.

The observed mutation rate per marker is:

(63±16)/750=0.084±0.021

Again, the correction factor for back mutations is negligible, 1.044±0.011, that is 4.4±1.1%, within a typical margin of error. However, let be it. The observed mutation rate per marker is 0.088±0.022. Using the mutation rate constant obtained by Chandler (2006) we obtain (0.088±0.022)/0.00052 = 169±42 generations, that is 4225±1050 ybp.

This figure fits the one obtained by my "opponent", though with slightly incorrect numbers:

Jean: >Now using estimated mean mut/marker/gen of Chandler et al (2006) of 0.00052 yields:
0.09935/0.00052 mut/marker/gen = 191 generations (4776 ybp).

It also in agreement (within the margin of error) with the value of 3625±370 ybp, obtained earlier.

The problem with the above three lines (in *italics*) is that my "opponent" keeps neglecting margins of error and confidence intervals. For him the figures, subject to statistics, apparently, have the absolute meaning.

Now, we can continue reading with a smile:

Jeanlohizun cont.:
So thus far it has become very clear that estimated mutation rates tend to underestimated TMRCA even for slow markers, and that calibrated mutation rates estimated from FTDNA projects for family clans fail when extrapolated to a different dataset.

Thus where does this leave us? We have to keep collecting more data of father-son pairs, and even three generation triples so it would at least give us a more decent picture of how mutation rates work. In any case, if we find a TMRCA using a set of slow STRs which is far greater than that of a combined set of STRs, chances are that the slow STRs TMRCA represents the true TMRCA, as the combined set might be affected by back mutations happening in the other STRs which even the correction factor might not account for.

MY COMMENT:
So, we have some gibberish again, except one phrase: "*We have to keep collecting more data of father-son pairs*". Good enough.

Anatole Klyosov:

*DP: >Linking these various languages (*presented by AK*) is a very controversial, albeit valid hypothesis. The link, however, of the proposed macro-family with R1b is completely arbitrary. What is the evidence that "Sumer" was R1b or that Sino-Tibetan (which is part of Sino-Caucasian) was R1b?*

A purpose of my "presentation" here is not to convince everyone, or not even lay out here all relevant facts and observations. There is no room for it, neither my desire, neither your intention to listen. A purpose is to show how science works: one collects some facts and observations, advance a hypothesis which explains a chain of things and events which are not explained as yet, and sometimes have not even been considered at the same angle, then, examine pros and cons, add some other facts and observations which were missed in the first version, adjust some parts of the hypothesis, etc. It is a never ending process.

Nothing is easier than to sit on a fence and criticize without adding anything to our knowledge in this particular case.

Nothing is easier than to say "The link, however, of the proposed macro-family with R1b is completely arbitrary". In fact, it is not. However, would you kindly offer another haplogroup, or several of them if you KNOW (based on DATA) which are those several ones might have been linked to the proposed language

family. Q? No, it is very unlikely. O? N? R1a? I highly doubt it. There is only one haplogroup, R1b1, which made this way, left a trek of R1b, and those R1b in Asia-Middle East today talk agglutinative languages with common elements between them. Some of them still speak very archaic and distinct variants of Turkic.

What is the evidence that "Sumer" was R1b?

Nothing in this concept is out of the blue. Assyrians as likely descendants of the Sumers have R1b as the predominant haplogroup compared with others. R1b1 in the Middle East present for 6000-5500 years, since the Sumerian times. Jews of R1b1a2 have the TMRCA of 5500 ybp, it is also Sumerian times. Sumerian language at different times was associated with Scythian language, Turkic language, Manjurian language, North Caucasian languages.

It is not my job to do a linguistic analysis, I am not qualified. However, it is my job to point in this direction.

>*First of all, R1b1 is not from the Altai even if R is from Central Asia (something that is uncertain in itself).*

I do not know how do you define the "Altai", however, South of Altai/Altay is located in Xinjiang, with the town named Altay there. Many Uigurs have R1b1, which is VERY different from European R1b, with an estimated common ancestor 16,000 ybp (Klyosov, 2008).

Gioiello:
I have expressed (also to Anatole Klyosov and to Ken Nordtvedt, who know mathematics better than me) these same concepts from many years:
1) mutations around the modal
2) convergence to the modal as time passes
3) clusters when a mutation (backwards or forwards) goes for the tangent (of course mainly of slow mutating markers).

Anatole Klyosov:
Maybe there are deep thoughts behind those three items above, however, the language employed in describing them effectively nullifies any use of them. Why wouldn't you give examples to illustrate what you mean?

