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La Scandale Genetique: part 4

October 20, 2018 //

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La Scandale Genetique part 4 by P Priyadarshi

The Mathematical Examination of Narasimhan and reichs Data

<https://www.biorxiv.org/content/10.1101/292581v1.full>

Any basic text book of basic genetics gives us the mathematical calculation on the basis of which we can judge whether a particular inference drawn from a set of data is correct. We shall use these mathematical formulas to assess whether Narasimhans’ inferences are correct or wrong or absurd.

If P_t is the frequency of an allele in a recipient population in generation t , P is the frequency of that allele in a donor population (or the average over several donor populations), and m is the proportion of the recipient population that is made up of new migrants from the donor population, then the allele frequency in the recipient population in the next generation, P_{t+1} , is the result of mixing $1 - m$ genes from the recipient population with m genes from the donor population.

Thus

Allele frequency $P_{t+1} = (1 - m)P_t + mP = P_t + m(P - P_t)$ Equation (1)

and

Change in allele frequency $\Delta P = P_{t+1} - P_t = m(P - P_t)$ Equation (2)

[Box 19.4, page 629; Griffiths, A.J.F. et al, An Introduction to Genetic Analysis, Eighth Edition, 2004]

Now we shall examine the Narasimhan data, in his article Fig 1B, and their supplement Fig S3.21. From these we get the admixture pattern of Onge and Ganj-Dareh Neolithic (Iranian Agriculturists of Narasimhans) genetic composition details. We shall compare the Admixture Analysis outcomes presented as histograms for Ganj Dareh Neolithic (taken as representative of the Zagros Agriculturists by Narasimhans), and that for the Onge.

We get from the Narasimhan histogram Fig S3.38 these figures. P is the dna coloured light blue in Ganj Dareh Neolithic. : P_t is the frequency of Zagros DNAs in Onge, and is 0.3 (i.e. 30%) by measurement of the blue colour in the Onge admixture-histogram.

And the value of P in the donor Zagros Agriculturist is 1.0 (i.e. 100%).



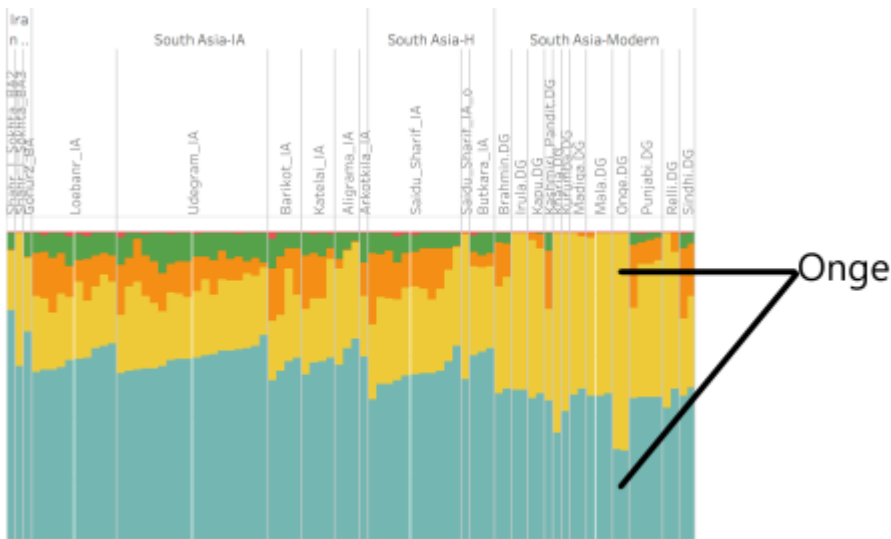


Figure PC2 S3.37 Narasimhan's supplement

Suppose 100 Onge couple (i.e. 200 persons) lived in an Andaman Island. And z is the number of Zagros Iranian males who arrived there and were successful in breeding. Now new total population would be $200+z$.

In the above situation, proportion of immigrants from Ganj Dareh to Onge would be, $m = z / (200+z)$

From equation 2 above,

$$\Delta p = m(P - P_t)$$

$$\text{Or } (0.3-0) = \{ z / (200+z) \} (1-0.0)$$

$$\text{Or, } 0.3(200 + z) = z$$

$$\text{Or, } 60 = 0.7 z$$

$$\text{Or, } z \text{ is } 87.$$

Alternatively if it is said that the arriving Iranian males would sexually replace the Onge males and thus the total number of men plus women would remain at 200, then the aboriginal people's number (100 women plus $100-z$ men) involved in genetic transfer to the next generation too will be reduced and would become $200-z$.

Calculation of z :

In the above situation, proportion of immigrants from Ganj Dareh to Onge would be, $m = z / (200)$

From the original equation 2 above,

$$\Delta p = m(P - P_t)$$

$$\text{Or } (0.3-0) = \{ z / (200) \} (1-0.0)$$

$$\text{Or, } 0.3 = z / (200+z)$$

$$\text{Or, } 0.3 = z / (200)$$

$$\text{Or, } 0.3(200) = z$$

$$\text{Or, } 60 = z$$

$$\text{Or, } z \text{ is } 60.$$

Therefore the number of arriving Iranian Agriculturist males and successfully breeding to Onge

village i.e. z was 60. Thus 60 Onge men were either massacred, or cannibalized or castrated-slaved. The war must have been fierce. The winner were certainly the Iranians. The remaining 40 Onge men in the village must have been allowed to survive as free-living slaves allowed to breed with their wives. This scale of invasion and domination must have resulted in language change. That means the current language of the Onge is derived from the Gunj-Dareh (Iranian Agriculturist) language.

These are the inevitable conclusions and deductions and corollaries which come out of the Narasimhan report.

Let in the world of science in future this phenomenon be known as the Narasimhan Phenomenon.

Addendum:

The story does not end here.

We today find that there are no Ganj-Dareh Neolithic/ Iranian Y-DNA or male haplogroups in Onge today. This means that after a few generation of subjugation and breeding by the Iranians, the Onge minority men slaves revolted and in a surprise attack killed all the male descendants of the Iranians. Academic Fraud..... ? Poor IQ.... ? Poor homework...? What is this?

Categories Uncategorized

La Genetique Scandale Part 3

September 29, 2018 //

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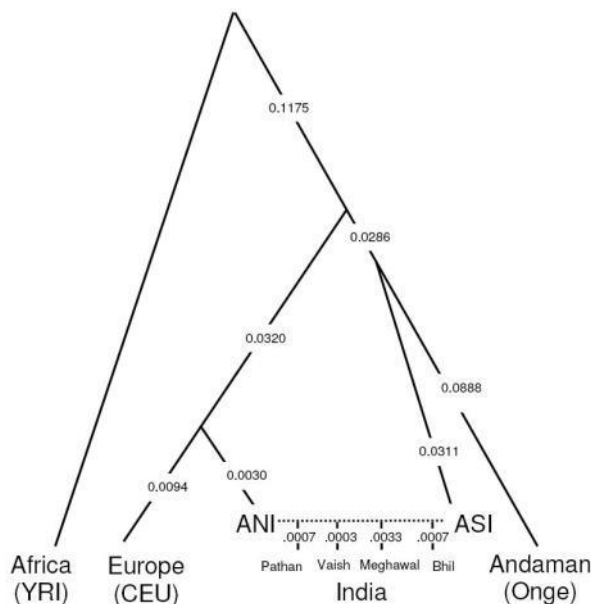
La Genetique Scandale

Part 3

P Priyadarshi

The article by the Narasimhans is full of mistake. If one looks even casually at any paragraph there is either a wrong calculation, or a self-contradiction, or a very obvious manipulation or evidence of the ignorance of the most well-known of the scientific facts. Let us see some of them.

The father of the ANA-ASI hypothesis (David Reich) who is also the master-mind of the group had never proposed that the ANI was formed by the mixing of people of Western Eurasian (European) or even steppe ancestry. He had proposed that the European (which he named CEU) and ANI had split from a common ancestor [which we can name as proto-ANI-Europe] and then diverged or ran parallel without further contributing with each other. This was explicitly depicted graphically in Figure 4 on page 492 in his original landmark article (Reich 2009).



See Original :

Figure 4 of the Reich 2009 article.

We know that science progresses by amendments. If this figure (above) and the hypothesis behind this were not correct in view of Narasimhan et al, they must have first suggested the necessary amendments to Reich's original hypothesis present in the year 2009, and then proceeded further. However they did not suggest that the original hypothesis must be amended.

However without doing this, the Narasimhans have gone straight on to proposing an entirely different hypothesis which contradicts Reich et al 2009, and claims that the ANI was formed by the admixture of the Onge (of Andaman), ancient Iranians and the MLBA-steppe (middle to late Bronze Age steppe) DNAs.

However Reich (2009) had written, "Two features of the inferred history are of special interest. First, the ANI and CEU form a clade, and further analysis shows that the Adygei, a Caucasian group, are an outgroup (Supplementary Note 4). Many Indian and European groups speak Indo-European languages, whereas the Adygei speak a Northwest Caucasian language. It is tempting to assume that the population ancestral to ANI and CEU spoke 'Proto-Indo-European', which has been reconstructed as ancestral to both Sanskrit and European languages, although we cannot be certain without a date for ANI-ASI mixture." [CEU means European in that article. This paragraph also suggests that the ancestor of the Adygei language was the original inhabitant of the Caucasus region and the Indo-Europeans had arrived from somewhere else. We have information that some parts of Caucasus region/ adjoining regions had Indo-European languages in history. These included Hittite in Anatolia, Maikop in North Caucasus, Armenian towards the south.]

Thus it had been made out clearly by them (Reich 2009) that the European population (called CEU in that article) had split from the proto-ANI-Europa trunk, and stayed segregated from the ANI branch for long before ANI and ASI admixed together to give rise to the later Indian (both north and south) populations.

Earlier Reich had thought and claimed that the ancestor ANI-European (call it Proto-ANI-Europa or PAE) reached Europe direct from North Africa. Then ANI split and migrated through Iran to India,

and the main trunk had stayed back in Europe from which Central Asian as well as West Asian people too originated.

However since 2015 (Haak's and all later works) made it clear that Europe was inhabited by dark-skinned, entirely different people up to at least 5500 BC and the newer people who now live there came into Europe from Asia in several distinct waves between 5500 BC and 1500 BC. This happened by two routes one to the north of and the other to the south of the Black Sea (Neolithic to Bronze Age migration). A third route through the Mediterranean islands has also been identified.

Now the genomic findings as depicted in the figure above (Fig. 4 Reich 2009) needed to be explained in a different way than he had thought. It was going to be the same as had been explained by Priyadarshi in the past. The findings of Reich 2009 would mean (following the Haak 2015 onwards) that the Ancestral Europeans (AE) split from the Proto-ANI-Europa, and lived long in isolation in some place which was not in Europe. It would imply that the ANI (Ancestral North Indians) and the ancestral Europeans had stayed at two (or more) different locations outside Europe for quite some time (as depicted in the Figure 4 of Reich 2009). By all available ancient DNA evidence these locations were going to be North India and Iran, also possibly the Pamir-Tajikistan-Tarim region. Thus Iran (and/or Pamir-Tajikistan region) was the intermediate homeland for the European languages.

However the Europa-gene could not stay pure. It got admixtures from East Asians and Africans to give rise to the modern European population. This admixture of the Europa with these several populations in varying combinations produced the several European nations, and these admixtures cause the distance found today between the genetic composition the modern European and modern Indus-Valley populations.

The far right wing Eurocentric supremacists, which dominated the Harvard Academics, could not digest this fact. David Reich being quite clever decided to stay at the back foot, and pretend a middle-path or centrist approach. Hence he himself claimed in his latest book that the homeland of the Indo-European was in Iran and/or Armenia. He wrote,

“This suggests to me that the most likely location of the population that first spoke an Indo-European language was south of the Caucasus Mountains, perhaps in present-day Iran or Armenia, because ancient DNA from people who lived there matches what we would expect for a source population both for the Yamnaya and for ancient Anatolians. If this scenario is right, the population sent one branch up into the steppe—mixing with steppe hunter-gatherers in a one-to-one ratio to become the Yamnaya as described earlier—and another to Anatolia to found the ancestors of people there who spoke languages such as Hittite.”. [page 145 of the pdf version of his latest book *Who We Are and How We Got There* 2018.]

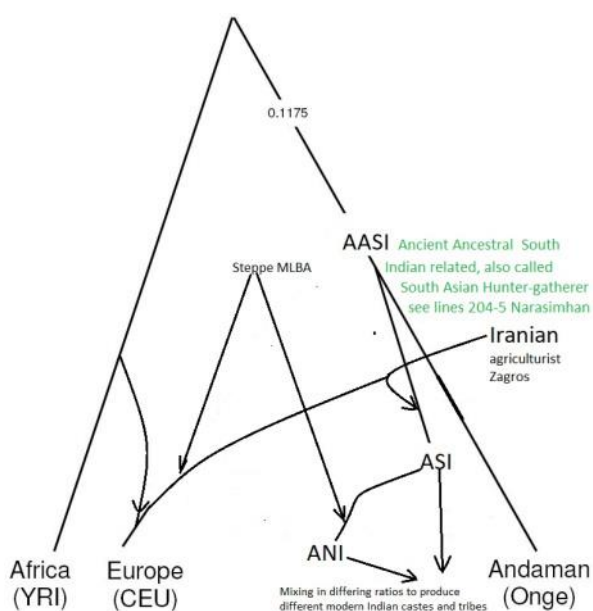
While himself maintaining the centrist posture, he sponsored now various young and ambitious Indian workers and students and job-seekers to re-create the myth of the steppe home of the Indo-European languages from a new crutch. Fellowships, grants and academic positions attract every academic person. Narasimhan, Moorjani, and Niraj Rai started working in a new line. People started writing copious reports after reports in support of the Far Right Wing (Nazi) ideologies which included the Ukrainian or Baltic homeland of the Indo-Europeans for a long time. However these reports were full of mistakes which even a casual reading could reveal.

Thus Narasimhans claim that before the Iranian admixture to Indian population the whole India consisted of Onge people. They named it AASI (Ancient Ancestral South Indian), as if Ancestral South Indian (ASI) concept itself was not sufficient to explain the things. In this new concept the ASI and ANI were not coming from the main trunk, but were coming from a further ancestor AASI (Onge), from which ANI and ASI had originated but the CEU (European) had not originated. In fact instead of emerging from the main trunk, the ANI and the ASI had been formed from admixture of the AASI and two other populations, Narasimhan et al claimed. While the AASI was from the main trunk, ANI was AASI+Iranian+Late Steppe; and ASI was AASI+Iranian. Iranians too were possibly from the main trunk they thought. The Middle to Late steppe population was a hybrid which had been made from ancient north European, Anatolian, East Asian and Iranian admixtures. And these were the people who invented the Indo-Iranian languages in the eastern parts of the MLBA-steppe distribution.

The first contradictory statement to Reich (2009, figure cited above) by Narasimhan is that the “Hierarchical Modeling Shows ASI and ANI Both Had Iranian Agriculturalist-Related Ancestry” (Lines 4811-4812, Supplementary Information, Narasimhan et al 2018).

They further write contradicting Reich 2009, “Line 4870: Simple Statistics Confirm Iranian Agriculturalist-Related Ancestry in the ASI”. Giving a deadly blow to Reich (2009) they write, “The ANI Cline represented mixtures in different proportions of Indus_Periphery- and Steppe_MLBA-related groups, and the ASI Cline represented mixtures in different proportions of Indus_Periphery and AASI.” [Lines 5135-5137; Narasimhan 2018 Supplementary.] While in the original concept by Reich the ANI and the ASI were two lineages of a common remote ancestor. He had proposed that one lineage gave birth to CEU (Europa, in fact Iranian) and Ancestral North Indians (left branch in figure) and the other branch (right one) had given gave rise to ASI and Onge-Andaman. Clearly this has been destroyed completely by Narasimhan’s article. So who is correct? Reich or Narasimhan? This is the main question.

The Reich et al (2009 figure 4) has now been fully replaced by a model by Narasimhan, which would now look somewhat like this:



The Narasimhan Model

Anatolia (Asian part of Turkey) has occupied a special place in the hearts of the Far Right Eurocentrics. Although they call it Asia Minor, they actually consider it 'Europe Minor'. This place was the cradle of Eastern Roman Empire, and the Constantinople is a reminiscence of that past. And the Levant (Jordan and Israel) is important to the Jews as they have copious mention in the Old Testament. It is important to the Western people in general as it is the home place of Jesus Christ.

In spite of the Far Right Eurocentric claims, the emerging facts did not prove that these two (Anatolia and Levant) had been the sources of the cultures located to their East like Iran and India. Archaeology did not support such views and the recent ancient DNA studies too tell the reverse.

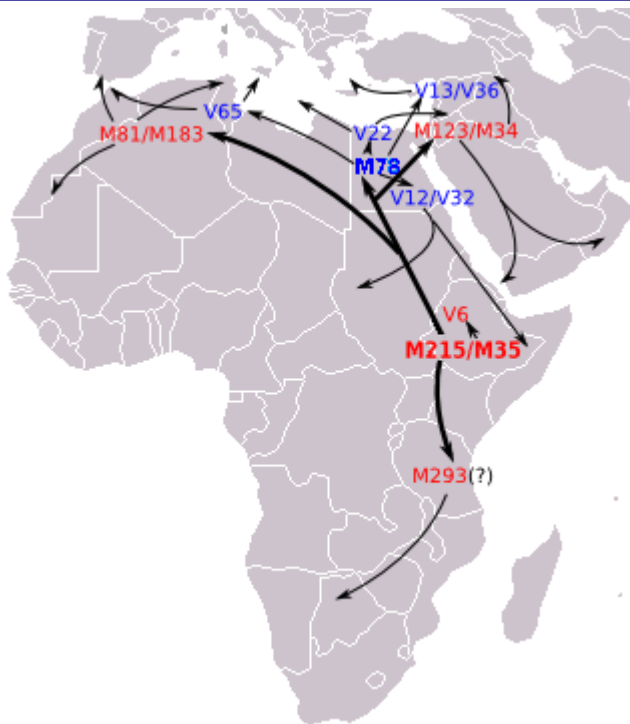
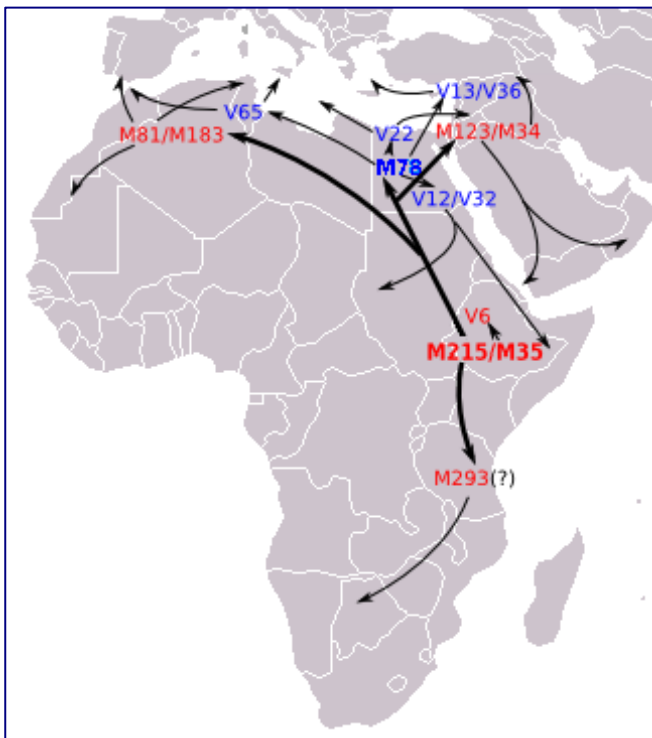
Kavita Gangal et al (2014) of the Newcastle University, UK, published an article in which she calculated the speed of migration of the farming/ pastoralism from Israel to India, and found it to be 0.63 to 0.71 kms per year. This article too was based on the assumption that the Mehrgarh was later than Israel and Iran. The distance from Israel to Mehrgarh is about 4,200 kms. And the Israeli people reached Indus Valley about the Bronze Age. Dorian Fuller also wrote many articles denying the originality of the Indica rice in India. Such articles were published in advance much before finally orchestrating a volley of a dozen articles and a book to prove something which was never a fact. Narasimhans denied the entire pre-Harappa archaeology of India.

To support their claims of later acquisition of agriculture in India from West Asian, they have cited Fuller (2003) and Fuller (2007) who is also one of the co-authors of the impugned article. However most of the discoveries in Indian archaeology have taken place after that. These authors have not consulted the articles on Mehrgarh written in 2008 by authors like Jarrige (the French excavator of Mehrgarh) and Peter Bellwood (an International doyen in Archaeology). The central Indian farming sites which pre-date the west Asian's have all been studied only after this time. The Ladakh farming sites of 7th millennium BC, and Assam early farming of almost equal antiquity have all been omitted (probably deliberately).

We should go by the facts. The first settlement at Jericho was established at about 7500 BC, and it lasted only 300 years. "At some point between 8000 and 7000 B.C., the first permanent settlement on the site was started by an unknown people who built extensive walls ..." [La Boda, Sharon, 1996, International Dictionary of Historic Places: Middle East and Africa, Fitzroy Dearborn Publishers, Chicago and London.]