What is "mutations around the modal"? Are 12→13 and 12→11 in, say, DYS388 are not "around the modal"? How about 12→13→14? Are they not "around the modal? What is new in what you have said? What problem does it solve?

What is "convergence to the modal as time passes"? Do you mean reverse

mutations? Of course some of them returned back to the initial, base haplotype. It is all described mathematically and it is the core of calculations in "my" approach.

What is "clusters when a mutation (backwards or forwards) goes for the tangent"??

Generally, it is good to have fast AND slow mutating markers in a haplotype dataset for calculations, since they balance each other. When a common ancestor lived only a few centuries ago, "slow" mutations are silent. So, effectively they are not there. Between, say, 2000-5000 ybp both slow and fast markers are good. For more then 10,000 ybp and to 100,000 ybp and older I have developed the 22 "super-slow" marker panel, one mutation in those happens on average in about 5,000 years.

A correction for back mutation is applied to the whole panel, not to single markers. It does not matter that some markers are slow and some fast. We work with average values. When you pump air into your tire, some molecules move like crazy, some slower. However, your manometer shows a stable, average pressure. Whole chemistry also stands on that concept, because molecules move very differently from each other.

When you toss a coin, heads and tails happen in various combinations, however, the average in 0.5, but only after MANY tosses.

Mutations in haplotypes behave in the same fashion.

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Обращения читателей и персональные случаи ДНК-генеалогии

LETTERS FROM THE READERS: PERSONAL CASES

Часть 31

Анатолий Клёсов

Newton, Massachusetts 02459, U.S.A.
http://aklyosov.home.comcast.net

LETTER 101

I live in Brazil. Please help me to make sense of a series of J1b haplotypes which I have extracted (in 43 marker format) from the Sorenson Molecular Genealogy Foundation (SMGF). I could not separate Iranian haplotypes from the Western Iberian ones. The haplotypes are as follows:

13 22 15 10 12 18 11 16 11 13 11 29 17.2 8 9 11 11 25 14 20 26 14 15 15 16 11 9 21 22 15 12 10 13 15 10 12 13 20 11 15 11 29 21 (Iran)

13 22 15 10 12 16 11 16 11 13 11 29 18.2 8 9 11 11 25 14 20 25 14 15 15 16 11 9 21 22 15 13 10 12 15 10 12 12 21 11 14 11 29 21 (Iran)

13 22 15 10 12 20 11 16 11 13 11 29 17.2 6 8 11 11 25 14 20 25 14 15 16 16 10 9 21 22 15 13 10 12 15 9 12 11 21 11 14 11 29 21 (Iran)

13 22 15 10 12 19 11 16 11 13 11 30 18.2 8 9 11 11 25 14 20 25 14 15 17 17 10 9 21 22 16 12 10 12 15 10 12 11 21 11 14 11 29 21 (Portugal)

13 22 16 10 12 19 11 16 11 13 11 29 18.2 8 9 11 11 25 14 20 25 14 15 17 17 10 9 21 22 15 11 10 12 15 10 12 11 21 11 14 11 29 21 (Brazil)

13 23 15 10 12 18 11 16 11 14 11 30 17.2 8 9 11 11 26 14 20 27 15 15 16 16 11 9 21 22 15 12 10 12 15 10 12 11 22 11 14 11 29 21 (Peru)

13 22 15 11 12 20 11 16 11 13 11 30 18.2 8 9 11 11 25 14 20 25 14 15 16 18 10 9 21 22 15 12 10 12 15 10 12 11 21 11 14 12 29 21 (Brazil)

Besides, I have two more J1b haplotypes from SMGF, but in a incomplete 43 marker format:

13 22 15 10 13 18 11 16 12 13 11 29 17.2 8 9 11 11 25 14 20 25 X X X X 11 X 21 22 15 12 10 11 15 10 12 11 20 11 14 11 29 21 (Iran)

13 22 15 10 12 19 11 16 11 13 11 29 18.2 X X 11X 25 14 20 23 14 15 16 17 10 9 21 22 X 12 10 12 15 10 12 11 21 11 14 X X 21 (Brazil)

Finally, I have three more Iranian J1 haplotypes from SMGF:

12 22 15 10 13 18 11 15 11 13 11 29 18.2 8 9 11 11 26 14 20 26 10 10 19 22 15 12 10 12 16 11 11 12 21 11 14 11 29 22 (Iran)

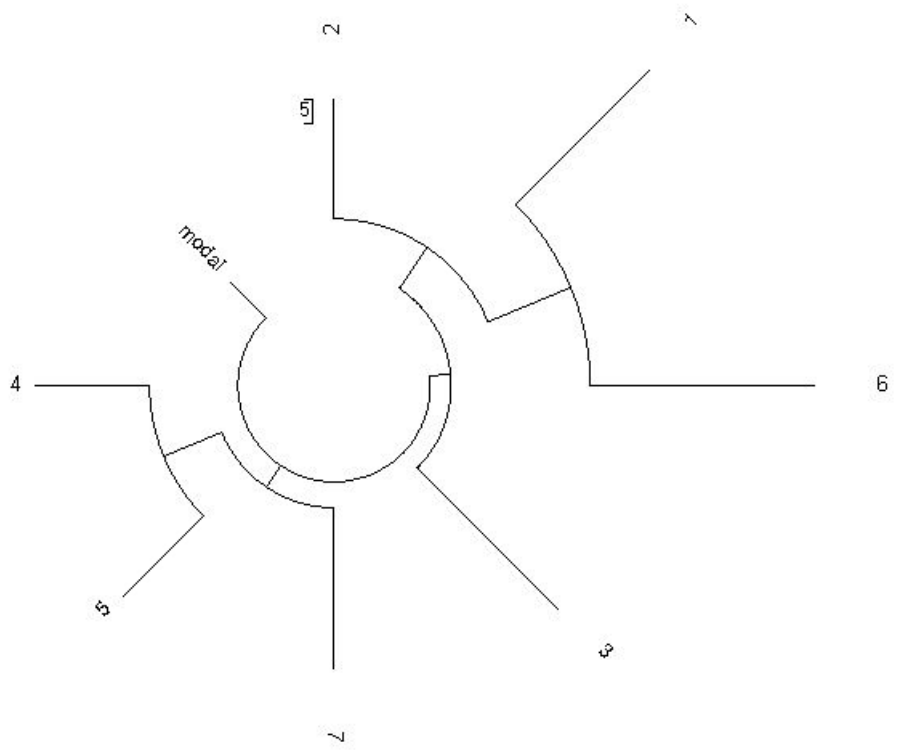
12 22 15 10 13 18 11 15 12 13 11 29 18.2 8 9 11 11 26 14 20 26 10 10 19 22 15 12 10 12 16 11 11 12 22 11 15 11 29 22 (Iran)

12 22 15 10 13 18 11 15 12 13 11 29 17.2 8 9 11 11 26 14 20 26 10 10 19 22 15 12 10 12 15 11 11 12 21 11 14 11 29 22 (Iran)

When those lineages could have been appeared?

MY RESPONSE:

The first seven J1 haplotypes from Iran, Portugal, Brazil and Peru are shown on a 43 marker haplotype tree (the numbering as shown above):



Of course, there are too few haplotypes on the tree for their detailed analysis, however, it shows two branches: one branch (on the left) contains haplotypes from Brazil (5 and 7) and Portugal (4), and the branch on the right shows Iranian (1, 2, 3) and Peruvian (6) haplotypes. Apparently, this separation makes sense, with Peruvian clearly almost identical to the Iranian (1) one, and is very likely a result of a "single" migration event.

The right branch (mainly Iranian) has 28 mutations from the base haplotype, which gives a common ancestor of 28/4/0.086 = 81 → 89 generations before present, that is 2225±475 years ago. It is rather young age for J1 haplotypes, the end of BC plus-minus a few centuries. There are not Jewish haplotypes, and their common ancestor with the Jews of J1 lived at least 4900 years ago. There were no Jews that time. It was well before "Abraham times".

The left branch (Portugal and Brazil haplotypes, that also makes sense) is very young, and contains only 9 mutations in three haplotypes from the base one. This gives 9/3/0.086 = 35 → 36 generations, or 900±310 years to a common ancestor.

There are 7 mutations (in the 43 marker base haplotypes) between the left and right branches' base haplotypes. This is a noticeable difference, and that is why the both branches are separated on the haplotypes tree. This difference places the common ancestor of the whole tree to 2800 years to a common ancestor of the whole tree. It is the beginning of the 1st millennium BC. Again, it is a "young"

lineage compared with “age” of J1 haplogroup, which is at least 16,000 years "old", and likely more.

Another three Iranian haplotypes (with DYS388=15) belong to another lineage. Those three haplotypes have a common ancestor very recently, only 575±280 years ago. However, they are VERY far away from the first series, that THEIR common ancestor lived about 8300 years ago.