The DNA analysis of the people found from Israel and Jordan Neolithic sites indicates that most of those who had arrived here were from Africa. This could be said because they harboured the African male DNA lineages (Y-DNA) E1b and its branches. From the Levant Neolithic, Lazaridis reported eight Y-DNA results. Out of these the sample number '1414' had Y-DNA haplogroup E, '1415' had E1b1b1 (PPNB; Pre-Pottery Neolithic B), '1710' had E1b1b1. These were post glacial arrivals from African corridor. However one sample numbered '0867' was Indian Y-DNA lineage H2. Thus out of the eight one was Indian and three were African. The other three were CT which might have arrived from South Asia about 50,000 years ago and can be considered local settled hunter-gatherer population of the Levant. One sample, numbered '1707', was Y-DNA T. (Lazaridis 2016, Supplementary Information p. 51, Table S6.1). T possibly originated in Andhra Pradesh of India. Similarly out of five Natufian samples three were the African E1b1 and E1b1b1b2 and two were CT. These lineages (E1b and its branches) did not migrate further east to Iran, as they are not

found from the Bronze Age samples from Iran. However they are found from Armenia and later steppe.



Y-DNA E1b1b spread during Neolithic

The Anatolian Neolithic too was characterised by a large number of Eastern arrivals particularly the East Iranian G2a and the Indian (Andhra Pradesh) H2. Later the African lineage E1 and its branches are found in the plenty in the Y-DNA recoveries from the Early Bronze age Anatolian skeletons.

The E1b1b etc came to Anatolia through the Levant (Israel and Jordan). (Lazaridia 2016 Supplement page 54; Barros Damgaard Excel Table S14).

They write, “While some Y-chromosomal lineages (such as H2, T, and G2a) span more than one early Neolithic population in West Eurasia, none of them are found in all of them (Levant, Iran, and North-western Anatolia/Europe), in agreement with the conclusion based on the analysis of autosomal data that the Neolithic of West Eurasia either began (or was taken up soon after its beginning) by genetically diverse populations.” In other words, the people who arrived at the north-west Anatolia to activate the Neolithic revolution had arrived there from several different sources. We can clearly see in the Y-DNA haplogroup constitution of northwest Anatolia that the Neolithic people had arrived there from India (haplogroup H2); Iranian Zagros (haplogroup G2a) and Northeast Africa (haplogroup E1b1b).

Finally they clarify that the Neolithic Iran and the Neolithic Anatolia are very different. Yet at the Chalcolithic (Copper Age) period they share some resemblance or components. This is not because the Anatolians migrated to Iran, but because the Iranians expanded to Anatolia, Caucasus and the steppe during the Chalcolithic period.

“However, the two are not a clade, and Chalcolithic Anatolia differs from the Neolithic by sharing more alleles with “eastern” populations from the steppe, the Caucasus, and Iran. Thus, at the western end of western Asia, the population seems to become more “eastern” just as at the eastern end (Iran) it became more “western”, confirming the visual impression from PCA (Fig. 1b) for highly differentiated Neolithic populations (Anatolia_N vs. Iran_N) but relatively similar Chalcolithic ones (Anatolia_ChL vs. Iran_ChL).” [p. 91]

“We first model Anatolia_ChL as a mix of Anatolia_N and a population A (Table S7.17). Only populations from Iran and Armenia work as sources of the input into Anatolia, confirming the visual impression from PCA. This input is quantified as at least $32.9 \pm 7.9\%$ when Iran_ChL is used as a source population A.” [p. 91]

La Boda also confirmed that the Israeli (Levant) Bronze Age was a product of arrivals from Iranian Copper Age. Haber “Showed that the Levant Bronze Age population from the site of ‘Ain Ghazal, Jordan (2490–2300 BCE) could be fit statistically as a mixture of around 56% ancestry from a group related to Levantine Pre-Pottery Neolithic agriculturalists (represented by ancient DNA from Motza, Israel and ‘Ain Ghazal, Jordan; 8300–6700 BCE) and 44% related to populations of the Iranian Chalcolithic (Seh Gabi, Iran; 4680–3662 calBCE)” La Boda, citing “Haber, M. et al. Continuity and admixture in the last five millennia of Levantine history from ancient Canaanite and present-day Lebanese genome sequences. *Am. J. Hum. Genet.* 101, 274-282 (2017).”]

The admixture analysis revealed that instead of the Israelis moving towards Iran, the Iranians had moved into the Israel region to produce the Levantine Chalcolithic population (Harney et al 2018 *Nature*). [“We conclude that while the Levant_N and Levant_ChL populations are clearly related, the Levant_ChL population cannot be modeled as descending directly from the Levant_N population without additional admixture related to ancient Iranian agriculturalists.” (p. 4, *ibid*)]

Similarly the radiocarbon dates from Gesher (or Sultania) is 7930 ± 140 BC (Gerfinkel, Y. and Nadel, D., 1989, The Sultania flint assemblage from Gesher and its implications for Recognising Early Neolithic Entities in the Levant, 15(2):139-151). No pottery, not any figurine, was found from these remains. Only flint spear-heads (a type of stone) chips were found. [see figure]. However these flint pieces were used for hunting, and therefore these people were mainly hunters.

One thing is clear that the Anatolian farmers did not move towards the East. “The origin of the Neolithic of Iran does not appear to be related to either Anatolia or the Levant, as the Neolithic and Mesolithic of Iran are symmetrically related to either population (Fig. S7.5), providing no evidence for gene flow from either region into the Zagros, but hinting strongly that whatever role the exchange of ideas and technology may have played in the emergence of the Neolithic in the Zagros, this was not accompanied with any substantial gene flow from other ancient Near Eastern Neolithic centers of domestication.” [Lazaridis 2016 Supplement p. 70].

Clearly this means that the Anatolian genetic cline found by Narasimhan’s study reaching up to Indian borders is artefactual resulting from mishandling/ manipulation/ tampering of the genetic data. In fact the Anatolian Neolithic was the product of arrival of the farmers from India, Iran and Africa into a region inhabited by local hunter-gatherers which were genetically continuous with the European hunter-gatherers before such arrivals. This is reflected in the following lines by Lazaridis:

“we observe that the Neolithic Anatolians are genetically shifted towards Europe in the PCA (Fig. 1b) and have ancestry from an ancestral population related to European hunter-gatherers according to ADMIXTURE analysis (Fig. 1c). This should not be interpreted as evidence of ancestry from actual hunter-gatherers from Europe; while this is not implausible for our sample from Northwestern Anatolia, we have previously seen that populations of the ancient Near East are also differentially related to European hunter-gatherers. This suggests that populations related to European hunter-gatherers existed in the Near East and may be included in the Epipalaeolithic/Mesolithic ancestors of the Neolithic Anatolians without any need for a direct migration from Europe”. [Lazaridis 2016 Supplement p. 74].

Also;

“Our finding that the Levant_ChL population can be well modeled as a three-way admixture between Levant_N (57%), Anatolia_N (26%), and Iran_ChL (17%), while the Levant_-BA_South can be modeled as a mixture of Levant_N (58%) and Iran_ChL (42%), but has little if any additional Anatolia_N-related ancestry, can only be explained by multiple episodes of population movement. The presence of Iran_ChL-related ancestry in both populations – but not in the earlier Levant_N – suggests a history of spread into the Levant of peoples related to Iranian agriculturalists, which must have occurred at least by the time of the Chalcolithic. The Anatolian_N component present in the Levant_ChL but not in the Levant_BA_South sample suggests that there was also a separate spread of Anatolian-related people into the region. The Levant_BA_South population may thus represent a remnant of a population that formed after an initial spread of Iran_ChL-related ancestry into the Levant that was not affected by the spread of an Anatolia_N-related population, or perhaps a reintroduction of a population without Anatolia_N-related ancestry to the region.” [p. 8; Harney]

Hafmanova also found,

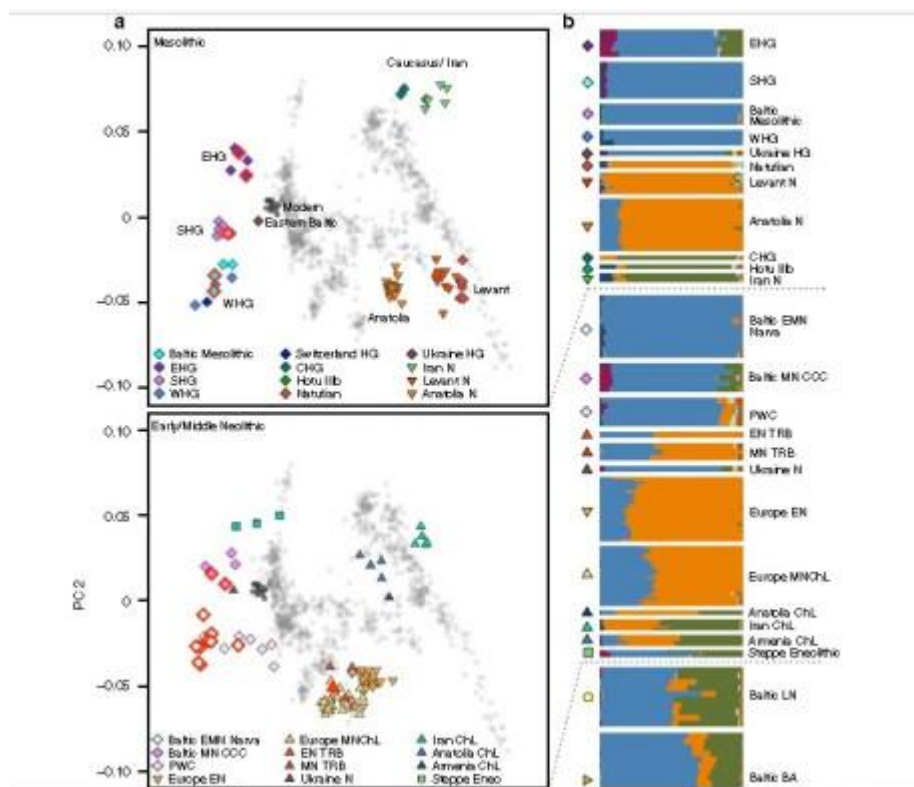
“Furthermore, when we form each Anatolian Neolithic genome as a mixture of all modern groups, we infer no contributions from groups in southeastern Anatolia and the Levant, where the earliest Neolithic sites are found (SI Appendix, Figs. S22 and S30 and Table S30; Dataset S3). Similarly, comparison of allele sharing between ancient and modern genomes to those expected under population continuity indicates Neolithic-to-modern discontinuity in Greece and western Anatolia, unless ancestral populations were unrealistically small” Hofmanova p. 6889

“The dissimilarity and lack of continuity of the Early Neolithic Aegean genomes to most modern Turkish and Levantine populations, in contrast to those of early central and southwestern European farmers and modern Mediterraneans, is best explained by subsequent gene flow into Anatolia from still unknown sources.” Hofmanova p. 6890.

This unknown source was also the source of Y-DNA haplogroup H2 found in the early Neolithics of these regions. Thus we can say that the unknown source was South Asia.

The last item for today is another article published this year and co-authored by Reich. The first author is Mittnik. The title is “The genetic prehistory of the Baltic Sea region”. Since it was not in the linguistic context, the Admixture analyses have not been tampered or manipulated.

They are below:



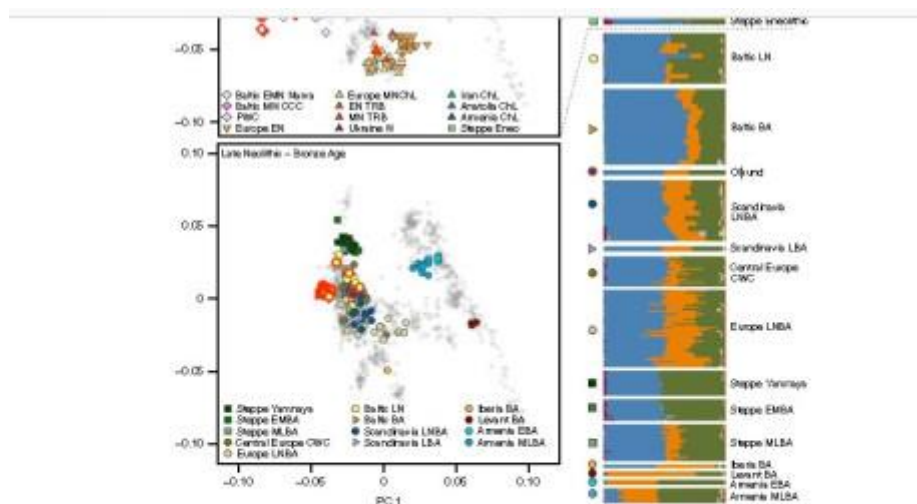


Fig. 2 PCA and ADMIXTURE analysis reflecting three time periods in Northern European prehistory. **a** Principal components analysis of 1012 present-day West Eurasians (grey points, modern Baltic populations in dark grey) with 294 projected published ancient and 38 ancient North European samples introduced in this study (marked with a red outline). Population labels of modern West Eurasians are given in Supplementary Fig. 7 and a zoomed-in version of the European Late Neolithic and Bronze Age samples is provided in Supplementary Fig. 8. **b** Ancestral components in ancient individuals estimated by ADMIXTURE ($K=11$)

It reveals that there are three larger principal components, blue, yellow and green.

Steppe-MLBA is having all the three colours. But the steppe-Yamnaya and the steppe-EMBA have only green and blue.

Yellow is the colour of Natufian (Israel Mesolithic) and Levant (Israel-Jordan) Neolithic. As discussed above, this is predominantly African in origin and its male lineage is African E1b1 and branches. Thus yellow colour is the marker of the African admixture.

Iran Neolithic and Caucasian hunter-Gatherer are predominantly green. In our interpretation the green colour should belong to the ANI and also the Indo-European linguistic groups.

Baltic Mesolithic and SGH (Sweden Hunter Gatherer, Motala) are blue. It means the original people of Europe belonged to almost pure blue. Ukrainian Hunter-Gatherers and the Ukrainian Neolithic are also largely blue indicating continuity with the original European population before the Neolithic period.

Thus it is the admixture of African (yellow, through Levant and Anatolia), Ancestral North Indian (green, through Iran and Caucasus) and blue (original European) which by combination produced the

If we mix Iran-Chalcolithic (see in figure) with the Ukrainian or European blue substratum, it gives exactly the same proportions of the colours which are there in Scandinavian and European LNBA (Late Neolithic to Bronze Age). Remember that in absolute time scales (calendar time) Iranian Chalcolithic is older than European Late Neolithic.

But the Early Bronze Age steppe is just a mixture of West Siberia-Steppe-Europe substratum (blue) plus ancient North Indian ANI (Green).

It is the addition of yellow (Anatolian/ Levantine) to EMBA steppe / or the Yamnaya steppe which produces the MLBA steppe, which has been linked by the Narasimhans with the Indic branch of IE migration. Clearly people from Iran and India had arrived into the steppe during the MLBA period, bringing the people speaking the Iranian and the Indic languages, clear enclaves of the two have been found linguistically in the Western Siberia and the steppe.

La Genetique Scandale By P. Priyadarshi

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La Genetique Scandale

By Premendra Priyadarshi

PART 2

Manipulation with data and Concoction

The Defective Design of Research: Systemic Bias

Bias in the modern scientific researches and concluding narratives is the rule rather than exception (Mullane and Williams, Eds., Biochemical Pharmacology, Elsevier Journal, 2013; Smith and Noble, British Medical Journal, 2014; Pannuki and Wilkins, Plastic and Reconstructive Surgery 2010). Narasimhans' paper is the first class example of how biases can be operative at all the levels and stages of research. If all the manipulations and biases in the book is listed it will form a 1000 page volume, which is not my intention to do. Because will consume at least one year of my time writing all that. Some very obvious things, which even lay readers can understand will be noted below.

The Admixture Analysis and the Identification of Component

In the admixture Analysis presented by them, they have identified some primary components or populations genetically, which were to act as components for the formation of other populations by admixture later in the history. We shall first see only three of them :

Line 197 (BioRxive) . “Iranian agriculturalist-related”: represented by 8th millennium BCE pastoralists from the Zagros Mountains of Iran (17, 18)

Line 201 (ibid). “West Siberian Hunter-Gatherer (West_Siberian_HG)-related”: a newly documented deep source of Eurasian ancestry represented here by three samples

Line 204 (ibid) . “Ancient Ancestral South Indian (AASI)-related”: a hypothesized South Asian Hunter-Gatherer lineage related deeply to present-day indigenous Andaman Islanders (19) [The Narasimhans have used the DNA of the ONGE Tribe of the Andaman Islands to represent this gene pool.]

ONGE

The Narasimhans (a handy word in lieu of Narasimhan and colleagues) have identified Ancient Ancestral South Asian- (AASI)-related population by the modern Onge tribe's genome, which live in the Andaman Islands today, and which are genetically related to the Papua New Guinea tribal peoples from the antiquity. Surprisingly the Narasimhans' hypothesis that there were people having identical genomic constitution as the modern Onge living in India until the Iranians and the steppe people arrived and admixed with them. These Indians have been labelled as the AASI in the paper. This is a new invention (Neologism) uniquely invented for the occasion. These Onge people of

North and South India admixed with Iranian and mid-to-late BA steppe genetic group to produce the modern Indian populations, Narasimhans conclude.

In their hypothesis the admixture of the Onge-genome with the Iranian one gave rise to the South Indian (Dravidian) population; and the admixture of this with the Middle-to-late-Bronze Age steppe population gave rise to the North Indian (Aryan) population, they hypothesize. In other words it is the resurrection of Elamite theory of the origin of Dravidian in addition to the Aryan Invasion Theory.

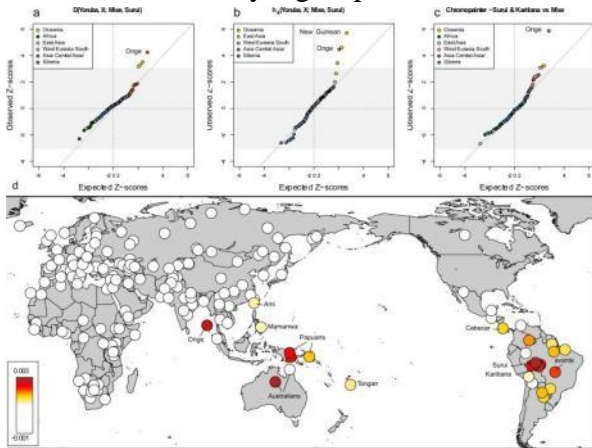
However the real story is different. Onge people could have been of the same genetic composition as the Indians about 70,000 to 50,000 years back, but not today, not even 10,000 years before today. These people (Onge) are the remnants of the people who migrated to the Andaman Islands, and also to the southeast Asia about 70,000 to 50,000 years back. Some had stayed in India; some had arrived into Andaman (ancestors of the Onge and Jorwa); and some others would migrate eastward towards Papua New Guinea and Australia. But they did not stop there. They migrated further east to South America.

Thus the Onge separated from the rest of the humanity about 50,000 to 70,000 years ago, noted Thangaraj et al (2005) in their genetic study: This was the same time when the Australians (and the Papuans) separated from the rest of the humanity. They are considered Australasian family, and must be considered much more remotely connected to the Ancient Ancestral South Asians than the European Cro-Magnons, Siberians, Iranians and the Central Asians who branched off from the main basal Eurasian trunk much later than the Onge did.

It is useful here to recollect what Thangaraj wrote about the Onge: “Our data indicate that two ancient maternal lineages, M31 and M32 in the Onge and the Great Andamanese, have evolved in the Andaman Islands independently from other South and Southeast Asian populations. These lineages have likely been isolated since the initial penetration of the northern coastal areas of the Indian Ocean by anatomically modern humans, in their out-of-Africa migration –50 to 70 thousand years ago.” [Thangaraj et al, 2005, Reconstructing the Origin of Andaman Islanders, Science, 308 (5724): 996.]

Thangaraj also noted that over the period of time the genetic composition of the populations of the Andaman-Onge and Indian-Mainland population drifted from each other due to changes taking place in the two independently. They note: “Analysis of the complete mtDNA sequences shows that none of the coding region mutations defining these two haplogroups overlap with the known Indian or East Asian mtDNA haplogroups (1–5). In our survey of 6500 mtDNA sequences from mainland India, none of the M lineages carried the coding region mutations specific to M31 and M32 (6).” (Thangaraj 2005). Thus we can see that genetically the Onge had deviated a lot from mainland India over the last 50,000 years of the separation. The Onge people are short-stature and dark skinned. (Thangaraj is one of the authors in Narasimhan’s article too).

In fact the article which claimed that the Onge had migrated east even up to South America had been authored by a group of authors which included the doyen David Reich himself.



<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4982469/figure/F1/>

Thus considering Onge as the Indian population at the onset of Neolithic marred the total work, and vitiated all the results. Instead of considering the Onge as single component, their admixture analysis found that it is an admixture of Iranian DNA. This error occurred because the authors failed to recognise that the Onge and the Iranians both had split from the mainland Indians, although in different eras. Hence there must be some elements common in the three the Iranian, the Mainland Indian and the Onge populations. However there would be some portions which would be distinct in the three populations.

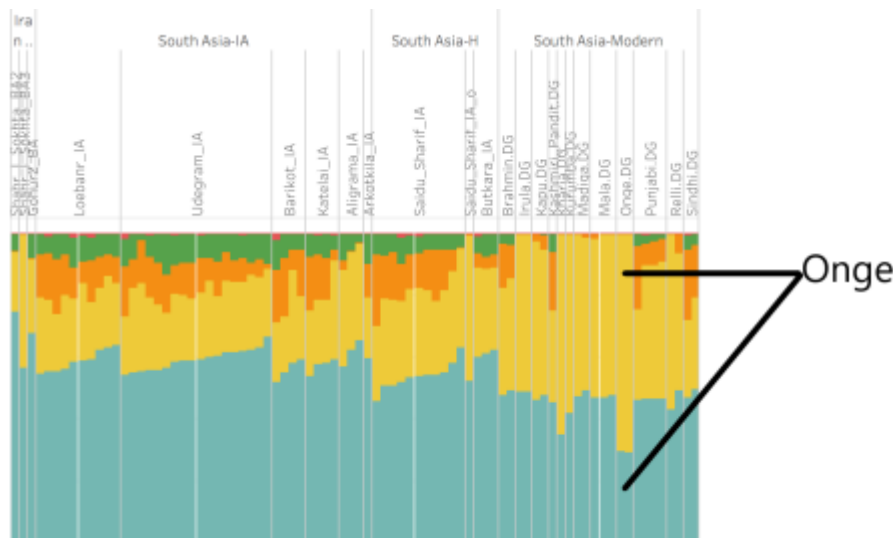


Figure: Onge as shown in the Admixture Analysis in the Figure S3.37; page 166 of the Supplement of the Narasimhan et al. Onge highlighted and pointed out by us. In this figure, Onge has almost the same components as the Mala, Irula, Shaidu-Sharif (Iron Age_0) and Shahar-i-Sokhta BA3, except that the latter ones have greater proportions of the Iranian component.

This failure to appreciate some commonality (due to origin) between Indian and Iranian DNAs resulted in considering the Iranian farmers as unmixed pure component. It was also compounded by the false and erroneous belief that nobody could ever have gone out of India. In an effort at negating the Indian components in the Iranian Agriculturists the authors used the parameters in such way as

that it read Iranian Agriculturists made up of a single component, coloured teal (light blue) in the Admixture Analysis.

Such distortion in the calibration vitiated the whole result in such a way that the mono-component genomes of the Onge (Andamanese) started showing made up of two components. One of them was blue (Iranian Agriculturists) as depicted in the histogram above.

How it happened can be seen in the figure below:

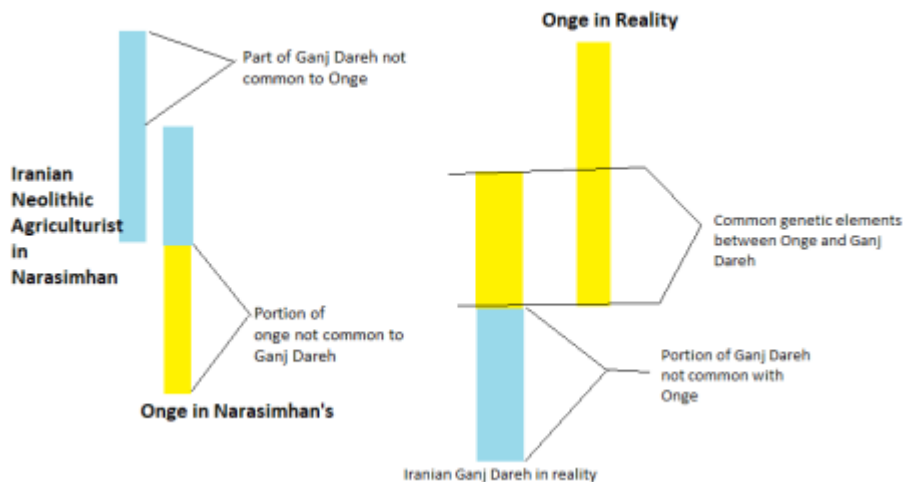


Figure: Onge (Andaman) as depicted in Admixture Analysis by Narasimhan, and as in reality it should have been. Commonality between Ganj Dareh (Iranian Agricult.) and Onge (Andaman) only means that a large proportion of the gene in the Ganj Dareh was same as Ancient Ancestral South Asians, today represented in mainland India by Mala, Irula etc, and in the Andaman as Onge. The Ancient Iranian Agriculturists have been shown as light blue (teal) colour and the Andaman-Onge are half light-blue (teal) and half yellow.

Iranian (Jagros Neolithic): Ganj Dareh

The Ganj Dareh has been postulated as the one of the principal components in the Narasimhan study. However it has clear ancestry from Northwest Indian sub-continent, where Pakistan is located today. Narasimhan's picture itself shows that the Ganj Dareh is only a sub-set of the larger set which is Onge, Mala etc Indian samples.

Unfortunately for the Narasimhans, the Ganj Dareh (Iran Neolithic) DNA was studied by another group of workers whose work was published in the Nature (which is not a biased journal like Science) found that:

“The mitochondrion of GD13a (91.74X) was assigned to haplogroup X, most likely to the subhaplogroup X2, which has been associated with an early expansion from the Near East and has been found in early Neolithic samples from Anatolia, Hungary and Germany.” (Llorente 2016)

“GD13a did not cluster with any other early Neolithic individual from Eurasia in any of the analyses.” (Llorente 2016)

[Interpretation: We need to remember that no South Asian Neolithic DNA has been reported so far. Thus if GD13a a matched none, possibly only one which remains to be tried is the South Asian Neolithic DNA.]

“We further investigated the relationship between GD13a and Caucasus Hunter-Gatherers using D-statistics to test whether they formed a clade to the exclusion of other ancient and modern samples (Table S4). A large number of Western Eurasian samples (both modern and ancient) showed significant excess genetic affinity to the Caucasus Hunter-Gatherers, whilst none did with GD13a. Overall, these results point to GD13a having little direct genetic input into later European populations compared to its northern neighbours.” (Llorente 2016)

[Interpretation: Thus the oldest Iranian Agriculturists of the Ganj Dareh had not directly migrated to Europe, although their mitochondrial DNA X2 certainly contributed to the modern European population. Other studies have shown (see below) that the Iranian Neolithic DNAs had migrated to Levant and Anatolia, and the Caucasus as well as the steppe. Clearly the Ganj Dareh DNAs were not the gross representative of the Iranian Neolithic, but they represent a segment which was very small and did not make much impact on later Europe, Caucasus or the steppe. It might have represented just a small number of the emigrants from a single village in Baluchistan or other part of the northwest South Asia, and might have represented only a tiny fraction of genetic variation which South Asia had at that time. On the other hand the people reaching the other locations in Zagros (Iran) at Neolithic might have originate from other villages of Pakistan/ Afghanistan resulting in the difference in the genetic composition within the Zagros Neolithic populations.]

“The individual analysed here was part of burial 13, which contained three individuals, and was recovered in level C in 1971 from the floor of a brick-walled structure. The individual sampled, 13A (referred to as GD13a throughout the text), was a 30–50 year old female; the other individuals in the burial unit were a second adult (13B) and an adolescent (13). The site has been directly dated to 9650–9950 cal BP, and shows intense occupation over two to three centuries. The economy of the population was that of pastoralists with an emphasis on goat herding⁷. Archaeobotanical evidence is limited but the evidence present is for two-row barley with no evidence for wheat, rye or other domesticates. This implies that the overall economy was at a much earlier stage in the development of cereal agriculture than that found in the Levant, Anatolia and Northern Mesopotamian basin.” (Llorente 2016)

[Interpretation: This information refutes the claim by the Narasimhans that the Mehrgarh farming culture had been borrowed from Anatolia (Turkey) through Iran (Ganj Dareh). The date cited above gives a date of 7,850 BC (mean). It may be noted that the Mehrgarh oldest layer has a date of 8,707 BC (mean).

While the Ganj Dareh Iranian people had only two-row barley (see above) at 7850 BC, the Mehrgarh had six-row barley at 8700 BC, which is an advanced stage of agricultural development and domestication of barley (Upinder Singh 120; Jarrige 2008). Jarrige wrote citing Lorenzo Costantini:

“Lorenzo Costantini has shown that the plant assemblage of Period I is dominated by naked six-row barley which accounts for more than 90% of the so far recorded seeds and imprints. He has also pointed out the sphaerococcoid form of the naked-barley grains with a short compact spike with shortened internodes and small rounded seeds.

According to him, such characteristics in the aceramic Neolithic levels can be ascribed to probably cultivated but perhaps not fully domesticated plants. Domestic hulled six-row barley (*H. vulgare*, subsp. *vulgare*) and wild and domestic hulled two-row barley (*H. vulgare* subsp. *spontaneum* and *H. vulgare* subsp. *distichum*) have also been recorded, but in much smaller quantities. According to Zohary quoted by R.H. Meadow, the distribution of wild barley extends today to the head of the

Bolan Pass. It is therefore likely that local wild barleys could have been brought under cultivation in the Mehrgarh area. Costantini has also identified a small amount of domestic einkorn (hulled: *Triticum monococcum*), domestic emmer (hulled: *T. turgidum* subsp. *dicoccum*) and a free-threshing form which can be referred to as *Triticum durum* (Fig. 10). ” (Jarrige 2006)

Thus these people of Iran had arrived here about 1000 years after the Mehrgarh took off. The Ganj Dareh site had been occupied by only a short period of 100 to 300 years (mean 200 years). On the other hand the Mehrgarh shows a continuous occupation till late. It may be noted that the domestication of the goat is not possible to take place in 200 or 300 years and about a thousand years are required to give domestication features to the animal skeletons. Clearly the people of Ganj Dareh were not local, and had arrived from somewhere else.]

“ADMIXTURE and outgroup f3 statistics identified Caucasus Hunter-Gatherers of Western Georgia, just north of the Zagros mountains, as the group genetically most similar to GD13a (Fig. 1B,C), whilst PCA also revealed some affinity with modern Central South Asian populations such as Balochi, Makrani and Brahui (Fig. 1A and Fig. S4).” (Llorente 2016)

[It is possible to interpret it as the Ganj Darh coming from a region within the locations Brahui, Baluchistan and Makaran of South Asia, now in Pakistan. Mehrgarh was in Baluchistan.]

“Also genetically close to GD13a were ancient samples from Steppe populations (Yamnaya & Afanasievo) that were part of one or more Bronze age migrations into Europe, as well as early Bronze age cultures in that continent (Corded Ware) in line with previous relationships observed for the Caucasus Hunter-Gatherers.”

[Yamnaya and Afanasievo of steppe/ Central Asia were much later than Ganj Dareh (Iran). The resemblance could be due to either the Iranian early farmers migrating into the steppe. But these people could have developed from the migrations from the northwest India/ Afghanistan/ Pamir region. The Pamir is a likely source of R1b which migrated by northern Iranian/ Turkmenistan wet corridor to south of Caspian and then from there to Armenia, Anatolia and then Southern, Western and Central Europe. Yamnaya and Afanasievo belong to R1b Y-DNA. See figures below.]

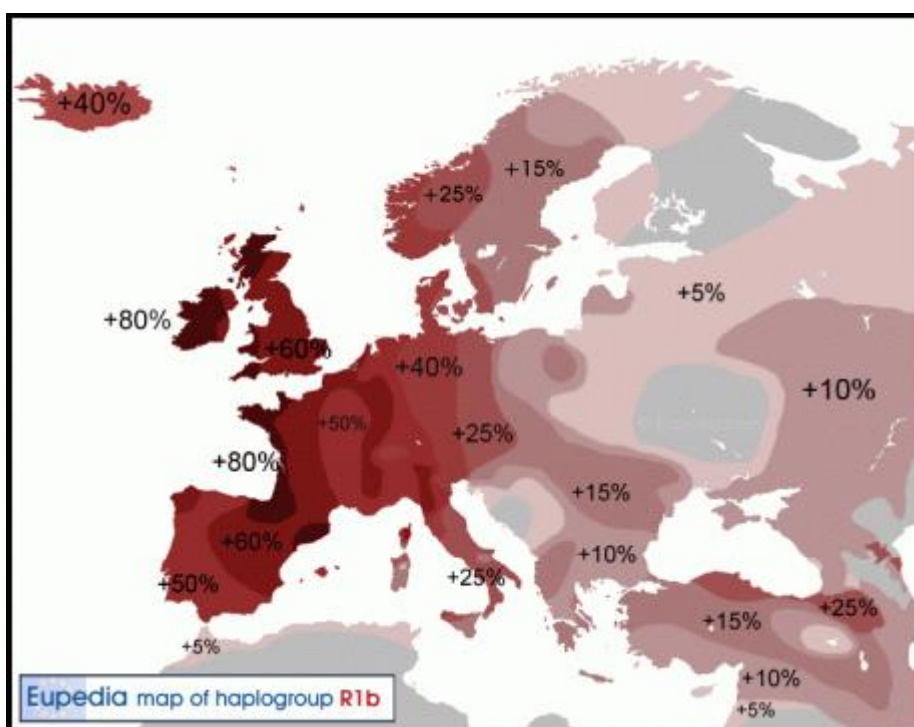


Figure: Eupedia map of R1b distribution in Europe. It is dominant in those parts of Europe which speak Centum languages like Scottish, Irish, Welsh, Italic (French, Spanish, Portuguese, Italian), Greek, Anatolian, Armenian and Germanic (English, Norwegian, German etc). The steppe language Tocharian was also Centum which was spoken by the Yamnaya and the Afanasievo people in the Bronze Age.

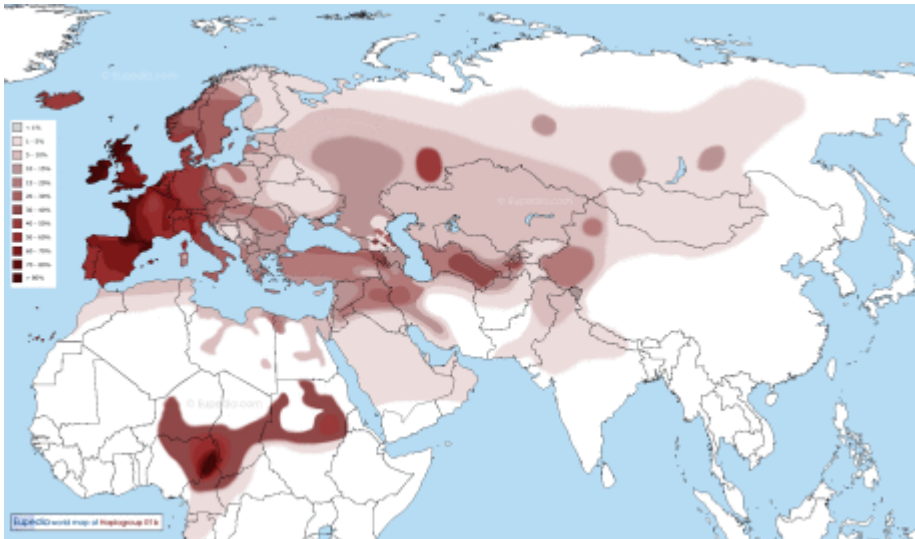


Figure: source Eupedia. The R1b might have originated in the region to the north of Kashmir i.e. Tajikistan, and migrated through Tajikistan to Armenia and further. It also went to Central Africa. In steppe and Central Asia it was replaced by later arrivals in Late Bronze Age by the R1a, which is dominant only in the Satem speaking groups like Russian, Ukrainian, other Slavic, Latvian, Lithuanian, Polish, Iranian, Indic etc.



Figure: Source Wikipedia. Map showing distribution of Centum and Satem branches of Indo-European

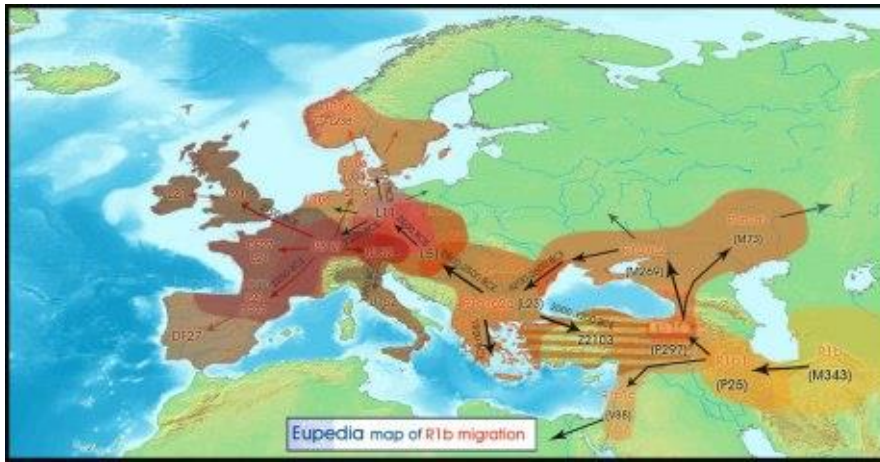


Figure: R1b Migration map suggested by Eupedia

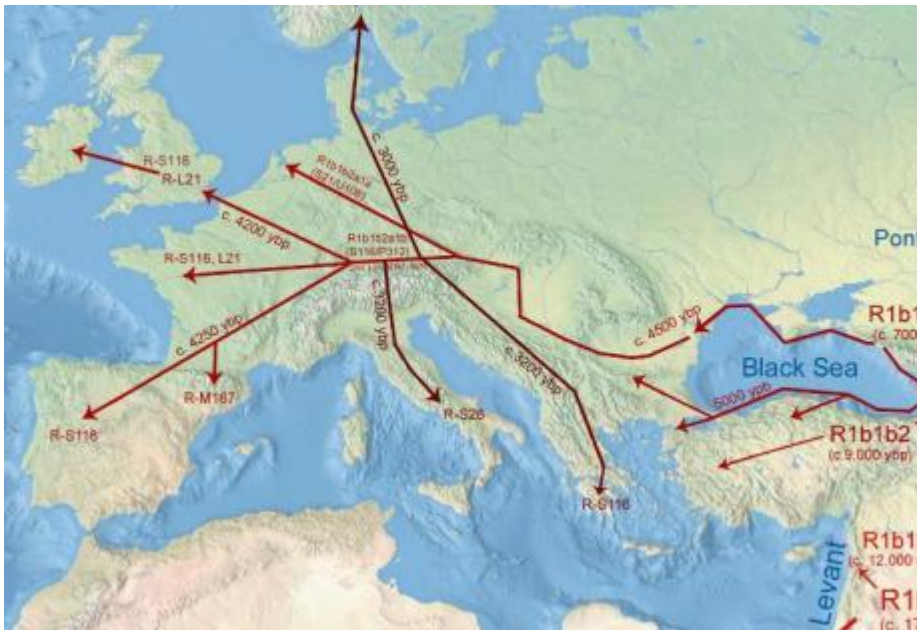


Figure: R1b Migration map as suggested by Wiki

Now we can also see regarding Ganj Darh what Llorente had to say further:

“We further investigated the relationship between GD13a and Caucasus Hunter-Gatherers using D-statistics to test whether they formed a clade to the exclusion of other ancient and modern samples (Table S4). A large number of Western Eurasian samples (both modern and ancient) showed significant excess genetic affinity to the Caucasus Hunter-Gatherers, whilst none did with GD13a. Overall, these results point to GD13a having little direct genetic input into later European populations compared to its northern neighbours.” (Llorente 2016)

[Later Europeans are products of another wave of migration namely R1b which came later in Bronze Age.]

“Thus, GD13a is the descendant of a group that had relatively stable demography and did not suffer the bottlenecks that affected more northern populations.” (Llorente 2016)

[Interpretation: This line points to India.]

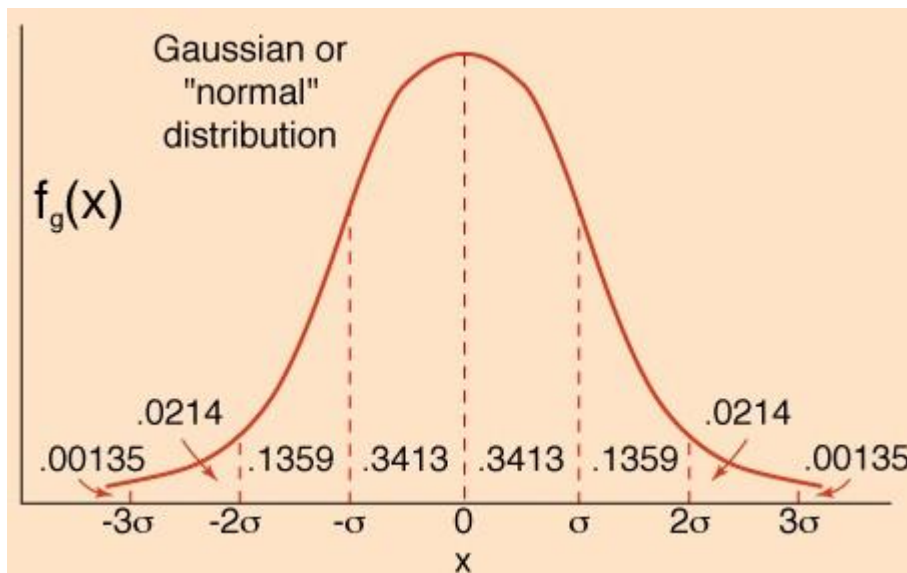


Figure: It may be understood from the Gaussian Normal Distribution curve that it is quite normal finding in any normal data that the extremes look different. It does not mean that they belong to two populations. However the naïve would take them as two populations.

What about other characters of the Ganj Dareh lady? Llorante noted the skin colour of the Ganj Dareh lady. :

“She lacked the derived variant (rs16891982) of the SLC45A2 gene associated with light skin pigmentation but likely had at least one copy of the derived SLC24A5 allele (rs1426654) associated with the same trait. The derived SLC24A5 variant has been found in both Neolithic farmer and Caucasus Hunter-Gatherer groups^{5,15,24} suggesting that it was already at appreciable frequency before these populations diverged. Finally, she did not have the most common European variant of the LCT gene (rs4988235) associated with the ability to digest raw milk, consistent with the later emergence of this adaptation^{5,15,21}.” (Llorante 2016).