Two more haplotypes, Iranian and Brazilian, have missing alleles, which does not allow to add them to the tree, shown above. However, they apparently fit well to the tree. They belong to the same or a similar lineages, rather recent ones.

CONTINUATION:

Thanks you for your interesting analysis. I agree with you that the Brazilians (5 and 7) and the Portuguese (4) are related to times of 900 years or even less, the time of the expansion of the Portuguese frontier after the Reconquista, a good time for the expansion of the Portuguese Y DNA stock in Western Iberia and later to Brazil. The Peruvian (6) haplotype is probably related to the Portuguese group as a member of a common Iberian cluster with a common ancestor differentiated from the Iranian cluster (1, 2, 3). I agree that the distance between Northern Iran and Western Iberia produced only one-time migration, only one historical movement, one opportunity and is not a regular movement connecting the two distant clusters. Therefore we have the Iranians (1, 2, 3) and the Iberians (4, 5, 6, 7) in two different branches. Is is interesting that the Peruvian is a rare haplotype, because so far there’s no other Spanish haplotype similar to that one in the Spaniard (FTDNA) or Mexican (FTDNA) big projects. The J1b M365 L136-, P58- subclade is quite distant from the other J1 L136+, P58+ L147+ subclade, perhaps almost 10000-9000 years, as you have found by the calculations.