Clearly she had the light skin colour gene SLC24A5 allele which produces light skin colour in the Europeans and the Indians (Basu Mallik et al 2013). This gene was not found in the Europeans until late Bronze Age. It was not present in the La Branda human of 5000 BC. However it was found present in many European people between 3000 BC and 1000 BC (Allentoft). This means the Ganj Dareh were not ancestral to the early Neolithic people of north of Black Sea who entered East Europe replacing the hunter-gatherers at about 5000 BC. In my hypothesis the light skin colour gene SLC24A5 originated in South India long back, and it migrated to other places including even Ethiopia from India.

<https://en.wikipedia.org/wiki/SLC24A5>

Another worker Broushaki (2016) noted that the Iranian Neolithic people from Wezmeh Cave were related to the Pakistani and Afghan people particularly to the Zoroastrians of Iran origin now living in India. “These people are estimated to have separated from Early Neolithic farmers in Anatolia some 46-77,000 years ago and show affinities to modern day Pakistani and Afghan populations, but particularly to Iranian Zoroastrians.” Clearly the Zagros (Iran) farmers had not arrived from Anatolian farmer community of the Anatolia Neolithic. In fact they are deeply related to Indian population.

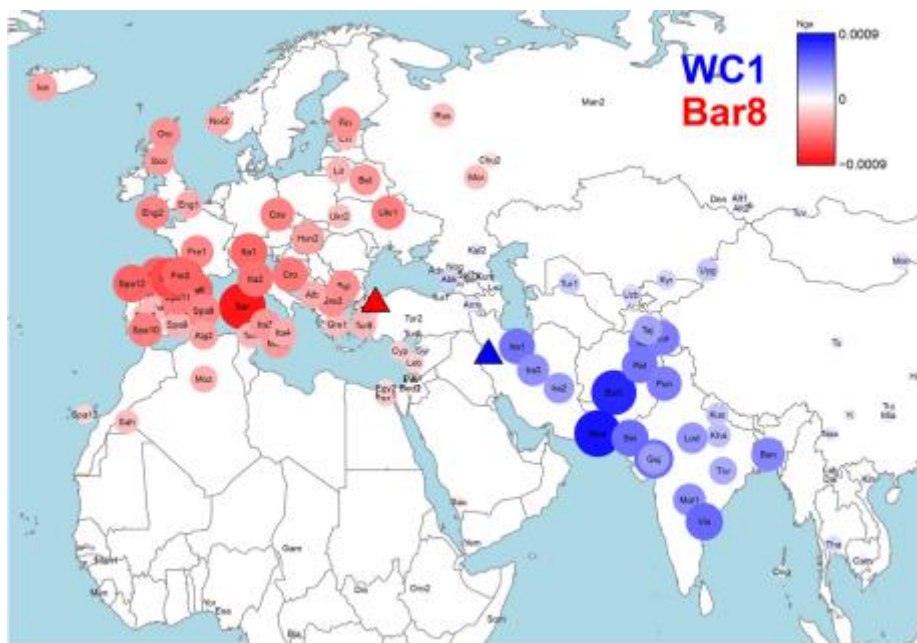


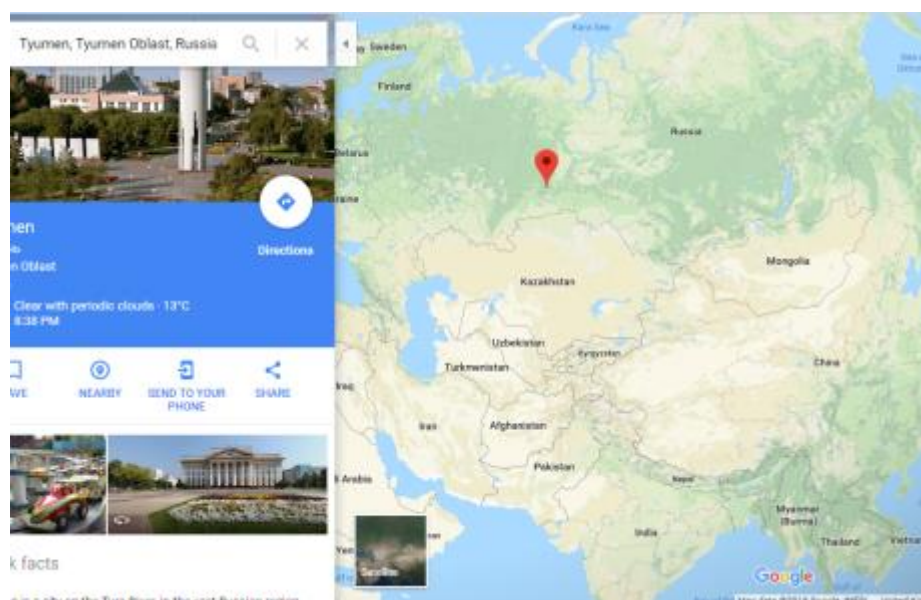
Figure Neolithic Iran as compared to Indian genome by Broushaki 2016

The Western Siberian Hunter Gatherers

Narasimhans have selected the following samples as representing the West Siberian DNA:

Sosnoviy-Ostrov, western Siberia, Russia (n=1); Tomsk10 (I5766): Date of 4230-3983 cal BCE (5261±33 BP, OxA-33486, d15N=+12.8 permil possible marine influence). Genetically female.;

Tyumen Oblast, western Siberia, Russia (n=2) Tyumen1, Kurgan 1 (I1958): Date of 4723-4558 cal BCE (5805±25 BP, PSUAMS-2359), Genetically female; Tyumen50, Kurgan 6 (I1960): Date of 6361-6071 cal BCE [6335-6071 cal BCE (7330±40 BP, Poz-82198), 6361-6086 cal BCE (7355±40 BP, OxA-33489, d15N=+15.3 permil possible marine influence)]. Genetically female.



Location of Tyumen Oblast, the Ancient West Siberia HG genes

These places Sosnoviy- Ostrov and Tyumen Oblast by foot are about 3400 kms to the north of Kabul. They had yellow colour (AASI, Indian, Onge) component about one third quantitatively in the Admixture Analysis. To mislead people denial of this fact was done, not by changing the colour of the component, but by considering it an entirely different component although it looked same as Indian.



Figure: West Siberia admixture Analysis at the top. Source Narasimhan.

Apart from this the Barros Damgaard too have provided another set of histograms for the Admixture Analysis of the same populations, with locations marked. This is more honest and correct and not tampered with.

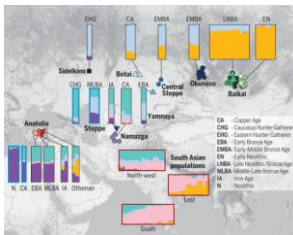
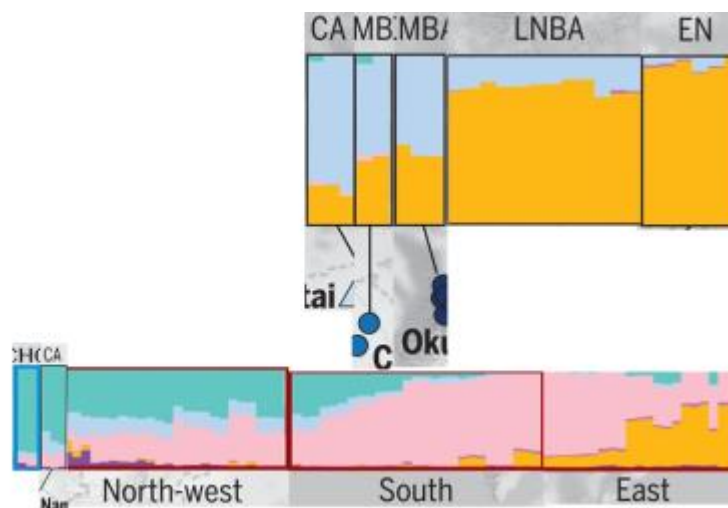


Figure: Barros Damgaard 2018, Admixture Analysis, Science

If rearranged, this picture gives the following outcomes:



This figure indicates that the Indian cline should be defined as East to South to Northwest in a folded shape or V shape. There is a gradual change in proportions of the golden, pink and teal (bluish-green) colours. Such arrangement indicates natural settlements with genetic movements not by migration but by the Brownian Movements of the genes.

If any arrival takes place, there is a breach in the cline, in the same way as Broushaki got one between Zagros and Anatolia during the Neolithic.

The further summations of the components indicates that the steppe may have originated from northwest India:

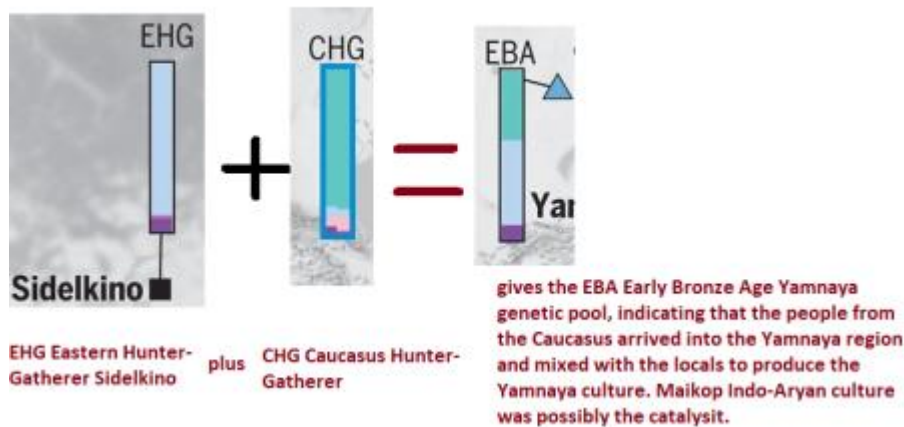


Figure: Eastern Hunter Gatherer (Sidel'kino location near Samara east of Volga river) plus Caucasus hunter gatherer gives if averaged, the Early Bronze Yamnaya. Clearly people coming through the Caucasus admixed with the local EHG to produce the Yamnaya culture. This happened during the R1b-Y-DNA expansion. Because the Yamnaya is mainly R1b. After reaching southern Caspian coast, the R1b people turned north. Established the Armenia Indo-European (Centum) and moved into Caucasus forming the Maikop (Maykop) culture in north Caucasus. It is believed that the Maikop people gave rise to the Yamnaya.



Figure: Admixture Analysis, Early Bronze Age Yamnaya plus Early Bronze Age Anatolia averaged gives the Middle to Late Steppe population.

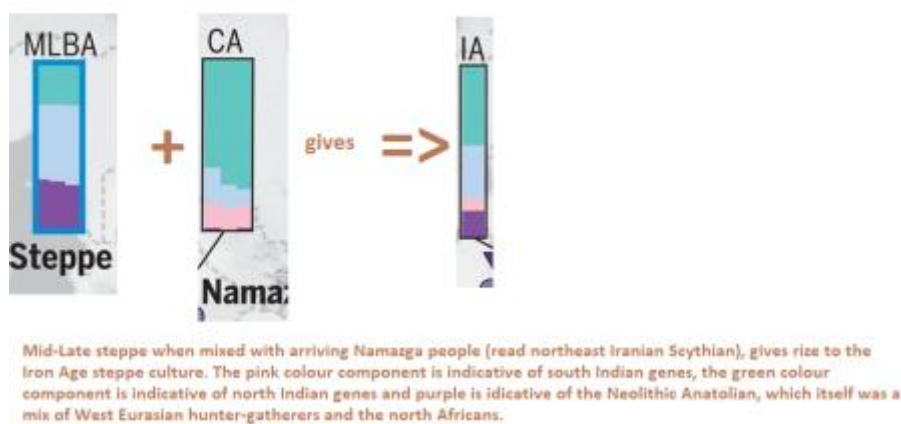


Figure: MLBA steppe and Namazga Copper Age when averaged gives the Iron Age steppe culture.

We know from other studies that lot of the ancient samples of Y-DNA H1 lineage, which is typically Indian and most probably of South Indian origin later expanding to North India, have been found from Eneolithic to Bronze Age periods from locations in Anatolia, Middle East (e.g. Namazga), and North of Mongolia (Lake Baikal region, Shamanka). Clearly Indians had been migrating to wider regions of Asia much before the steppe culture took off during the Bronze Age period. (See Supplementary matter Excel Table aar7711_Table 14, of Barros Damgaard, Science 2018).

Thus we can conclude as this picture:

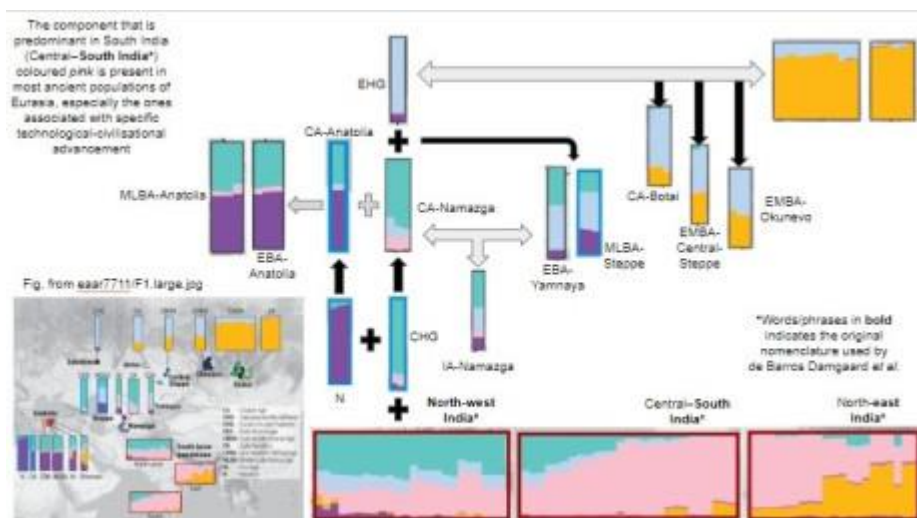
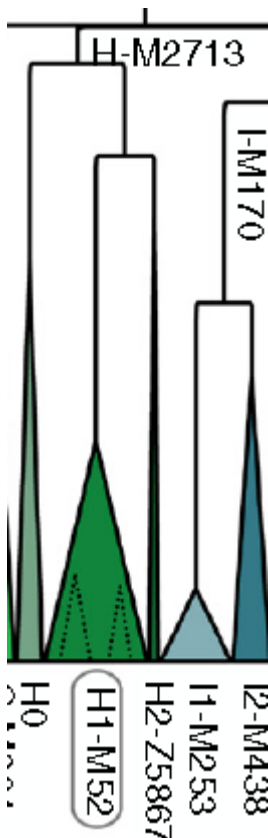


Figure: Barrow and Damgaard data rationally reorganised to produce understandable conclusions; (courtesy significant contribution from Dr Murali V.)

The H1 had a sibling H2 which has been found from Neolithic of Levant and Anatolia, and Sardinia. It has also been found from West Lake Baikal Shamanka region from Eneolithic period (sample number DA339 in Barros Damgaard 2018, see table). H3 is another branch which is found in the Romania. The early branch H0 which had split the earliest from the main trunk of H is also found in India only.



Family tree of Y-DNA H: Poznik 2016 Figure 2 enlarged

Categories Uncategorized

La Genetique Scandale

August 27, 2018 //

3

La Genetique Scandale

A critique of the recent articles particularly one by Narasimhan

(This will be in 4 parts)

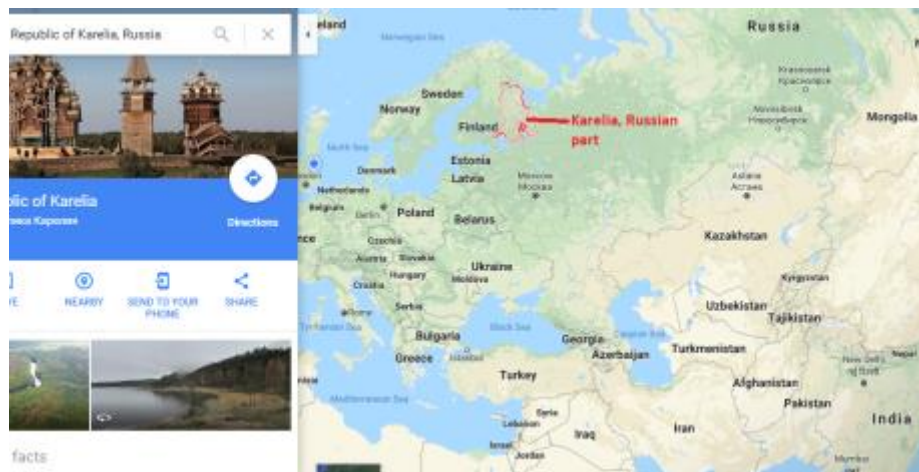
By Premendra Priyadarshi

PART 1

Cracking the Narasimhan Code

The article by Narasimhan et al (BioRxiv) uses a large number of words, abbreviations and location names, most of which have been created arbitrarily and may be misleading to the reader. I believe, it was done by them inadvertently, not intentionally. To understand the impugned article as you go into it you need to understand these words/names first. I have explained them below. Where necessary, I have pointed out the flaw in the hypothesis/inclusion of the name.

1. Karelian: The word Karelian is central to the article. The ultimate goal of the somersaults in the article is to prove by hook or by crook that the Baltic region (Karelia) was the home of the Proto-Indo-Europeans. Karelia is a region now divided into two parts—one in Finland and the other in Russia. Its language is not Indo-European, but Finnish, which belongs to the Finno-Ugric Language family. The Eurocentric Aryanists have long been claiming that the Finnish (and its sister Hungarian) have come to their present locations from Siberia.



Karelia

Source: Google Map.

While the rest of the region of Europe to the south of Karelia was having Mesolithic and later agricultural revolution, and the mode of subsistence was changing to farming and pastoralism, the region surrounding Karelia was still having hunter-gatherer-fisher existence until quite late.

Hence when the word Karelian Hunter Gatherer is used it should be considered to be belonging to a much later period, later by several thousand years, as compared to the Neolithic periods of India, Anatolia and Iran. In fact when it was Neolithic in India and Anatolia, it was Mesolithic in Europe in general and Hunter-Gatherer (Upper Palaeolithic) in the northern Europe.

Two ancient human DNAs have been retrieved from Karelia for this study. One dated 6425 BC (Y-DNA hg R1a-M420); and the other 5250 BC (Y-DNA hg J). The R1a-M420 is today common in Iran, Caucasus and Eastern Arabian Peninsula. Narasimhan claim that Karelian DNAs have more of Ancestral North Eurasian (ANE) ancestry than any other ancient or modern population. As evidence to this they allege that it is close to the sample from Afontova Gora (ca. 15980 BC), located to the west of Lake Baikal.

The resemblance of Karelian to Western Lake Baikal HG DNA only means that the c. 16,000 BC Lake Baikal, c. 6500 BC Karelia and c. 5250 BC Karelia individuals had been derived from some common ancestral population located to the southern latitudes of Asia. This could have been somewhere between the Pamir and South Caspian bank or the region located somewhat north of this line.

This assumption is necessitated by the fact that Karelia (and also West Bank Baikal) suffered two episodes of depopulation between 16,000 BC and 5250 BC. This we know from geological studies. One was at the Tardiglacial about 11,500 BC and the other was about 6200 BC (8.2 Kilo-climatic-event). In fact, the Baikal 16000 BC human sample was also the result of a migration from the south, initiated in response to the de-glaciation event which started at 18,000 BC. These DNAs must have prevailed in India and Iran too during those days. However the sporadic and focal bursts of the Neolithic promoted some newer lineages leading to the extinction of most of the Indian lineages of Upper Palaeolithic India. The same fact is true for Anatolia and much of Iran too.

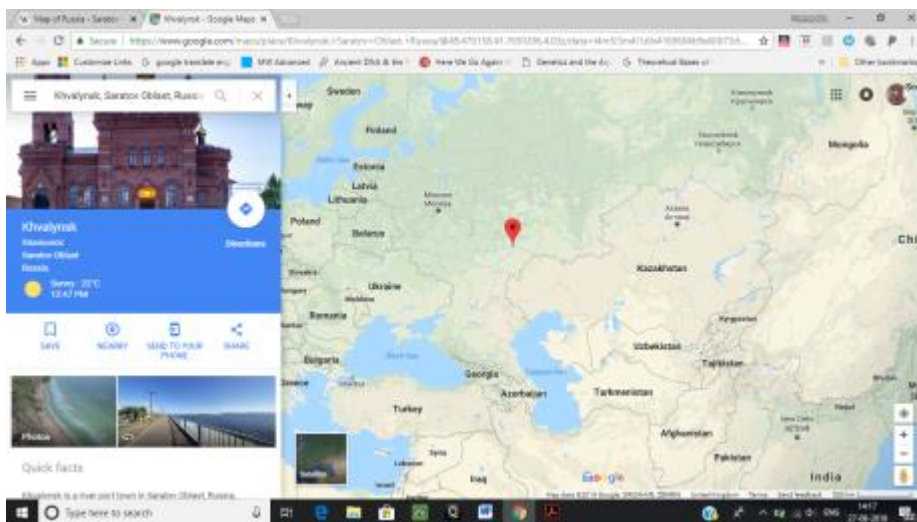
The 6500 BC Karelia sample could have been due to the migration initiated from West Asia and Mehrgarh in response to the Neolithic revolution and consequent population explosion in Europe and Asia. At this time we get Mesolithic culture in Southern and Central Europe. Its R1a-M420 Y-

DNA indicates the source from Asia. The 5250 BC Karelian sample was from West Asia through Caucasus and North Pontic regions; secondary to the adoption of Neolithic in that region about 5500-5000 BC. This we can say from the Y-DNA J, and also from the study of the ancient DNAs of Neolithic Iran, Caucasus and steppe.