Thanks for your contribution and insights

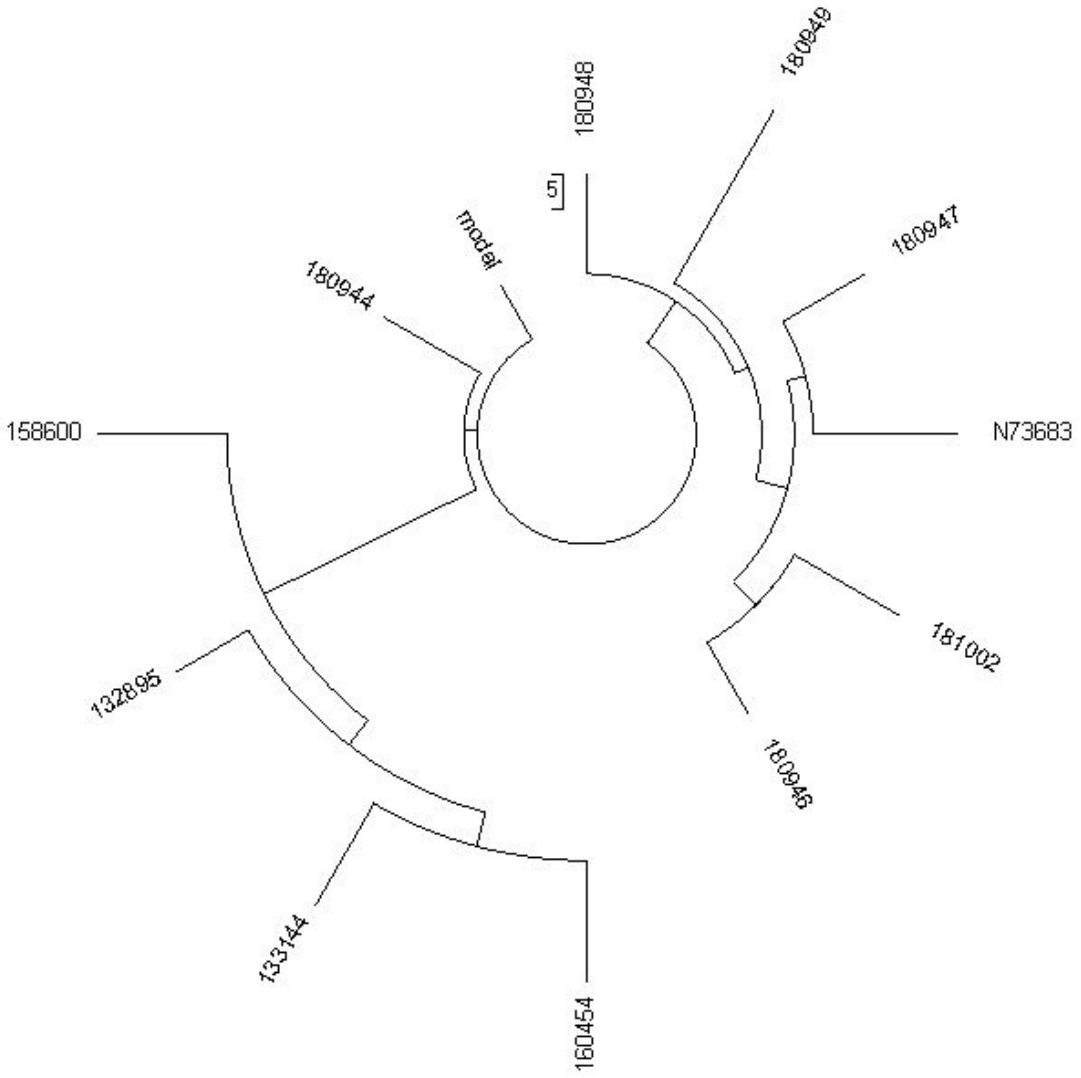
LETTER 102

I am administrating a project on FTDNA, and we run into problem of estimating TMRCA of one Lithuanian family of seven individuals, each one having 67 marker haplotypes in N1c1 haplogroup. Currently the TMRCA which we are trying to calculate fluctuates from 750 to 1100 years before present. However, we need more precise estimation of TMRCA, if possible. The seven haplotypes are attached. The 7th person, however, has a different surname than the others. So, we do not know if he belongs to the same family. Besides, there are four more

individuals which are descendants of a person who lived in the period between 1260-1340 (it is a historical fact).

MY RESPONSE

The pattern is quite clear. The extended family tree of all eleven individuals is attached, including those four distant relatives, to make the tree more informative and have "an internal control".



The four 67 marker haplotypes on the lower left side indeed form a pretty distinct branch. All four haplotypes have 13 mutations from the majority of other alleles (I call it "13 mutations from the base haplotype"). Since the mutation rate constant for 67 marker haplotypes equals to 0.12 mutations per haplotype per a conditional generation of 25 years (the last one is a mathematical value which has

nothing to do with a common "generation" which is a floating value), we have 13/4/0.12 = 27 → 28 generations, that is 700 years to a common ancestor (for the margin of error see below). 27 → 28 is a correction for back (reverse) mutations. The basis of all those calculations was published in my papers in detail. 700 years to a common ancestor means that he lived around 2011-700 = 1311 AD. You can compare it with your 1260-1340 in your letter above.

For the other branch I can tell that the suspect N73683 is just fine. It perfectly fits to the family, albeit with a different surname. 1800944 is not very clear whether he belongs to the family (the branch). He does, as an examination shows. I have calculated the branch in two versions – excluding N73683 and including him. If we (temporarily) exclude him, the six haplotypes have 23 mutations overall, which gives 23/6/0.12 = 32 → 33 generations, that is 825 years to a common ancestor (around 1186 AD). In we include him, it gives 28 mutations, that is 28/7/0.12 = 33 → 34 generations, that is 850 years to a common ancestor (around 1161 AD). As you see, it is practically the same values. You cannot expect a better fit.

Margins of error. Science requires us to provide a confidence interval, or margins of error. It depends how picky we want to be. If to apply "reasonable" expectations, common for DNA-genealogical studies, and employ the respective formulae (it is also published in my works), I obtain for the first case 1311±210 AD, and for the second two cases (two variants) 1186±190 and 1161±180 years, respectively. As you see, I am rather generous with those margins of error. In reality they are often smaller, as in this particular case. However, I would prefer to use those wide confidence intervals to be "mathematically fair".

With respect to the overall historical context, all those haplotypes belong to the so-called "South Baltic" branch of N1c1 haplogroup, unlike "Ugro-Finnish" N1c1 branch. The distinct feature of the first one is 14-14-15-15 or a mutated 15-15-15-15 quadruplet in DYS464 (in fact, it is 14-15 as a duplicate); in the Urgro-Finnish branch it is 13-13-14-14 and 13-13-15-15 (in fact, 13-14 and 13-15). A majority of Lithuanians and the Polish N1c1 belong to the South Baltic branch.

CONTINUATION:

Thank you very much for the estimations. Your date of 1186 AD makes a perfect sense historically. You mention that in reality the margin of error is smaller than ±190 years. To me the date 1186 would fit very well with one particular individual who lived around 1150- 1225 AD. My question would be how close we could come to this individual with our calculations? Can you please comment on realistic margins of error you think are present in this case.

Another important question – what is the distance do you think exists between the two analysed groups of people. Some estimates are to be about 2200 years back, other 2900-3000 years back. Would you say that in fact relationship between these two groups is closer?

MY RESPONSE:

Q.1: the margin of error. Generally, it is us who set it. If one wants to see the date with 99% confidence, it would be, say, 1186±1186, that is I guarantee (I am confident with 99% guarantee) that the ancestor lived between 2370 years ago and today. It is safe to give the data this way.