The article (Narasimhan et al) uses the words EHG and Karelian Hunter Gatherer interchangeably. The ultimate aim is to prove that Karelia was the source of the MLBD_steppe's Indo-European speaking component.

2. EHG : EHG has been explained by Narasimhan as Eastern European Hunter-Gatherers. The Main Article explains this component of Eurasian ancestry as "Eastern European Hunter-Gatherers represented by hunter-Gatherers from the diverse sites in Eastern Europe". However in the supplement to the text where actual discussions have been done, the article means, implies and uses only the Karelian genes/DNA/Genome (and probably also Samara_HG) for this purpose. I don't think that it (the nomenclature EHG given to Karelia_H_G) was deliberately done to mislead people. It was a product of poor naming, writing and editing skills. In fact the EHG (Eastern Hunter Gatherer) name should have been given to East Eurasian Hunter Gatherers from Japan, Korea and coastal East China.

3. Khvalynsk_EN: Khvalynsk Eneolithic (EN here meaning Bronze Age, and not the Early Neolithic). Its period is 5000-4500 BC. The PCA by the authors found that the Khvalynsk population consisted of people from Karelia of Finland:



Khvalynsk Location

Map showing Location of Khvalynsk (Google Maps)



Location of Khvalynsk in flattened map

They write, “Khvalynsk_EN can be modelled with Karelian HGs as a primary source of ancestry and about 20% Iranian agriculturalist related ancestry. This shows that the results of our modeling procedure are consistent with the observations in refs. (75) and (83), where a slightly modified qpAdm procedure and different sets of outgroups were used (Table S3.45).” [Lines 4116-4120, Narasimhan Supplement]

The plain English meaning of this quoted passage is — The Bronze Age people of Khvalynsk region, which is located to the East and north of Ukraine, came from Finland at about 5000 BC.

This interpretation by the authors is naïve because Finland and adjoining Baltic regions had very low food productivity until as late as about 2000 BC. It could not provide immigrants to a distant region like Khvalynsk at 5000 BC. Moreover the rule in Archaeology and history is that the farmers penetrate into the hunter-gatherer territories, not the vice-versa. The fact of resemblance between Karelian and Khvalynsk at this time needs to be interpreted as follows:

The Khvalynsk 5000 BC should be considered to be composed of two components. One arriving here and settling much earlier, even before 6200 BC, from a source population locate in Pre-Ganj-Dareh Iran/ Caucasus. This would be of the same stock as the Karelian samples as the Karelian too might have arrived from this region to Finland earlier. This human genetic layer formed the existing substratum of people in the region between Volga and the Baltic region, when the people with Neolithic arrived from the south at about 5000 BC. Thus Khvalynsk was retaining 80% of this gene pool between 5000 BC and 4500 BC. Further arrivals from the south would further dilute this gene component with time.

And the other (20%) component of Khvalynsk arrived to this region in a Neolithic wave from North-West Iran after 5000 BC, and this event was after the establishment of the Ganj-Dareh population in west Iran, which had taken place about 7700 BC, but fresh wave of these people reached north of Caucasus only after the 8.2 kilo-event had passed. We know from the other studies (Lazaridis 2016) that migration from Iran through Caucasus to Volga and north Pontic-Caspian region took place about 5500 to 4500 BC. We have to understand also that it is this latter Iranian population (from Ganj Dareh stock) only which has been named as Iranian Agriculturalist in the article by Narasimhan.

4. Iranian Agriculturists: The authors mean the six Ganj-Dareh ancient human samples dating about 7900-7700 BC only by the term “Iranian Agriculturists”. They do not include other Iranian agriculturists in this term e.g. Wezmeh Cave Zagros Farmers (Broushaki 2016). [Quote from Broushaki: “These people are estimated to have separated from Early Neolithic farmers in Anatolia some 46-77,000 years ago and show affinities to modern day Pakistani and Afghan populations, but particularly to Iranian Zoroastrians.” Broushaki: Abstract. Clearly Broushaki is talking about the split into two of the Early Eurasians coming westward from coastal western India (Gujarat-Sind) and one moving ahead to give rise to the European and Anatolian Hunetr-Gatherers (Cro-Magnons) and the other staying back in Pakistan-Afghanistan–East Iran region. This we can understand from the received knowledge about early Eurasian migration.]

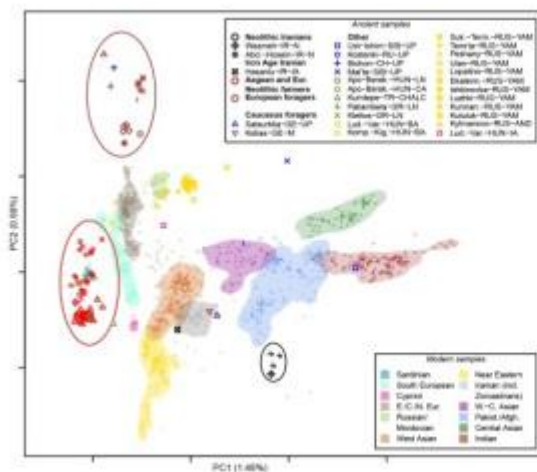
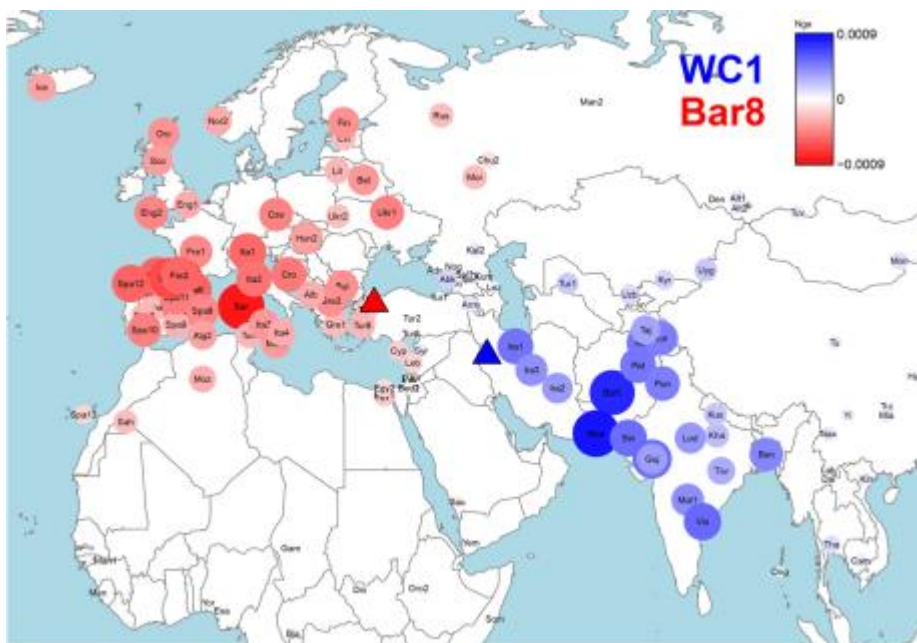


Fig. 2. PCA plot of Zagros, European, and Near and Middle Eastern ancient genomes. Comparing ancient and modern genomes. Neolithic Zagros genomes form a distinct genetic cluster close to modern Pakistani and Afghan genomes but distinct from other Neolithic farmers and European hunter-gatherers. See Animation S1 for an interactive 3D version of the PCA including the third principal component.

bioRxiv preprint doi: <https://doi.org/10.1101/071111>; this version posted July 18, 2016.

Thus in fact the expression ‘Iranian Agriculturist’ must have included Wezmeh Cave within its meaning, who had migrated to Zagros from a location within Pakistan/ Afghanistan. The Wezmeh DNA could have been named ‘Iranian Agriculturist II’. In that case it would have been all right.



Source: Broushaki 2016:Fig 4. Wezmeh is related to Indian, and Europeans are related with Barcin Anatolian. There is a break or discontinuity between Anatolian DNAs and West Iranian DNAs at this time. This indicates recent arrival from the Eastern countries to West Iran. Long-standing

coexistence would later create clines between Iran and Anatolia, which was absent at the Neolithic period.

5. Anatolian Agriculturist: It is another misnomer in the article. Anatolian farmers were not one people. Originally there lived Hunter-Gatherers in Anatolia who were homogeneous with the people of Europe and Caucasus before the Holocene. But Holocene brought first the Mesolithic people from somewhere else to Anatolia. Then another wave brought Early Anatolian farmers. These were replaced by Mid- to Late- Neolithic farmers from Iran arriving in Anatolia.

6. Samara: Samara has been considered EHG (East European Hunter Gatherer. However Middle Bronze Age population had received about half of its genome from Armenia (Indo-European speakers) located to the north of west Iran. “Poltavka Middle Bronze Age (2900-2200 BCE) population that followed the Yamnaya in Samara, are all genetically homogeneous, forming a tight “Bronze Age steppe” cluster in PCA (Fig. 1b), sharing predominantly R1b Y-chromosomes^{5,7} (Supplementary Data Table 1), and having 48–58% ancestry from an Armenian-like Near Eastern source (Extended Data Table 2)” [Mathieson 2016:page 4] This fact has been concealed by Narasimhan, and they have projected a different source of Samara Middle to Late Bronze Age population. They think this source was Baltic region. But no evidence has been provided.

7. Late Bronze Age Steppe (MLBA_steppe): They think it was formed from arrivals from Baltic Europe and Baikal region inputs. However it has been clarified by Mathieson (2016 Nature) as this: “Further evidence that migrations originating as far west as central Europe may not have had an important impact on the Late Bronze Age steppe comes from the fact that the Srubnaya possess exclusively (n=6) R1a Y-chromosomes (Supplementary Data Table 1), and four of them (and one Poltavka male) belonged to haplogroup R1a-Z93 which is common in central/south Asians¹², very rare in present-day Europeans, and absent in all ancient central Europeans studied to date.”

8. West Siberia: They have used the words West Siberian Hunter Gatherers and West Siberian Neolithic. West Siberian HG has been considered a primary component in the article. The region is not at all located in the west. Ironically it is straight to the north of Mehrgarh, in the same longitude. Its yellow colour in the PCA histogram provided by the Narasimhan makes clear that it had significant Andamanese/ Ancestral South Asian component in it. It is located just to the north of Kazakhstan borders.

Narasimhans write: “West Siberian Hunter-Gatherer (West_Siberian_HG)-related”: a newly documented deep source of Eurasian ancestry represented here by three samples” [lines 201-2 main article]

However the PCA picture indicates that this component itself is formed of two segments, one from Onge (India) which is yellow; and the other from local older population which is green.



West Siberian Neolithic shown in top line. The green component in it is original hunter-gatherer West Siberian population which is two-thirds. However the Neolithic of the West Siberia does include the yellow (Indian) component in about one third quantity. Clearly it indicates arrival from Mehrgarh in response to population expansion caused by Neolithic in Mehrgarh at about 8000 BC, much before the Yamnaya etc were formed.

The take home summary for today is that the whole story has been created in such a way as to appear that it is the Karelia (Baltic) component which contributes to the Steppe population to make it MLBA (Indo-European Speakers). The long-term game plan of the authors will become more clear to you as you will understand bit-by-bit the whole plot of the impugned article by Narasimhan. Thus on the ultimate analysis, we can perceive that the Narasimhans want to prove the out-dated concept that ultimate home of the Proto-Indo-European is Karelia or the Baltic Peninsula of the North Sea. This was originally called the Lachs Theory (Lachsargument) of IE origin given by German Scholar Schrader and later adopted by Thieme. See in the link.
https://en.wikipedia.org/wiki/Salmon_problem

To be continued as Part II next week.

Categories Uncategorized

A Critical Appraisal of Narasimhan et al 2018 bioRxiv. by P. Priyadarshi

April 29, 2018 //

6

Let us start our discussion from the most significant paragraph of the article:

“Third, between 3100-2200 BCE we observe an outlier at the BMAC site of Gonur, as well as two outliers from the eastern Iranian site of Shahr-i-Sokhta, all with an ancestry profile similar to 41 ancient individuals from northern Pakistan who lived approximately a millennium later in the isolated Swat region of the northern Indus Valley (1200-800 BCE). These individuals had between 14-42% of their ancestry related to the AASI and the rest related to early Iranian agriculturalists and *West_Siberian_HG*. Like contemporary and earlier samples from Iran/Turan we find **no evidence of Steppe-pastoralist-related ancestry in these samples**. In contrast to all other Iran/Turan samples, we find that these individuals also had negligible Anatolian agriculturalist-related admixture, suggesting that they might be migrants from a population further east along the cline of decreasing Anatolian agriculturalist ancestry.” (Narasimhan 2018 bioRxiv: page 9 lines 276 to 285).

This paragraph provides us with two crucial pieces of information:

1. The Gonur and Shahr-i-Sokhta samples dated from 3100 BC to 2200 BC had no evidence of the Steppe-pastoralist-related ancestry in them.
2. These Gonur and Shahr-i-Sokhta people had the same ancestry profile as the 41 ancient individuals from northern Pakistan living between 1200 BC and 800 BC.

Impression from these two findings: This gives the most parsimonious impression that the ancestry or the genetic profile of the people from North Pakistan, Indus-Harappa proper and the Greater Indus Valley which included the regions up to east Iran and southern Turkmenistan had a genetic continuum in space and time, and they all were the same people.

1. These people (Gunur, Shahr-i-Sokhta, Swat etc North Pakistan, henceforth called **GSP**) had negligible ancestry from Anatolia.

1. These people (GSP) had not arrived from steppe-pastoralist culture of the Late Bronze Age.

Impression from points 3 and 4 : There was no arrival from either the Neolithic Anatolian farmers, nor had been any arrivals from the steppe-pastoralist cultural location, prior to or up to 800 BC.

Now let us look at the definition of the word AASI used in the quoted paragraph. It is ““Ancient Ancestral South Indian (AASI)-related”: a hypothesized South Asian Hunter-Gatherer lineage related deeply to present-day indigenous Andaman Islanders” (Narasimhan bioRxiv lines 204-205). This means that the Indians (both North and South) had a hunter-gatherer population whose ancestry was exactly the same as the present day Andaman islanders before 8th millennium BC, the time of arrival of Neolithic in India. It also by implication means that Andaman Islanders and the Hunter-Gatherer Ancient Indians had not diverged genetically or evolved at all in spite of having been separated genetically and spatially for 30,000 to 60,000 years. Another important thing to understand here is that this new name AASI means the same thing as the ASI coined by Reich (2010). In other words, Narasimhan assumes that the Andaman Islanders like people (ASI) had occupied the whole of India, and were not restricted to the south India, and hence they have been given a new name AASI replacing the older name ASI.

However this assumption cannot be supported on the basis of received information so far. We know from the data supplied by the Narasimhan article as well as earlier articles by various authors that the Y-DNA haplogroup of the Andaman Islanders had stayed the same—the oldest Asian ones—D1 and C2. On the other hand people who had stayed in the mainland India had developed newer haplogroups like F*, C5, H1 etc in their Y-DNA profile, and these newer Y-DNAs have largely replaced the oldest lineages D1 and C2 in the mainland India by this time. Hence the identification of the pre-Neolithic Indians by modern Andaman Islanders gene is essentially flawed, and is fraught with the danger of misleading the entire study towards wrong conclusions.

Now we should examine another statement regarding the GSP population: “These individuals had between 14-42% of their ancestry related to the AASI and the rest related to early Iranian agriculturalists and *West_Siberian_HG*.” (lines 279 to 281).

This statement at least confirms that the early Iranian agriculturists were genetically related to the GPS (Bronze Age Gonur, Shahr-i-Sokhta, North Pakistan) people. Although Narasimhan et al assume that the Zagros Iranian agriculturists (ZIA) were ancestral to the GPS, there is another possibility that the GPS and ZIA had descended from a common ancestor who was located more likely in Pakistan than in the Zagros.

The latter possibility is supported by stouter evidence. It has been noted that there was a genetic discontinuity, a break in the cline, between the Zagros people and the Anatolian farmers of the 7th millennium BC (Lazaridis 2016; Broushaki 2016). Such break is produced always by either a new arrival of a population, or an insurmountable long time geographical barrier between two adjacent populations. Broushaki had studied the Wezmeh sample from another Zagros cave. Broushaki also noted,

“We sequenced Early Neolithic genomes from the Zagros region of Iran (eastern Fertile Crescent), where some of the earliest evidence for farming is found, and identify a previously uncharacterized population that is neither ancestral to the first European farmers nor has contributed significantly to the ancestry of modern Europeans. These people are estimated to have separated from Early Neolithic farmers in Anatolia some 46-77,000 years ago and show affinities to modern day Pakistani and Afghan populations, but particularly to Iranian Zoroastrians.” (Abstract). Thus, the Wezmeh DNA seems to be a part of wider Indo-Iranian ancient pool, having maximum concentration in Pakistan as in this picture.”

<https://drive.google.com/file/d/0B9o3EYTdM8lQYzF0U2pWS0NVakU/view>

Figure from Broushaki et al., Early Neolithic genomes from the eastern Fertile Crescent, *Science* 14 Jul 2016, DOI: 10.1126/science.aaf7943

This effectively proves the arrival of the Neolithic Zagros farmers from the northwest Indian Neolithic, and the continuation of the same people in Pakistan/ Northwest India since the early Neolithic days.

More will follow in coming days. Please place your queries.

Priyadarshi

Categories Uncategorized

Factual Mistakes Committed in the article of Silva, Martin and Others’ (2017, BMC Evolutionary Biology)

June 27, 2017 //

The DNA data which Silva *et al* provide us in their article, are mostly wrong and confabulated. The whole conclusion rests over the foundation of huge lies. Alternatively they could be result of poor home-work . These have vitiated the conclusion of the article.

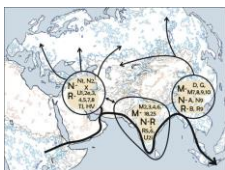
Let us first see some example of the misrepresentation of data in the article regarding the Mitochondrial DNAs:

- Silva *et al* say: “....analysis of several “non-autochthonous” N lineages present in South Asia (H2b, H7b, H13, H15a, H29, HV, I1, J1b, J1d, K1a, K2a, N1a, R0a, R1a, R2, T1a, T2, U1, U7, V2a, W and X2—all subclades of West Eurasian haplogroups),...” (page 3 of pdf)

In this passage the Silva list these above-mentioned mtDNA lineages found in India and claim that they are West Eurasian (i.e. European) in origin, and have arrived into India with Aryan Invasion/migration.

He does not site any evidence to support his view other than the weight of his academic position. This reflects his poor study of published literature. Let us see a few of the above mentioned lineages.

In the list above, he mentions R1a (mtDNA; it is not the same as R1a Y-DNA). This R1a mtDNA is found more in the tribes than in the upper-caste or north Indian population. Metspalu (2004) wrote, “Haplogroup R1a, previously associated with the putative Indo-Aryan invasion, was found at its highest frequency in Punjab but also at a relatively high frequency (26%) in the Chenchu tribe. **This finding, together with the higher R1a-associated short tandem repeat diversity in India and Iran compared with Europe** and central Asia, suggests that southern and western Asia might be the source of this haplogroup. ” (Metspalu Abstract). See Metspalu’s map below. In the quoted sentence Western Asia stands for East Iran (see below).. So from where did Silva get the information that the mtDNA R1a is European?



M, N and R all mdDNA originating in India

It must also be understood here that Iran which is a sibling of India linguistically (Indo-Iranian branch of IE Family), has been considered as a part of West Asia by the Eurocentric authors, and this practice is wrong. The map below shows how they define West Asia or Middle East in a way to include Iran in it (See map below). And then they say, West Asia is near Europe, hence West Asian DNAs are European DNAs. Thus Iranian DNAs become European DNA by manipulation of geographical description.



However because of linguistic and prehistoric unity of East Iran with Indus Valley, Iran must not be considered West Asia but as western part of Indo-Iran Civilization. East Iran was certainly within the Greater Indus Valley Civilization, and people from East Iran came and settled in India since the Indus Valley Period up to the Mughal period. Most of the mtDNA lineages listed by Silva are in fact East Iranian, and they are found up to Punjab amounting up to 20% of the population, but not further East in India. In fact the East Iran was a an extension of the Vedic Civilization, and it has been demonstrated again and again by comparison of the Avesta and the Vedas and their practices. The mtDNAs HV, T2, etc fall in this category. And considering these DNAs as Europeans is totally arbitrary and wrong.

Migration was bi-directional between East Iran and India. The climate led earlier migration was from India to Iran, attested by the presence of 10% Indian lineages (mtDNA) in Iran overall, 5% of the mtDNA in Iran today are constituted by the Indian M lineage itself. (See Metspalu 2004). But later when Indus Valley Civilization became the world centre of culture, people from every part of Asia and Eastern part of Africa came and settled there as traders, businessmen and artisans, just as people flocked to London from every part of the world in the last century. This fact was proved by Valentine and Kenoyer et al in their study of the skeletons of the Indus Valley..

In fact the N1a, T2 and HV (mtDNAs) listed by Silva as European, also originated in Iran, and they reached India when the Indus Valley became a trade center of world, and the traders from every part of the world came and settled in the Indus valley in small numbers during the Bronze Age. (see Valentine, Kenoyer et al 2015). East Iranian arrivals due to economic factors is understandable, and they were the largest numbers among the foreign settlers in India. Link:

<http://journals.plos.org/plosone/article/file?id=10.1371/journal.pone.0123103&type=printable>

<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0123103>

However, there are pure Indian mtDNA lineages also which have been depicted by Silva as European, one of which (mtDNA R1a) we just described.

None of the above named DNAs, which Silva has listed as European (Western European) mtDNAs, originated in Europe (West Eurasia). These are the mtDNA lineages which reached Europe from Asia after 5500 BC. In fact only a few original paleolithic DNAs of Europe have survived till today. In the great freeze of 8200 BP known as 8.2 kilo year event, nearly all of the European people died. So did the people of the steppe and Central Asia.

Thus to quote Brandt, “Ancient DNA studies have revealed genetic **discontinuities between indigenous hunter-gatherers and early farmers and between later and present day Europeans.** (Brandt 2013: page 257).

Links to Brandt’s ancient DNA study of 2013

Full Article <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4039305/>

Abstract: <https://www.ncbi.nlm.nih.gov/pubmed/24115443>

Brandt’s study establishes (by means of ancient DNAs recovered from the fossils) that the newer people continued to arrive into Europe, through the Turkish corridor and the north Black Sea highway, from the Caucasus, Iran and Central Asian during the various stages of the Neolithic.

Brandt’s study of the aDNAs reveals European transition from foraging to farming introduced by the LBK (Linear Pottery Culture), which reached Central Europe *circa* 5500 calibrated BC (calBC). MtDNA data from Central European hunter-gatherers, *i.e.* the **people who were the original inhabitants of Europe, comprises only of some U lineages (viz. U, U4, U5, and U8) and not even U2 and many other lineages found today in Europe.** On the other hand the later Europeans (after 5500 BC) had entirely new DNAs arriving from Asia.

The oldest farming culture of Europe is the LBK. The LBK (*i.e.* Central Europe after 5500 BC) is characterized by a distinct mtDNA haplogroup (lineages) profile including N1a, T2, K, J, HV, V,W, and X. Although Silva-team have addressed these in the impugned article as European DNAs, these are Iranian in origin and went to Europe only after 5500 BC. Brandt named these haplogroups a mitochondrial “Neolithic package”, and these comprise around 79.4% of the diversity in the LBK, whereas hunter-gatherer lineages are rare comprising only 2.9% (Brandt 2013: page 260). So, the original Europe became minority and got reduced to 2.9% of the population during the LBK period.

Silva *et al* also claim in the same impugned line, about mtDNA U7, that U7 too is European and migrated from Europe to India. However another article published by a closely allied group of authors Sahakyan, Villems et al (2017) published only recently finds that this mtDNA U7 was present in India about 11,500 years back, and reached Europe about 8000 years back. This also must have originated in Indo-Iran region. We know that Indo-Iranian was one culture before split. And it is useful to describe its territory as Indo-Iran.

Link to Sahakyan 2017 : <https://www.nature.com/articles/srep46044.pdf>

also, <https://www.nature.com/articles/srep46044> (This is another example of these scholars doing poor homework in the haste of being published).

The Claim that Bronze Age migrations were male exclusive is lie

Not only Iranian female lineages migrated into Europe, but also several Indian female lineages (mtDNA) did migrate to Europe in significant numbers, and out of them mtDNA M itself is found in the Eastern Europe, Hungary, Poland etc up to the extent of 3 to 5 percent of population today. This is not a small number. This is almost the same frequency in which the Indian mtDNA “M” lineages are found in Iran today.

So when the Iranian people migrated to Europe with their families, there were Indians (NRIs, Non Resident Indians) too in their group who had earlier arrived into Iran with the farming and other culture. These Indian lineages are scattered all over East Europe and Central Europe and also in Iran, Tajikistan, Uzbekistan, Kazakhstan, Arabia and Caucasus. Discussing them all here is beyond the scope of this blog.

The Indian female migrant lineages which are found in Europe today include M5a, M5a1, M35 etc. Malyarchuk (2008). Malyarchuk found that one of the Slovak female lineage (mtDNA) actually had even belonged from Andhra Pradesh in South India. They named it M35b. (Malyarchuk, page 230, column 1, last but 3rd line).

Link: <https://www.ncbi.nlm.nih.gov/pubmed/18205894>

Unfortunately, the Eurocentric academicians label all the Indian DNAs found amongst the Europeans as to be brought there by the Roma Gypsy migration and date them to about 1000 years back. However my study of the Roma DNA found that they migrated to Europe at the late Indus Valley period, when the drought started creating migration pressure on the people of the Indus Valley. Hence Roma also reflect a Late Bronze Age Indian population, while the other Europeans who are from Indian lineages probably migrated between middle Neolithic period to as late as the Scythian Period.

In fact ancient mtDNA recovered from Central Asia’s Tarim Basin (Xiaohe location) dating to the Bronze Age have many Iranian and Indian lineages. “Nowadays, the M5 variant observed in this study is found mainly in south and southwest Asia. The presence of hgs U7 and M5 in the Xiaohe people suggests that populations of west/south Asia contributed to the gene pool of the Tarim Basin during the Bronze Age.” [Chunxiang Li 2015: page 5 of 11] Tarim Basin spans from Altai to Mongolia.

Link: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4495690/>

In fact today Indian mtDNA M constitutes 72% of Altaian Kazakh population, indicating that this is the place where Indians came in the maximum numbers. (Tarlykov 2013: page 20, Table 1). This matches (overlaps) well with the migration of Indian branch of male lineage R1a known as R1a-Z93. (see Z93’s Eupedia Map).

Lalueza-Fox (2004) was the pioneer of the ancient human DNA studies. Se also found significant Indian DNA presence in Kazakhstan, and she thought that these came from Indo-Iran.

“The general west–east Eurasian composition of the prehistoric samples in the period after the arrival of east Eurasian sequences (after the seventh century BC) is, despite the small sample size (n = 14), quite similar to the values found in the modern Kazakh population: east Eurasian (42.9%), west Eurasian (50%) and Indian (7.1%). Interestingly, the only sequence of Indian origin that was observed, belonging to the M4 haplogroup (Bamshad et al. 2001), originates from a site in the

south of Kazakhstan. This fact could correspond to **an independent, Indo-Iranian genetic infusion into the steppes.**

More direct evidence of Indian migration to Iran, Middle East, Caucasus is provided by the ancient DNAs.

The Indian M52 (mtDNA) has been found from the remains of the Maikop culture which was an Indo-European culture dating back to 3700 BC to 3000 BC. (Solovak *et al*). Link: <http://www.sciencedirect.com/science/article/pii/S0305440316301091>

Hence we can say that the Indian families had migrated to north Caucasus region about 5700 years back and these families had gone there with cows and buffaloes and Indo-European language. Clearly they had crossed Armenia before reaching north Caucasus. Armenia is another Indo-European speaking country which shows lot of Indian mtDNA and Y-DNA both.

Hence the conclusion from mtDNA is that the Indo-European migration from India to Europe took place not male specifically but it was both male and female, and often entire families had migrated to Iran, Tajikistan, Uzbekistan, Mongolia, Armenia and Caucasus, and to a lesser extent as a secondary migration to Eastern Europe up to Romania, Slovakia, Russia, Hungary and Poland.

Y-DNA (male lineages) too migrated from India to Europe

The Silva et al write about R1a branches as their prime evidence. They write (on page 14 of their published pdf document):

“R1a-M17 (R1a-M198 or R1a1a) accounts for 17.5% of male lineages in Indian data overall, and it displays significantly higher frequencies in Indo-European than in Dravidian speakers”. Perhaps Silva has not studied all the papers honestly. This matter has been sorted out much earlier. It has been found that it is not only Indian but in certain Austro-Asiatic tribes of India, its frequency has even been higher than the IE speakers (Sahoo 2006; Sengupta 2006; Sharma 2009; Underhill 2010), and I will not discuss any further this naïve statement by Silva.

Now examine another statement,

“Moreover, not only has R1a been found in all Sintashta and Sintashta derived Andronovo and Srubnaya remains analysed to date at the genome-wide level (nine in total) [76, 77], and been previously identified in a majority of Andronovo (2/3) and post-Andronovo Iron Age (Tagar and Tachtyk: 6/6) male samples from southern central Siberia tested using microsatellite analysis, it has also been identified in other remains across Europe and Central Asia ranging from the Mesolithic up until the Iron Age (Fig. 5).”

Now this statement is a clear example of academic deception. The authors do not reveal here that the ancient samples from Sintashta etc belonged to which branch—Indian branch or European branch. The fact is that they all belonged to the Indian branch Z93. Mathieson has clarified this matter unequivocally:

“Further evidence that migrations originating as far west as central Europe may not have had an important impact on the Late Bronze Age steppe comes from the fact that the **Srubnaya** possess

exclusively (n=6) R1a Y-chromosomes (Supplementary Data Table 1), **and four of them (and one Poltavka male) belonged to haplogroup R1a-Z93 which is common in central/south Asians,** very rare in present-day Europeans, and **absent in all ancient central Europeans studied to date.**” (Mathieson 2015: page 2 of pdf full article in Nature). Link:

<https://www.nature.com/nature/journal/v528/n7583/full/nature16152.html>

Clearly, Silva did not read this article before sitting down to write a paper.

The European branch never came to India but the Indian branch did go to Europe. Underhill wrote, ““Importantly, **the virtual absence of M458 chromosomes outside Europe speaks against substantial patrilineal gene flow from East Europe to Asia, including to India,** at least since the mid-Holocene.” (Underhill 2010:Abstract)” Had people come from Europe to India or even from Ukraine to India, this European branch R1a-M458 must have arrived to India.

On the other hand the Indian branch R1a-Z93 is present in Europe up to Hungary and Poland. Even in Sintashta, which is considered the Cradle of Europe’s Indo-European culture and language, the ancient DNAs recovered are of the Indian R1a-Z93 and not the European variety, which was reproduced only after the main trunk reached well inside Europe.

Extremely poor knowledge of Silva of the wider picture like human associated migrations of animals, diseases etc

There have been other studies which indirectly prove migration from India to Europe.

Otzi Man and *H. pylori* infection :

Otzi Man or the European Iceman was recovered from the Alps frozen. His mtDNA and Y-DNA reflected Iranian ancestry, yet the *Helicobacter pylori* bacteria recovered from his stomach was of the Indian breed. This finding established that fact that the *H. pylori* infection reached Europe from India (read details in the link).

Link: <http://www.nature.com/news/famous-ancient-iceman-had-familiar-stomach-infection-1.19127>

Mice Migration:

The domestic mouse is a domestic pest of farming culture. It has been shown by a large number of studies that the domestic mice, shrew and rat have originated in India, were domesticated in India, and they migrated with the humans with the Neolithic migration. It is an indirect or circumstantial evidence of Indian origin of farming culture and the Indo-European speakers.

Link:

https://www.academia.edu/2504657/Of_Mice_and_Men_DNA_Archaeological_and_Linguistic_correlation_of_the_liked_journeys_of_mice_and_men

Cow Migration:

It had been found that all the zebu cows of the world are of Indian origin (Chen). Link:

<https://academic.oup.com/mbe/article/27/1/1/1127118/Zebu-Cattle-Are-an-Exclusive-Legacy-of-the-South>

It has been shown that the Ukrainian cows, as well as East European Piedmont etc and Mongolian and Even South Chinese cows migrated from India in a domesticated form long back. Even the Central Asian cattle recovered from Neolithic and Bronze Ages belong to Indian variety (Zebu). (Chen; Kantanen).

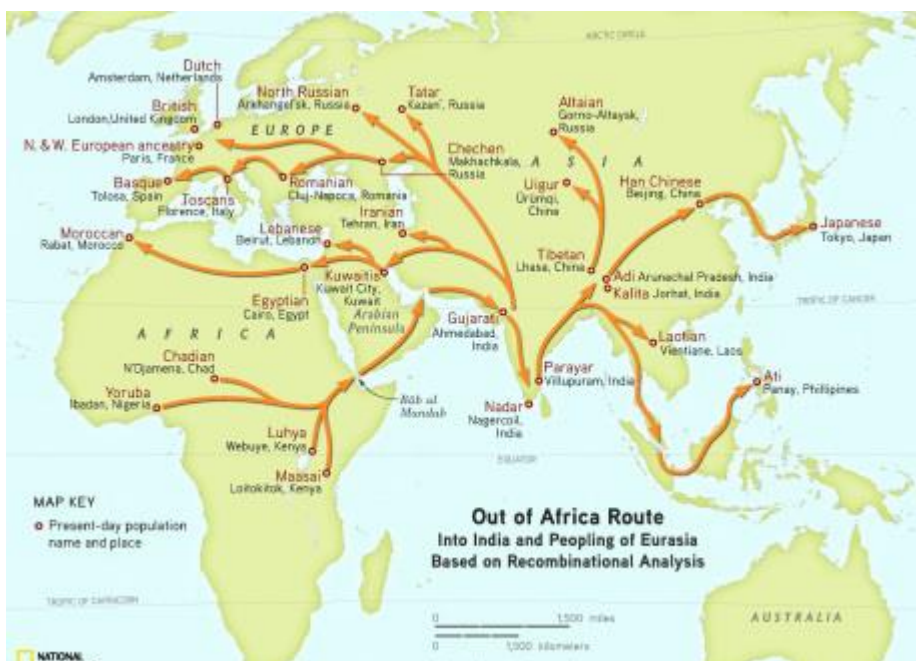
Link: <https://www.ncbi.nlm.nih.gov/pubmed/19603063>

The authors also show a gross ignorance of published literature pertaining to the migration issues. Man did not migrate alone. It migrated with its diseases, its pets and pests.

They Do Not Know about Recombinant Technology:

The most sophisticated method of study for the purpose of finding out the Out of Africa route was adopted by the Genographic Project which was funded by IBM, the computer giant. The method was so refined that it could map each step of a thousand mile journey. This method was the most accurate also. It produced the following map of the routes of human migration. It was based on the study of recombination. Every time a sperm is formed or an ovum is formed there is meiosis in which parts of chromosomes crossover. This crossing over takes place in each generation at a different point of the chromosome causing a permanent print of the past all ancestors on the chromosome.

This study found that the humans first came to India (from Africa) and then migrated to all over the world as depicted in this map.



Link Genographic Project web site. <http://www-03.ibm.com/press/us/en/photo/35881.wss>

also, <https://www-03.ibm.com/press/us/en/pressrelease/35877.wss>

Silva does not know that only southern route to India is the valid route.

It has been settled so many times by several repeated studies that the modern man came out of Africa from the horn of Africa (Djibouti) crossing Bab-el-Mandeb Strait then through coastal Arabia to Sind-Gujarat region of India (Quintana-Murci 1999; Oppenheimer 2003; Maccaulay 2005; Mellars 2006; Thangaraj 2005; Field 2007; Armitage 2011; Mele 2012). And it has also been conclusively decided that the human migration out of Africa took place only once and not the second time again.

Categories ancient DNA, archaeology, history, linguistics

ANI, ASI, R1a and Indian ancestral origins.

June 25, 2017 //

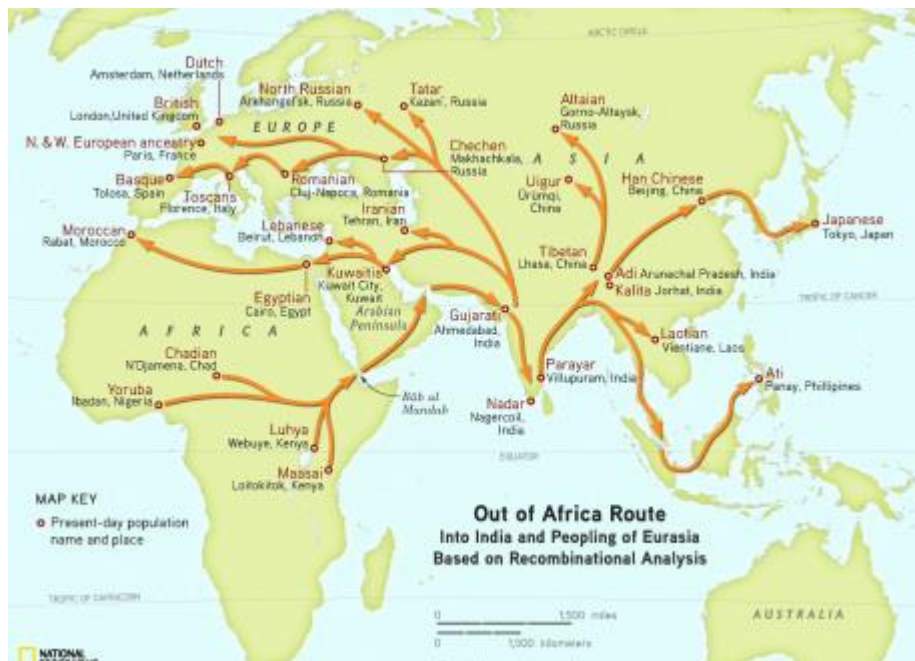
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What are ANI and ASI? What are the European and Indian R1a branches? Some explanations to the findings of David Reich et al 2009 and later works

by P. Priyadarshi

It has been settled so many times by several repeated studies that the modern man came out of Africa from the horn of Africa (Djibouti) crossing Bab-el-Mandeb Strait then through coastal Arabia to Sind-Gujarat region of India (Quintana-Murci 1999; Oppenheimer 2003; Maccaulay 2005; Mellars 2006; Thangaraj 2005; Field 2007; Armitage 2011; Mele 2012). And it has also been conclusively decided that the human migration out of Africa took place only once and not the second time again.

The most sophisticated method of study for the purpose of finding out the Out of Africa route was adopted by the Genographic Project which was funded by IBM, the computer giant. The method was so refined that it could map each step of a thousand mile journey. This method was the most accurate also. It produced the following map of the routes of human migration.



Source: Genographic Project web site. <http://www-03.ibm.com/press/us/en/photo/35881.wss>

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Their press release said, “Over the past six years, we’ve had the opportunity to gather and analyze genetic data around the world at a scale and level of detail that has never been done before. When we started, our goal was to bring science expeditions into the modern era to further a deeper understanding of human roots and diversity. With evidence that the genetic diversity in southern India is closer to Africa than that of Europe, this suggests that other fields of research such as archaeology and anthropology should look for additional evidence on the migration route of early humans to further explore this theory.”

However this good advice was ignored by later workers, however, Priyadarshi (2014) tried to look for additional evidence in archaeology and anthropology to correlate with this route, and he achieved remarkable success. The results of the Genographic team’s study were largely ignored by the Eurocentric dominated academic community which is dominant.

The workers of the Genographic Project also said, “The new analytical method looks at recombinations of DNA chromosomes over time, which is one determinant of how new gene sequences are created in subsequent generations. Imagine a recombining chromosome as a deck of cards. When a pair of chromosomes is shuffled together, it creates combinations of DNA. This recombination process occurs through the generations.”

“Recombination contributes to genome diversity in 99% of the human genome. However, many believed it was impossible to map the recombinational history of DNA due to the complex, overlapping patterns created in every generation. Now, by applying detailed computational methods and powerful algorithms, scientists can provide new evidence on the size and history of ancient populations.” (source web site, link provided below the figure above).

An article was published on the basis of this study which said in its Abstract, “We also observe that the patterns of recombinational diversity of these populations correlate with distance out of Africa if that distance is measured along a path crossing South Arabia. **No such correlation is found through a Sinai route, suggesting that anatomically modern humans first left Africa through the Bab-el-Mandeb strait rather than through present Egypt.**” (Mele *et al* 2012:Abstract).

The article further noted, in the context of the other method based on SNPs, “And the two approaches may reflect processes taking place in different time frames with the recombination-based analysis being more sensitive to more recent events.” (Mele 2012:28) Thus the migrations taking place during the last 10,000 years, particularly the Indo-European migrations can be best described by the migration routes described by the Genographic Project’s study. Thus it is settled that there was only one route out of Africa and people using the Arabian coast reached India to expand further.

However an obsession to stick to his untenable position of the Egyptian route to Europe, West Asia and Central Asia, kept Reich and his group continuously making mistakes after mistakes in analysing the data emerging from all the later studies.

Thus in light of the above discussion, if we examine the data of Reich (2009), it gives entirely different inferences. Metspalu (2004) and Sahoo (2006) had demonstrated that there is a paucity of mtDNA and Y chromosome lineages in the Indian gene pool that have been assigned a Central Asian origin (Metspalu *et al.* 2004; Sahoo *et al.* 2006). This in other words means there was no measurable, if at all, arrival from Central Asia to India. Metspalu (2004) also noted that about 10% of mtDNAs (haplogroup M) of Iran were of Indian origin.

Sahoo *et al* (2006:847) demonstrated that although the DNA haplogroups of South Asian (India-Pakistan) origin are found in West Asia, other common lineages of West Asia are not found at all in India-Pakistan; and therefore they concluded that no migration from Middle East had taken place to Indian subcontinent, although migrations from India to Middle East had taken place.

Sahoo *et al* had actually written the following words: “The perennial concept of people, language, and agriculture arriving to India together through the northwest corridor does not hold up to close scrutiny. Recent claims for a linkage of haplogroups J2, L, R1a, and R2 with a contemporaneous origin for the majority of the Indian castes’ paternal lineages from outside the subcontinent are rejected, although our findings do support a local origin of haplogroups F* and H.” (p. 847). They also rule out arrivals from Southwest Asia because West Asian haplogroups (like Y-Hg G) are not found in India.

Kivisild's findings (2003:322, column 2) too had shown that humans could not have arrived from West Asia into India because of lack of West Asian Y-hgs E, G, I, J* and J2f in India. Kivisild *et al* wrote, "When compared with European and Middle Eastern populations (Semino *et al.* 2000), Indians (i) share with them clades J2 and M173 derived sister groups R1b and R1a, the latter of which is particularly frequent in India; and (ii) lack or show a marginal frequency of clades E, G, I, J*, and J2f."