However, you would not like it, would you?

That is why we pick, how safe the date should be. The more narrow is the margin of error, the less confidence. If I say that the date is 1186±25 years, I certainly would not feel confident. Maybe 5% or less confident. Furthermore, it does not make sense to give the margin of error of less than ±25 years, since it is close to the length of generation.

Practically, a common sense plus experience gives as a formula which we employ for calculations. When I gave you 1186±190, it is a range into which my DNA-genealogical calculations typically nicely fit when compared with actual data. It might be exactly 1186 (well, give or take at which age of the father the child was born). For example, in one case I have calculated 1718, and it turned out it was 1715, when the boy was born. Still, the margin of error was ±150 years. It all depends on how many haplotypes are in the dataset and how many mutations they collectively have.

As you see, it is more or less philosophical question. 23 mutations in the dataset are not many. It could have easily been – statistically – 22, or 24, or 21, or 25. You see, it is already 10% uncertainty. For 100 descendants it would have been much more accurate.

When I gave you 1186±190, it meant that the most likely it was around 1186, but the size of that "around" depends on many factors. 190 is just a "safe" margin.

Q.2. The distance between the two lineages, and when THEIR common ancestor lived.

Actually, the same approach is applicable to those numbers that one I gave you earlier. It does not mean that my numbers are exact, because some factors I cannot control. However, the methodology is the most examined and verified one.

Having said that, let me explain how the principal question should be answered. Here are two base (presumably ancestral) haplotypes for the two lineages:

For the 7 haplotype branch:

14 23 15 11 11 13 11 12 10 13 14 16 – 17 9 9 11 12 26 14 19 28 15 15 15 15 – 11 11 18 20 13 15 18 20 35 35 14 10 – 11 8 15 17 8 8 10 8 11 10 12 21 22 14 10 12 12 17 7 13 20 21 17 12 11 10 11 11 12 11

For the 4 haplotype branch:

14 23 15 11 11 13 11 12 **10.5 14 15** 16 – 17 9 9 11 12 **25** 14 19 28 **14 14** 15 15 – **10** 11 18 20 13 **14 15 18 36 36** 14 10 – 11 8 15 17 8 8 10 8 11 10 12 21 22 **13** 10 12 12 **16** 7 13 20 21 **16** 12 11 10 11 11 12 11

Mutations between them are marked. There are 15 mutations between them (some of them are fractional, some are recLOH mutations, so their counting is not that simple). 15/0.12 = 125 → 143 generations, that is 3575 "lateral" years between them. In other words, it takes 3575 years to make 15 mutations – on average – in a 67-marker haplotype. THEIR common ancestor lives (3575+850+700)/2 = 2560 years ago. I would round it up to 2600 years before present. It is a VERY long time ago for a N1c1 population in Europe.

CONTINUATION

Thank you very much for a very interesting information.

If you do not mind, I will ask you a few additional questions.

According to your analysis, kit. No. 1800944 is placed at the origins of the family. The 1186 AD was basically obtained because the individual 1800944 was included. Lithuanian chronicles, I believe mistakenly, state that all family members (with the same surname) originate from the single person who was a young man in year 1282.

At the same time No. 1800944 has the allele of 20 in DYS576, while all members have 17 or 18. Some argue that No. 1800944 got 20 in DYS576 instead of 19, because it is typical for N1c1 to have a jumping effect in this marker. If calculations are done with No. 1800944 taking this allele as 19, one gets calculation for all 6+1 family members centered on the date 1283 AD, which corresponds to the chronicles.

I need to counter argue this position – that is to prove that jumping effect in DYS576 is impossible and the real family establishment periodization must be shifted to around 1180 AD.

I look forward to your comments on jumping effect in DYS576.

MY RESPONSE:

>*According to your analysis kit. No. 1800944 is placed at the origins of the family*

1. 1800944 is not placed at the origins of the family. In fact, he is apparently the youngest member (in terms of mutations accumulated on the "evolutional way from the common ancestor"). The ancestral allele is 18, he has 20 in DYS576. His "remote" position on the tree reflects this fact, because the program was confused with that 20, and did not know where to place him.

> *The 1186 AD was basically obtained because the individual 1800944 was included.*

2. 1186 was obtained not because of 1800944. It was when it has been removed. With it, the year was 1161, that is practically the same within the margin of error, with only 25 years difference.