The Root Cause of Continuing Confusion

There were mtDNAs as well as Y-DNAs which were present in both—India and Iran on the one hand and in Europe on the other hand. This led the Eurocentric academia to proclaim that these were Western European DNAs. These included for example, Y-DNA J2, R1a, R1b etc and mtDNA H, U, T etc. This assumption was used as evidence favouring Indo-Iranian arrivals from Europe. The sharing of ANI (Ancestral North Indian) genes by European, West Asian and Central Asians as shown by Reich (2009) was considered as proof of about 50% of north Indians having arrived from Central Asia, West Asia and Europe (Tamang, Singh and Thangaraj 2012; Metspalu 2011). However the other possibility that the Ancient North Indians (ANI) people might have migrated to Europe, West Asia and Central Asia was not given any heed. The Aryan Invasion Theory was working hard in these minds.

Mist Cleared by Ancient DNA

Ancient DNA or aDNA are DNAs recovered from the skeletons recovered from part. Recently the technology has advanced much and now we know the things much better about the humans of the past. The ancient DNA (aDNA) studies showed that the population of Europe had been replaced by people arriving there from East Asia, Caucasus, West Asia and Iran during the Holocene. The original hunter-gatherer population of Europe became almost extinct except in some warmer regions like Iberian Peninsula (a fraction of people of Spain). People arrived in Europe starting about 7000 BC, but mainly after 5500 BC. The most of the modern population of Europe came there from Asia between 5000 and 4000 BC. However, many continued to arrive even up to 1000 BC. This is in nutshell the peopling of modern Europe as derived from ancient DNA studies (Olalde 2014; Haak 2015; Allentoft 2015; Der Sarkissian *et al.*, 2013; Fu *et al.*, 2016).

Thus, today's European or Western Eurasian haplogroups are not European in origin but are in fact Asian in origin; and the European or Western European gene or haplogroup is a misnomer and now needs to be discarded.

The R1a Controversy

The current debate is over the place of origin of the R1a or R1a1 (named differently in different articles). Underhill (2010) had noted that, “Importantly, the virtual absence of M458 chromosomes outside Europe speaks against substantial patrilineal gene flow from East Europe to Asia, including to India, at least since the mid-Holocene.” (Underhill 2010:Abstract, last line). The R1a-M458 is the European branch of R1a1. Had people come from East Europe like Ukraine etc moved to India this branch must have come to India. But it did not happen. It is not found in India today.

The fuss created by some people about two different branches of R1a Y-DNA—one Indian and one European—can now be sorted out by means of the ancient DNAs, and there is no room for speculation. The Indian branch of R1a, *i.e.* R1a-Z93 is exclusive of India, Pakistan and Afghanistan. It originated in India and migrated through the Pamir route during the Bronze Age to Altai region and even to Sintashta (Ukraine), the Cradle of Western Indo-European culture.

Brief story of R1a Controversy

The Y-chromosomal DNA haplogroup R1a was identified by a marker M17. This Y-DNA R1a or M17 is widespread in the living population of Eurasia—from India to Europe through Central Asia. This finding prompted many authors to link it with the Indo-European migration. Wells (2001) claimed that the humans made their first settlement in Central Asia, and that the M17 was born in Central Asia from where it reached India with the Aryan invaders in about 1500 BC. “This pattern of high diversity is consistent with an early settlement of Central Asia by anatomically modern humans, perhaps 40,000–50,000 years ago (see below), followed by subsequent migrations into Europe, America, and India,” (Wells 2001: 10247)

By 2006, another identifying mutation M198 was identified by the scientists for the same DNA, and the particular DNA was given the new name R1a1-M198 (or, R1a1-M17). This is now its preferred name. Regueiro (2006) claimed that the DNA R1a1-M198 had originated in the Kurgan culture of the steppe from where it migrated into India. He noted, “This finding supports the inferred migration of the Indo-Iranians during the period 3,000 to 1,000 B.C. as proposed by Mallory” (Regueiro 2006:140).

However such views were based on the Aryan Invasion Theory; and there was no supporting evidence regarding the direction of migration. Later Evidence favouring Indian origin of R1a1 Later on, voluminous DNA evidence emerged which proved that the place of origin of this DNA was India and that it had later migrated into Central Asia, from there to Volga-Ural region and from there to East and then Central Europe. Yet, ironically, in general many authors till date ignored the recent evidence and continued to say that this DNA originated in Ukraine from where migrated to Central Asia, India and Europe. Stephen Oppenheimer too holds this view privately as communicated to me in a meeting held at Lalit Hotel in Delhi.

Several researchers pointed out on the basis of the further analysis that this male lineage of DNA known as R1a1 had not arrived from outside but was indigenous to India (Sahoo 2006; Sengupta 2006; Sharma 2009). These researches also noted the formidable presence of this DNA (R1a1) in the Dravidian speaking South Indians as well as the Austro-Asiatic speaking tribal groups. In fact this DNA had migrated to Southeast Asia also from where it even reached Madagascar.

Underhill (2010) further examined this DNA and found that the oldest haplotypes of the DNA was present in India and it expanded from India (Indus Valley region) to Central Asia and then to Europe as well as Mongolia (Underhill 2010:Fig.1). He was able to identify two branches within this lineage with the help of two markers. One branch identified by the marker M434 was distributed in West Asia and it also migrated into Arabia. The other branch was identified by the marker M458 and it was restricted to Europe with a particularly high concentration in East Europe like Ukraine.

However not a single person belonging to this branch could be found in India or Iran. Thus Underhill ruled out any migration from Ukraine or from the adjoining steppe to India or to any other part of Asia. “Importantly, **the virtual absence of M458 chromosomes outside Europe speaks against substantial patrilineal gene flow from East Europe to Asia, including to India,** at least since the mid-Holocene.” (Underhill 2010:Abstract)

Pamjav (2012) was able to find finer details about the branches of the R1a1 lineage. He noted that the M458, earlier identified by Underhill, and another branch Z280 were found in Europe, whereas the branch Z93 had split from the main trunk in India. Thus it became clear that the main trunk M198, gave birth to branch Z93 in India from where it spread to Uzbekistan and Mongolia, as well as to Southeast Asia (Pamjav 2012:2). Some members of this Indian branch Z93 also reached up to Hungary independently of any Roma migration (*ibid*: 3). This means Indians certainly migrated to Mongolia, Central Asia and Hungary after the birth of this branch. And of course they could have migrated before the birth of this lineage in the earlier eras.

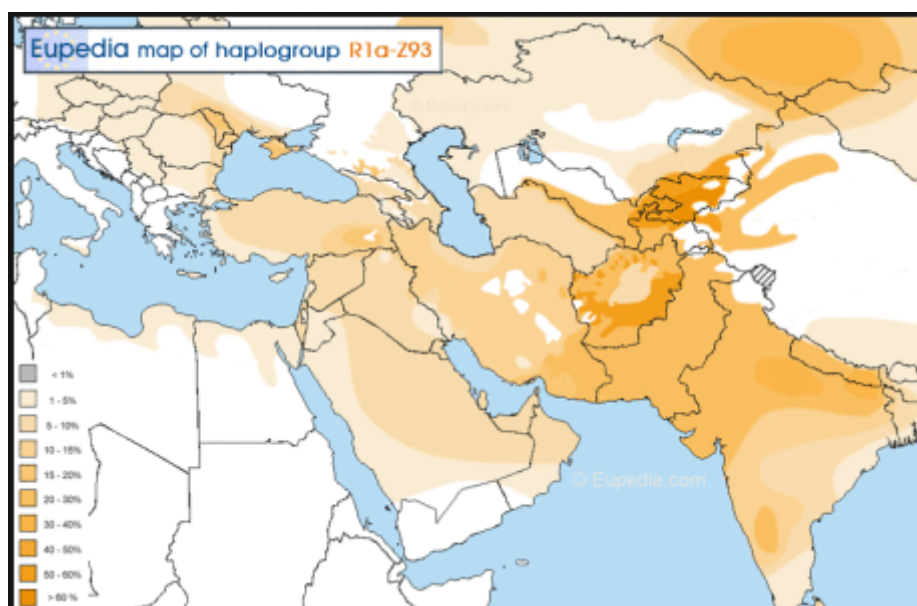


Fig. Source Eupedia. The distribution of Indian R1a-Z93 indicating its origin in India and migration through the Pamir to Tarim Basin and Altai, and from there to the steppe.

The European branches of R1a1 namely M458 and Z280 originated while the main trunk was passing through the Caucasus region and the steppe (Pamjav 2012:Abstract). Then the whole group of people moved forward into Europe through the North Black Sea region. Hence we get M458 and also Z280 in the steppe, East Europe and Central Europe but not in India or Iran. “Inner and Central Asia seem to be the overlap zones for the R1a1-Z280 and R1a1-Z93 chromosomes as both forms were observed at low frequencies.” (*ibid*:3)

This is because the Indian branch Z93 also migrated into Central Asia along with its parent main trunk M198. But the European branches found in Central Asia and the steppe never came to India. It is big evidence which clarifies the direction of human movement. Hence the Indian branch can be found today in Mongolia, Central Asia and even in Hungary today. But the European branches (M458 and Z280) cannot be found in India. This finding irrefutably fixes the direction of migration as to be from India to Europe, and leaves no room to any further argument in the matter.

Underhill (2015) was made pariah for his bold statement made in Underhill (2010). Yet even under great pressure he never accepted the European or steppe origin of the R1a trunk. He further worked on this lineage and found that the R1a1 has several branches which can be grouped into two. One set of branches are found in India and Central Asia, where as the other set of branches are found in Europe.

Of the European samples of R1a, 96% belonged to Z282, and 98.4% of Indian and Central Asian lineages belonged to the lineage Z93. Underhill (2015) found that one branch M558 originated in Volga-Ural area and migrated with the group further west into East Europe. The branch M458 broke off after that. Only after these, the branches M282 and M284 originated.

The Indian branch Z93 is quite common today in South Siberia, Altai region of Russia, Kyrgyzstan and Iran. The further branches of Z93 lineage are 1. Z2124 found in Pashtun Afghanistan, Caucasus and Iran; 2. M750 in India, Pakistan, Afghanistan and Himalayas; 3. M560 in Burushaski, Hazara, and Iranian Azeri (Underhill 2015:11).

Underhill in his latest work proposed the place of origin of R1a somewhere “near Iran” (2015:11-12). But instead of saying “near Iran”, saying Indian sub-continent would have been more accurate. His conclusion does not take into account of the R1a lineages present in the Indian tribes and Dravidian speakers. They were not included by Underhill (2015) in his study. His study also did not include the study of R1a present in several eastern regions of India like Bihar, UP, as well as R1a present in Myanmar, Thailand, and Indonesia etc.

The Y-DNAs R1 (M173) and R* (M207) are found in large numbers in Bali (Indonesia) today, and they have migrated there from India (Karafet 2005:Table 1). In fact at least 12% of Balinese male lineages were found to be of Indian origins in this study. These R1 DNAs are ancestral to R1a1. Kusuma (2015) found that R1a lineage has reached Madagascar (Malagasy) also when people of Indonesia migrated to this island. Such findings only prove that R1a1 originated in India and not in Iran.

More truth is revealed by the recovery of the R1a1 samples from the archaeological samples of human remains. One R1a1a has been found from 5100 BC Spain at Els Trocs site (Haak 2015). This is a descendant of R1a1a. This could have migrated there with the goat-pastoralist migration which took place from India to Southwest Europe through Ganj Dareh (Iran) about that time. One R1a1 has been found from Oleni Ostrov (Northwest Russia) dated 6,400 BC (Mesolithic Culture; Haak 2015). Earlier than these two findings, there has been no R1a1 lineage in Europe.

Also, five samples of India branch that is R1a-Z93 have been found from the Bronze Age Sintashta (Ukraine) about 2500 BC (Mathieson 2015: page 4). Sintashta is currently being considered the cradle and source of the Indo-European language and Culture of Europe. It has been repeated by these authors that Indo-Aryans and Iranians came to India and Iran from Sintashta. However the presence of Indian DNA there clearly indicated whether Indo-Europeans came to India from Sintashta, or went from India to Sintashta.

Apart from these two examples, the R1a1 did not migrate to Europe in large numbers during the Neolithic period. Its general migration from India and Iran to Central Asia and Europe took place mainly during the Copper, Bronze and the Iron Ages, which was also the time of rise and fall of the Indus Valley Civilization. This shows that this lineage got established in the Indus Valley just before its rise in about fifth millennium BC, and it also proves that the Bronze Age Indus Valley Civilization was Indo-European civilization.

The Tarim Basin mummies recovered from Xinjiang in Central Asia had all males in the R1a1 (M198A) lineage (Li 2010), which is Indian. The date was late Bronze Age to Iron Age. Since the lineage was not present in Europe in such large frequency at that time and before this time, its arrival could have been only from India or Iran. The high frequency may be because of the founder effect. Other evidence also shows migration during that period from India/ Iran. Li (2015) further clarified that the Tarim Basin mummies carried Indian maternal DNAs in good frequency.

Recent finding of ancient DNA from the Indo-European Maikop culture dating 3700 BC in North Caucasus further adds weight to Indian origin of Indo-European. Skolov (2016) found that several of the ancient mtDNAs recovered from Maikop belonged to the Indian M52 type. Thus proving that the Maikop people had arrived from India, and they had included female migrants too.

Understanding Reich *et al* 2009 in light of the foregoing

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David Reich's problem was that he failed to reconcile himself with the fact that there was no other route of Out of Africa than the coastal Arabian route to India, and thereafter expansion and migrations took off from here. He continued to harbour the concept of the second route to Europe and Central Asia through Egypt and Sinai to West Asia and then beyond. This created distortions in all the interpretations done by himself or the group of his follower scholars. In light of the ancient DNA findings, and also some robust extant DNA studies, it is desirable that 'Reich *et al* 2009' should be re-explained in more simple English once again so that people may wash their prejudiced views.

Reich *et al* (2009) nowhere said that there was any flow of west Eurasian (European) gene into South Asia. To quote their own words, "These results do not mean that the Indian groups descend from mixtures of European and Austro-Asiatic speakers, but only that they derive from at least two different groups that are (distantly) related to CEU and Santhal." (p. 4 pdf, col 1).

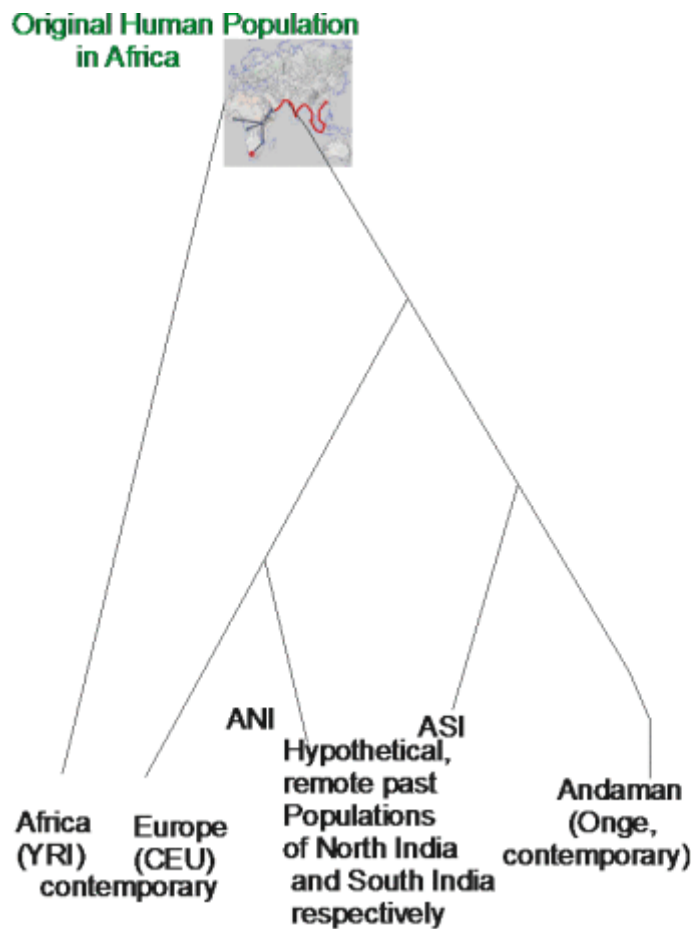
Relatedness does not at all imply gene flow from CEU (Europe) to India, however it means a common ancestor for both north ancestral Indians and CEU. This common ancestor had existed after split from the African main trunk, and after the Ancestral South Indians too had been split. Reich *et al* depict this situation by means of a figure (Fig. 4 of Reich *et al*). The figure of migration which Reich *et al* produced can be seen at the link below:

(<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2842210/figure/F4/> or,

http://www.nature.com/nature/journal/v461/n7263/fig_tab/nature08365_F4.html

or, see Fig 4, page 4 of pdf of the article.)

Figures for family tree can be constructed from the text itself actually. Reich *et al* write, "the tree (YRI,((CEU,ANI),(ASI, Onge))) provides an excellent fit to the data". This gives us a family tree for five populations, *viz.* 1. YRI (West African), 2. CEU (Modern Europeans), 3. ANI (Ancestral North Indians), 4. ASI (Ancestral South Indians) and 5. Onge (a Modern Andamanese tribe)—if drawn graphically would be like this:

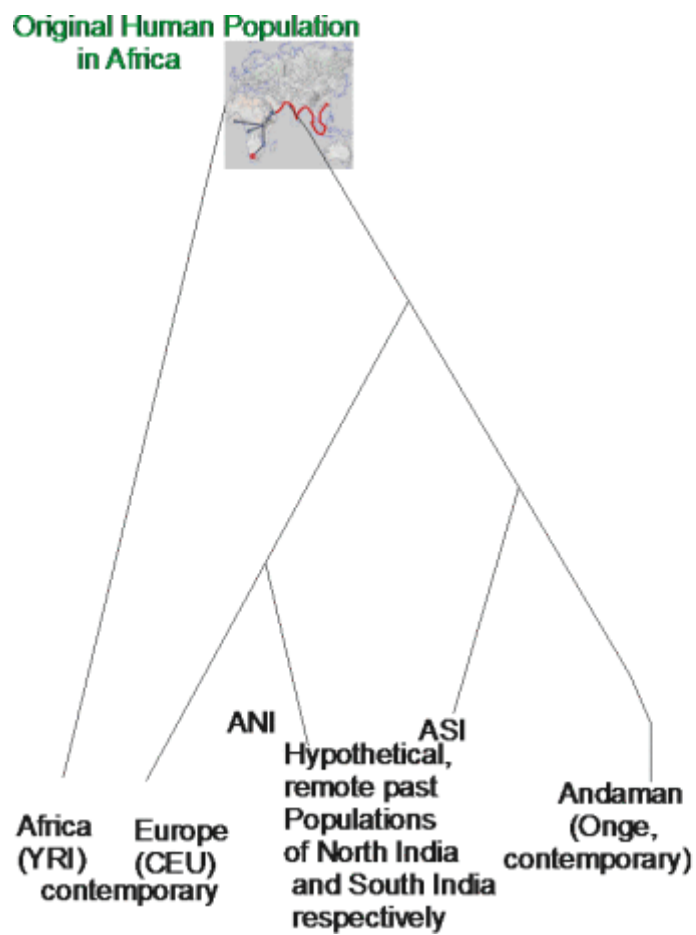


The top inset from Stephen Oppenheimer's *The Journey of Mankind*, Bradshaw Foundation has been added as a ready-reminder to African-Eurasian split and relationship. Source: <http://www.bradshawfoundation.com/journey/>

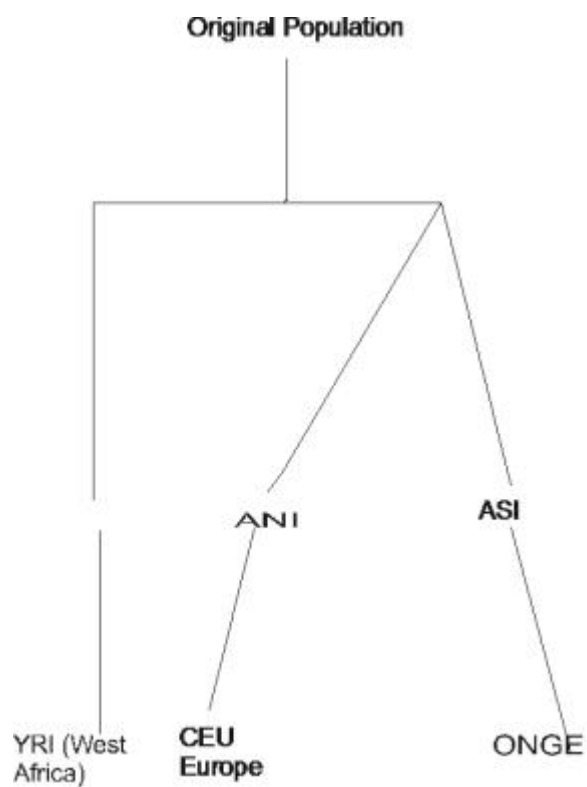
This is clarified further in the text of Reich *et al*: “the fact that different Indian groups have inherited different proportions of ancestry from the ‘Ancestral North Indians’ (ANI) who are related to western Eurasians, and the ‘Ancestral South Indians’ (ASI).”

Here we note that, in spite of the fact that ANI were related to Western Eurasians (Europeans) in remote antiquity, the current Indian populations (both north and south Indian) derive from admixture of ANI and ASI, and not by admixture from any third population. It is the Ancient Europeans which derived from Ancestral North Indians.