>*Some argue that No. 1800944 got 20 in DYS576 instead of 19, because it is typical for N1c1 to have a jumping effect in this marker.*

3. No, it is not. DYS576 is not "jumpy", it is just a fast marker. Among 213 N1c1 haplotypes in the N1c1 FTDNA Project, "15" repeats 26 times, "16" 71 times, "17" 51 times, "18" 48 times, "19" 15 times, and "20" 2 times. The base (ancestral) allele among those 7 haplotypes is "18", and "20" is only two steps from it. From "19" to become back "18" or forward "20" is equally probable. So, it is a normal mutation.

> *If calculations are done with No. 1800944 taking this allele as 19…*

4. You cannot do it. It is a no-no. It is called manipulation with data. The data reflects a random process of mutations, and should be treated that way, impartially.

CONTINUATION:

Thank you for clarifications and communication.

I am trying to understand how 1800944 must be placed on the family tree in reality, as it seems tricky to determine. I am trying to understand if it is a separate family branch which starts from the first ancestor or else.

What would be your opinion – where he should be placed on the tree (or to which family members he is more related)? I understand the program did not know where to place him exactly.

Thank you for your comments.

MY RESPONSE:

The very fact that the TMRCA is practically the same with that haplotype or without it tells me that it is the same family. If we had 50 haplotypes of the descendants, the haplotype in question would have been among them in a nicely shaped branch. With only 7 haplotypes the program is very sensitive to mutations.

LETTER 103

I live in Flanders (Belgium) and descended from the region Antwerp-Brussels. I've got from the University of Leuven my DNA results. Can you please give me your opinion on this matter as expert on DNA-readings.

I have been looking on your website but it is a little complicated for a non-professional to analyse the data.

MY RESPONSE:

Your ancestry is in the "Young Scandinavian" branch of R1a1 group. This branch has appeared 2300±300 years ago from the "Old Scandinavian" branch, which has split about 3500±400 years ago from the population of R1a1 people at the Russian Plain (aka East Europeam Plain). Its ancestor lived there 4800 years ago, and a part of the Russia Plain branch had migrated to the East around 4500 years ago, and moved to Iran and India as the Aryans.

So, your ancestry is among the same people who were the Aryans. Of course, those historical Aryans had nothing to do with the Aryans who were bastardized by Nazi Germany. The real Aryans were not a separate "race", they were the Europeoids, that is Caucasoids, they spoke the Indo-European language (which became “Indo” after they came to India), and before that they spoke the Aryan languages. Archaeology has plenty evidences about them.

Your particular branch of ancestors moved not to the East, but to the West in the 1st millennium BC, and many of them became the Vikings. Very many people in the R1a1 haplogroup, who have a very similar haplotype with yours, live in Norway, Denmark, and in the British Isles, and also those who moved to the Isles as the Vikings in the 9th-10th century AD, and then in the 11th Century along with the French troopes and Williams the Concurer. Apparently, your ancestors left behind, and did not go to the Isles.

I hope you will find this useful.

By the way, the MacDonald Clan belongs to the same group, but they are the "younger" lineage, originated some 650 years ago.

CONTINUATION:

Thank you for clarifying some items. Can you position my personal haplotype to the haplotype tree of the Scandinavian haplotypes? And is this correct that YCAII=19,21 belong to the Norwegian region instead of Denmark?

MY RESPONSE:

In order to position your haplotype properly among the Young Scandinavian branch, you need to have 67 marker haplotype. 37 marker haplotypes miss 30 markers, which are important. As a result, 37 marker haplotypes have some uncertainty on the tree.

19,21 haplotypes belong not to "Norwegian" or "Denmark", since when they arose, there were no Norway and Denmark. There are plenty of those 19,21 haplotypes in the British Isles, particularly in Ireland. Haplotypes do not have national passports. They go across the borders.

Best regards.

LETTER 104

I have a high level of confidence in my calculations from which I am building family trees and branches, and which I have learnt from your published papers. My favorite is the logarithmic method, which is very easy to use and which typically gives very reasonable data in my genealogical studies. The only issue I

now have is using standard deviation to compare the results from the logarithmic and linear methods.

Q1: what percentage difference is acceptable between the calculation methods? I am trying to interpret the results of my initial cluster example. I understand std dev as the measure of the confidence in statistical conclusions and it is the square root of the variance. Although I have a minor in engineering math with three semesters of calculus, I think I have been doing too much accounting lately and am missing the point of how to compute std dev for two numbers. All your other math calculations I have been able to interpret.

For example, for 12 markers with 18 haplotypes, the logarithmic result is 5.35 generations and for the linear method it is 5 generations. This appears within a reasonable range but I would like to use a better method for comparing the results numerically.

For 25 markers with 18 haplotypes, the logarithmic result is 1.24 generations and for the linear method is 0 generations. How would you interpret the difference? From the single difference, I would assume that this is a clean result.

For 67 markers with 18 haplotypes, the logarithmic result is 32 generations and for the linear method is 20 generations. There are 33 mutations and I assume this is not a clean result.

Q2: for 12 markers, the 5 generations is the TMRCA? This number just appears low. I have a very homogeneous population which makes the number of generations low. A greater number of differences would increase the TMRCA. I'm building out family trees and branches so the population set will be relatively homogeneous. I'm having a difficult time interpreting this low number and it's meaning.

I am making a repeatable solution for numerous Case Studies based on your work. I'm anticipating having to answer questions that I haven't completely been able to interpret. Many other FTDNA project admins will be using the repeatable solution to build their own family trees and branches.

MY RESPONSE:

I am glad that you are acquiring a vision in DNA genealogy. Thus is an important accomplishment.

>*The only issue I have is using standard deviation to compare the results from the logarithmic and linear methods.*

This is easy. A margin of error is directly determined by a number of mutations in the linear method, and a number of base haplotypes in the logarithmic method. It should be "felt" even using a common sense.

>*Q1: what percentage difference is acceptable between the calculation methods?*

"Acceptable" depends on a confidence interval you would like to see. If you are a control frik, 1.02 ratio between the two is acceptable, and everything beyond that would drive you nuts. If you are a relaxed person, 1.1-1.2 would be fine. 1,3 would be "something is wrong" at any rate. It would mean that you have a mix of lineages.

>*... I am missing the point of how to compute std dev for two numbers.*

For 100 mutations in a dataset (it does not matter how many haplotypes) std dev is 1/(the sq root (100)), that is 0.1 (one sigma, that is 68% confidence) or 0.2 (two sigma, that is 95% confidence). That is, 100 mutations is in fact 100±20 mutations with 95% confidence.

The same thing is with 100 base haplotypes (it does not matter how many haplotypes in the dataset).

>*For 12 markers with 18 haplotypes, the logarithmic result is 5.35 generations and for the linear method is 5 generations. This appears within a reasonable range but I would like to use a better method for comparing the results numerically.*

It seems that you have a series of 18 haplotypes, which have only two mutations in all of them. The other 16 haplotypes do not have mutations at all. They are clearly ancestral, or base haplotypes. In this case 2/18/0.022 = 5.05 generations and [ln (18/16)]/0.022 = 5.35 generations.

It is very good. I typically round up to the nearest number in those cases. That is you gave 5 and 5. You cannot ask for better. This is statistics. Flip a coin 18 times. Do you think you will have a better fit between a number of heads and tails?

>*For 25 markers with 18 haplotypes, the logarithmic result is 1.24 generations and for the linear method is 0 generations. How would you interpret the difference? From the single difference, I would assume that this is a clean result.*

I assume that this is a different dataset, otherwise you already have 2 muttaions in the first 12 markers. However, there is something strange here. You mean that 17 haplotypes are the same (base haplotypes) and one haplotype has 1 mutation? But even in that case you have 1/18/0.046 = 1.2 generations to a common

ancestor by the linear method. It is NOT “0 generations”. For the same system ln(18/17)/0.046 = 1.24 generations. Again, there is no difference between the numkbers obtained, 1.2 and 1.24. What is strange, is 18 individuals and all of them have just one generations from their… presumably, father. 18 sons??

>*For 67 markers with 18 haplotypes, the logarithmic result is 32 generations and for the linear method is 20 generations. There are 33 mutations in the series, and I assume this is not a clean result.*

It is not a clean result indeed. There are at least two lineages in the dataset. You have to split them.

It seems that you have obtained 43 mutations in those 18 of 67 marker in order to get 43/18/0.12 = 20 generations. However, you wrote that you have 33 mutations. Something is wrong here. For the logarithmic method in order to get 32 generations you need less than 1 base haplotype, which does not make sense. Even in this case you get [ln(18/1)]/0.12 = 24 generations, which is less than 32. Something is terribly wrong here. Please check your gata.

>*I have a very homogeneous population which makes the number of years low. A greater number of differences would increase the TMRCA. I'm building out family trees and branches so the population set will be relatively homogeneous. I'm having a difficult time interpreting this low number and it's meaning.*

The low number of generations to a common ancestor means that there is a low number of generations to a common ancestor. As simple as that. When a common ancestor lived just a few generations back, you do not expect a high number of mutations in haplotypes of his descendants.