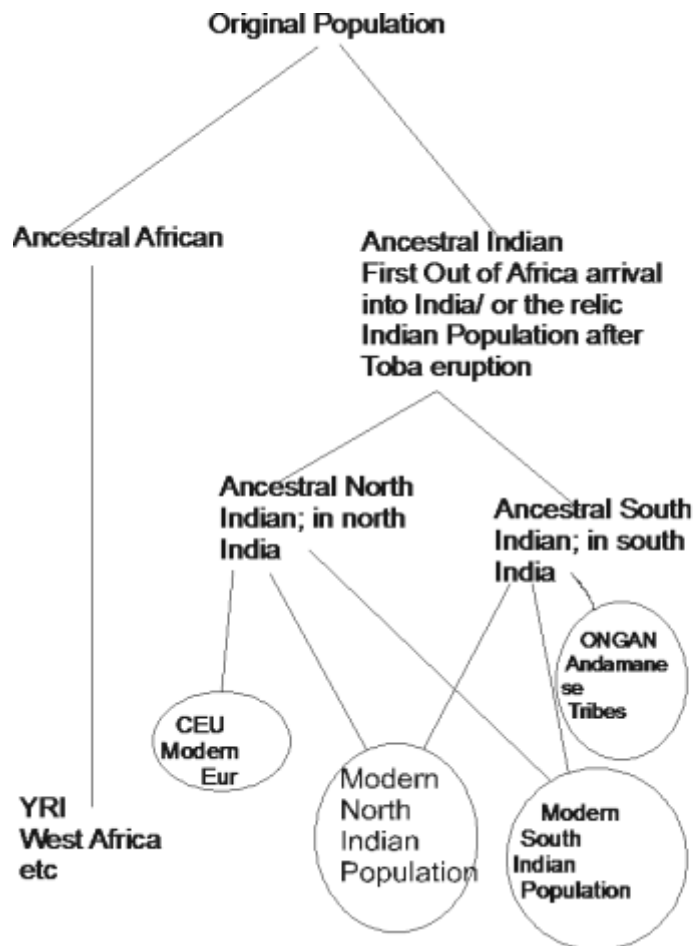
The family-tree (Fig 4 of Reich) is good. Yet it does not take into account the dates and places. It should be noted that ANI and ASI are past populations, and hence need to be placed nearer the source than the YRI (Africa), CEU (Europe, Central Asia, West Asia) and Onge (Andaman) populations, which are contemporary living populations. Therefore the picture needs to be corrected, to adjust placing for time. Then the picture would look like this:



However we know, that the stem of the non-African limb of the graphic was located in South Asia. Hence the real picture would be like this:



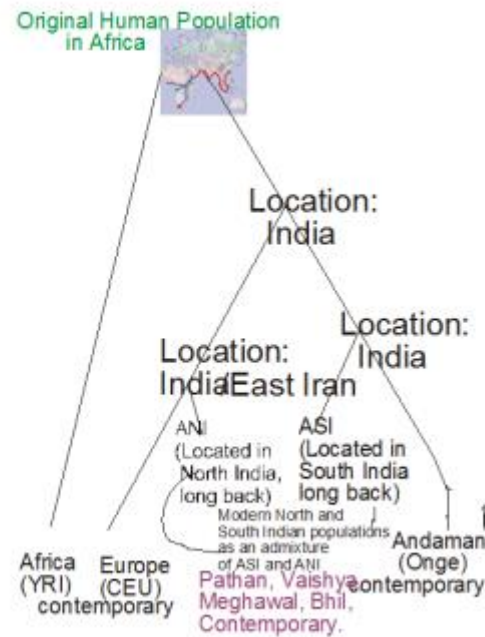
However, this model ignores the fact that many other populations than the CEU and Ongan had been derived from ANI and ASI. Hence the picture needs to be modified further to accommodate modern north Indian and South Indian populations:



This picture is consistent with both the important conclusions of the Reich's article:

1. "These results do not mean that the Indian groups descend from mixtures of European and Austro-Asiatic speakers, but only that they derive from at least two different groups that are (distantly) related to CEU and Santhal." (Reich *et al*, p. 4, column 1). This rules out any admixture of Europeans and Austro-Asiatics.
2. "Applying our model-fitting procedure, we find that the tree (YRI,((CEU,ANI),(ASI, Onge))) provides an excellent fit to the data from Indian groups."the tree (YRI,((CEU,ANI),(ASI, Onge))) provides an excellent fit to the data" (, p. 4, col 1).

Hence a full synthetic figure would be like this:



At the end it is useful to add that often statements by great authors are best not forgotten. Western Eurasia was formed of populations migrating from Asia and during recent Neolithic times from Africa. Hence if plotted, European genes cannot form any cline towards Asia or Africa, while African and Asian genes will always show clinal pattern of expansion into Europe.

The seminal words of Cavalli-Sforza remain valid even today, "...both Africans and Asians contributed to the settlement of Europe, which began about 40,000 years ago. It seems very reasonable to assume that both continents nearest to Europe contributed to its settlement, even if perhaps at different times and maybe repeatedly. It is reassuring that the analysis of other markers also consistently gives the same results in this case. Moreover, a specific evolutionary model tested, i.e., that Europe is formed by contributions from Asia and Africa, fits the distance matrix perfectly (6). In this simplified model, the migrations postulated to have populated Europe are estimated to have occurred at an early date (30,000 years ago), but it is impossible to distinguish, on the basis of these data, this model from that of several migrations at different times. The overall contributions from Asia and Africa were estimated to be around two-thirds and one-third, respectively". (Cavalli-Sforza 1997:7720).

The End

Q.E.D.

Categories Uncategorized

Ancient DNA tells how climate change caused the Indo-European migration

February 11, 2017 //

1

[Citation: Priyadarshi, Premendra, 2016, “The Climate Change and the Environmental basis for the Human migrations during Holocene”, Concept Paper presented to the seminar *Chronology of Indian Culture since the beginning of Holocene through Scientific Evidence*, organised by Institute of Scientific Research on Vedas (I-SERVE), Delhi on 16 July 2016.]

The Climate Change and the Environmental basis for the Human migrations during Holocene

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1. The Ancient DNA and the New Story of Holocene Migration

- Up to 6000 BC, Europe was inhabited by dark skinned meat-eating hunters, who were completely ignorant of farming and pastoralism (Olalde 2014; Haak 2015; Bramanti 2009; Der Sarkissian *et al*, 2013; Fu *et al*, 2016). They were hunters. Their primary food was meat. Their DNA reflects that they could not digest milk (Olalde 2014; Allentoft 2015). There is formidable new archaeological evidence to suggest that they practiced cannibalism and attacked and predated the newly arriving farmers from Asia (Boulestin 2009; Orschiedt and Haidle 2007; Orschiedt 2008). These dark-skinned people of pre-Neolithic Europe were nearly completely replaced by the arriving light-skinned Asians who brought farming to Europe, and these Asian farmers also carried the gene for digesting milk (Olalde 2014; Allentoft 2015; Haak 2015). The light skin colour later became nearly universal in most of Europe by the process of Natural Selection of a particular gene. Milk digesting gene took longer to become universal in North Europe.
- The farmers arrived for the first time in Europe between 6000 BC and 5000 BC and they appear in Germany, Hungary and Spain almost simultaneously (Haak 2015). These Asian newcomers in Europe brought farming and pastoralism. They spoke Indo-European language (Haak 2015:Abstract). Their arrival in Europe continued to take place up to 1000 BC. The arrivals were through the north of Black Sea (Ukrainian) corridor, as well as through Anatolia (Turkey) route located to the south of the Black Sea. Both the group of Asians arriving in Europe—those arriving through Anatolian route as well as those coming by the north Black Sea route—spoke Indo-European languages. These new people certainly had a common source of origin to the further east. These people brought the Indo-European language to Europe by both of the routes, the southern as well as the northern. In all probabilities this common location from where both limbs of migration had emerged was in Iran and to the further east.

- One of the two routes of arrival of the farmers in Europe was through West Asia. It has been clarified by ancient DNA studies that there were three genetically different populations of farmers living in West Asia at early Neolithic. These three populations were located in Anatolia, Fertile Crescent and Iran (Zagros) respectively. It was at a later time, i.e. by the Bronze Age or Late Neolithic that the intermixture of the three populations took place (Surugue 2016; Lazaridis 2016). Lazaridis (2016) made it clear that those farmers who migrated to Egypt and North Africa mainly included the farmers living in the Levant (Israel, Jordan, Syria).

The people who entered Europe during Early Neolithic mainly migrated from Anatolia which is modern Turkey (Lazaridis 2016). However these Anatolian farmers too spoke Indo-European language and had had some Iranian DNAs in significant frequencies, indicating that the Anatolian farming too had been originally catalysed by arrival of some Iranian farmers. The DNAs of Iranian (and Indian) origins which migrated from Anatolia to Europe included mtDNAs X, T and N (*vide infra*; also see Fig. 1), indicating the prior arrival of these DNAs from Iran to Anatolia. In fact the ancient DNA recovered from the Zagros Neolithic has confirmed that these people were genetically same as the Pakistani or Afghani populations (Broushaki 2016), indicating their arrival to Zagros from northwest India.

But Harvella (2015) found that these early Neolithic Anatolian immigrants do not represent the ancestors of modern European genetically. In fact there was a larger emigration from Anatolia later during late Neolithic and early Bronze Age which laid the actual foundations of the modern population of Europe genetically. This emigration certainly took place after the Zagros-Iran Neolithic farmers had infiltrated Anatolia much thoroughly by the process of demic diffusion.

“On the other hand, populations of the Middle-Late Neolithic (Boian, Zau and Gumelnița cultures), supposedly a second wave of Neolithic migration from Anatolia, had a much stronger effect on the genetic heritage of the European populations. In contrast, we find a smaller contribution of Late Bronze Age migrations to the genetic composition of Europeans. Based on these findings, we propose that permeation of mtDNA lineages from a second wave of Middle-Late Neolithic migration from North-West Anatolia into the Balkan Peninsula and Central Europe represent an important contribution to the genetic shift between Early and Late Neolithic populations in Europe, and consequently to the genetic make-up of modern European populations.” (Harvella 2015:Abstract).

However the main bulk of the early Neolithic migration ‘out of Iran’ took place into the Caucasus and the steppe, and Central Asia as the result of Iran’s population expansion from the Neolithic practices (see Fig. 1). This happened because the great freeze of the 6250 BC (8.2 Kilo Event) had caused large scale death of the humans in these colder areas, and had left these regions with negligible sparsely scattered human populations. A better climate after 6000 BC preferentially

promoted Iranian migration into these relatively vacant areas (*vide infra*). Iranians who has learned farming and had domesticated goat migrated into the vacant landscape as soon as the improved climate permitted. However, people from East Siberia, China, Tibet, and Hindu Kush etc. too arrived into this vacant inner Asian region (Comas 2004; Lalueza-Fox 2004; Dulik 2011:2 Table1; Berezina 2011; Tarykov 2013; Haak 2015). All these studies just cited also confirm the presence of Indian DNAs in Central Asia-steppe. A further migration from this region to Europe would bring the Eastern DNAs into Europe which is detectable even today.

Thus the Iranian Neolithic farmers migrated into the steppe i.e. the region north of the Caspian and the Black Seas and the area to the east in large numbers. This has been confirmed by the ancient DNA studies (Surugue 2016; Lazardis 2016). One of the routes of this migration was Caucasus, because ancient goat skeletons have been recovered from South Caucasus (West Azerbaijan) dated 6000 to 5500 BC (calibrated) which prove that the goats in South Caucasus had not been domesticated locally but had been brought from Zagros, Iran (Kadowaki 2016). This migration of ancient Iranians through Caucasus with Neolithic could have been the source of the Iranian language found in the steppe. Presence of Iranian language in the steppe in the remote antiquity has been inferred from the presence of the Iranian (and also Indic) loanwords in modern Russian, Finno-Ugric etc. in many comparative linguistic studies (Burrow 2001; Witzel 2003; Parpola and Carpelan: 2005; Priyadarshi 2013). At that time Burrow had considered it the evidence of Iranian people's (imagined) original home in the steppe (Volga region). The words were borrowed from Iranian into the steppe-languages, but not the vice-versa. The linguistic flow is unidirectional. In fact the linguistic data produced by these authors only suggest the contact between Iran and the steppe regions and that the contact was probably due to the migration, however in the reverse direction of what was suggested by Burrow etc.

Figure 1. Map showing the migration of the Iranian mtDNA T vertically to the north from South Iran to the Volga region, and also into Arabia, Turkey and South Europe on the basis of two different mtDNA parameters. Courtesy Fernandes *et al*, 2015.

- The ancient DNAs from India have not been studied so far. However by comparing the DNAs of the existing people of Iran and India it has been inferred that the Iranian gene pool shares a large percentage of DNAs of Indian origin, particularly mtDNA haplogroup M and its branches like M5. These DNAs which are shared between Iran and India are in fact India specific or “Indian origin” DNAs (Metspalu 2004: Abstract). The Indian mtDNA U7 is present in Iran in about 7% of population. The Indian mtDNA haplogroup M is present in 5.3% of Iranian population (Metspalu 2004:3). There are many more Indian DNAs present in Iranian population. But discussing them all here is beyond the scope of this article.
- The light skin colour gene, which is the hallmark of the Europeans or the white people today, too originated in India. In fact the original Europeans before 6000 BC were black skinned (*vide supra*). The European light-skin colour gene is exactly the same as that found

in India (both, north and south India; Basu-Mallik 2013). It was not known whether it had originated in India, Iran or Central Asia. However, a recent study makes it clear that this gene appeared for the first time in India. It is from India that it migrated to Europe particularly during the Bronze Age. In this DNA study of the existing populations of Europe and Asia, Canfield found that the oldest or the original of the light-skin-colour gene is found in the Gujarati Indians. Canfield and colleagues noted, “Interestingly, the greatest diversity of B-region haplotypes associated with C11 is found in GIH (89% B6).” (Canfield 2013:2063). The GIH in this study stands for Gujarati-Indian-Hindus. The data obtained from the GIH (the Gujarati Indians included in this study) showed that the light skin colour gene originated in Gujarat (India). So, at the most, the gene must have originate in a region spreading from India to Iran, but not to the further north, the authors concluded (*ibid*:2059 Abstract). Hence this study settles the issue as to where be the place of origin of the light-skin-colour gene. This gene spread from India to Iran; and from Iran to the steppe, and also to Anatolia and Arabia.

The light skin colour gene came into existence at about 10,000 years back by a genetic mutation. This happened in India in the form of a new mutation called A111T (Cheng 2014, quoted by Zolfagharifard 2014). It soon spread in Northwest India, Iran and Afghanistan. Later it spread to Central Asia and steppe from Iran. In the northern latitudes of India as well as in Iran and Afghanistan and further north, the light skin colour gene underwent Natural Selection leading to the increase in its frequency. In Central Asian regions like the Tarim Basin, and also in Europe its frequency went on increasing by the process of the Natural Selection until late Bronze Age.

The Natural Selection which was exerted on the light skin colour gene was enforced by farming related vegetarian diet which was poor in Vitamin D, and the lower intensity of sunlight caused the Vitamin D deficiency in the darker skinned people who had reached these northerly regions. The dark-skinned humans were eliminated over time and lighter skinned among them were promoted to survive. This process of Natural Selection was spread over generations over thousands of years, and it happened because the light skin colour helped get more of Vitamin D from the sunlight. Ultimately making the entire population white skinned in North Europe. In South Europe, the sunlight was more powerful than North Europe, and people would have more of Vitamin D. Hence in South Europe some dark-skin gene has survived and is found in the Greek, Spanish and the Latina populations even today.

Figure 2. Origin and Spread of Light Skin colour gene from India. Figure Courtesy Basu-Mallik *et al*, 2013.

- The people who lived in northwest India had developed pastoral practices and they had the milk digesting capacity during the adult life, a capacity which is present in the infants, but is lost in most of the people of the world in the adult life. The presence of the milk digesting capacity in the adult life is due to the Lactase Persistence gene (LP Gene). There are quite a few types of LP Genes present in the world. But the particular LP Gene which is shared by the people of North and South India, Arabia and Europe is the same (named as -13910*T).

Thus only three places of origin of this gene can be suggested—India, or Arabia or Europe (Romero 2011).

This gene although has been found from the Neolithic Sweden (a single sample) and Spain (Basque Neolithic, 7 out of 26 skeletons) about 5000 BC, it becomes absent from Central Europe for a long period of time. This means that some of the humans who arrived in Europe between 6000 and 5000 BC had originally this LP Gene. But the gene could not survive long because of the lack of adequate pastoral and milk-drinking practices getting firm roots in the European land. The food largely consisted of meat obtained by hunting even after the arrival of Neolithic in Europe, and the meaning of Neolithic often remained restricted to the presence of pottery. Hence later this gene was reintroduced from Asia in late Bronze Age and after.

Some samples from Hungary (Central Europe) from the Medieval period (900-1100 AD) revealed only 33% prevalence of the LP Gene, whereas the modern prevalence there is greater than 60%. Almost from the same period of Germany (950-1200 AD) at village of Dalheim in Nordrhein-Westfalen, the DNA recovered from ancient bones revealed 71% presence of this gene. This frequency is almost the same as the modern prevalence (Krutli 2014:2). That means in the western part of the Central Europe, the Natural Selection had achieved the modern levels of the LP Gene as late as 1200 AD, however much of Central Europe did not have modern frequencies of this gene even by that time. Hence the European origin of the gene can be ruled out.

Presence of this gene (LP Gene) from 25% of the human skeletons from the Neolithic layer of the Basque country of Spain (dating 5000 BC) is important. This LP Gene was found not in association with cow pastoralism, but with goat pastoralism. No goat had ever been domesticated in Europe, and all the goats of Europe have been imported there after having been domesticated in Asia. Fernandez (2006) reported the DNA of goats from skeletons recovered from an adjoining location in France dating 5000 BC that the goats present there had arrived from two different routes. These goats belonged to two lineages A and C, and had reached Southwest Europe from two different routes. The lineage A had reached from Pakistan through Iran and Anatolia route, and the lineage C which is also found in Central Asia but not in Iran or Anatolia had reached there by the north of Black sea route (Priyadarshi 2014:343).

The Indo-European type of the LP Gene is product of a mutation which is found in high frequency in northwest India, North Europe and Arabia. However it is present in South India in significant frequency, and sometimes in quite high frequency like in about 45% of the members of the Toda tribe of Tamil Nadu (Romero 2011:253). This indicates that the gene actually originated in South India, but it could not get the benefit of Natural Selection in this region, because of the very late arrival of Neolithic in Tamil Nadu at about 1500 BC owing to the desert like conditions of South India because of decline in the Bay of Bengal monsoon before this time. In all probability there was a population expansion in South India leading to the northward migration of the Dravidian speaking people at the onset of the Holocene (*vide infra*). This took place when the Mehrgarh and Lahuradewa-Koldihwa were flourishing with Neolithic.

- When people started trying milk as food in Mehrgarh and other parts of North Indian Neolithic culture, this gene was very helpful in digesting milk. Because of this gene people did not develop diarrhoea after drinking milk. The presence of this milk-digesting LP Gene provided a huge survival advantage to those who drank milk as their main or sole food. Milk provided them not only the general nutrition but also Vitamin D and Vitamin B12. Not getting diarrhoea after drinking milk provided a distinct advantage to those who possessed this gene. Those who did not have the LP Gene developed diarrhoea and they could not drink milk. In the northern latitudes where milk was essential for survival of the vegetarians, the Natural Selection favoured the LP Gene.

In Arabia it helped digest camel's milk when camel pastoralism developed in Arabia about 1000 BC. The camel's milk was the staple food in the Arabian Desert after 1000 BC, leading to Natural Selection of the LP gene in Arabia. Hence we get high frequencies of this gene in Northwest India and Arabia.

Vitamin B12 is found only in milk and meat diet, and for survival man has to take either or the both of the two. Thus adoption of Neolithic non-meat diet without simultaneous adoption of milk in food would result in disease and death. However it did not happen in India miraculously. In India those vegetarians who drank milk, or did not drink milk, both survived equally. And this happens even today in India that many vegetarians who cannot afford milk survive well. This is because, uniquely in the Indians, but in no other population of the world, there lives a commensal bacterium which produces the vitamin B12 in human intestine (Albert 1980).

Because of this reason, when these Neolithic people lived in India, the presence of the vitamin B12 in milk did not provide any additional survival advantage to its drinkers. But because the vitamin B12 is found only in milk and meat at least one of the two is essential for those who live outside India. Hence any vegan (those who take neither milk nor meat) cannot remain healthy outside India where this bacterium is not found. When Indians left India and reached Central Asia and Iran and Arabia, as farmers who no more depended on hunting and meat, the LP Gene provided a survival advantage to those who drank milk. Hence the LP Gene was selected by a strong Natural Selection once people came out of India, and particularly when they reached North Europe. This gene migrated to Central Asia and Europe with migrating farmers. By continued process of the Natural Selection it was not firmly established even by 1000 BC in the north European gene pool where more than 70% of the population possesses it by now (*vide supra*).

Figure Courtesy Andrew Curry 2013.

- **Correlation of the New History from DNA with available ancient literature**

Recently the period of the Rig-Veda has been fixed to between 8000 and 6000 BC by several authors (Priyadarshi 2014; Bala and Mishra 2012; Bag 2015). The Rig-Veda mentions at one place, that the daughter of Manu named *Parshu*, migrated to Persia (in south Iran) and gave birth to 20 children (RV 10.86.23). The *Rig Vedic* people had contact with the Parsu people (Fars, Iran) and they imported horse from there (RV 8.6.46).

The Baudhayana Srauta Sutra mentions the migration of three people to Iran, Bactria and Armenia (Ararat) respectively during the chalcolithic period (Priyadarshi 2014:119; Kazanas 2012:224; Lal 2009; vide infra). A more extensive examination of literature is required to give us information about what it says regarding the migration from India to Iran and other places during the Holocene.

2/ Some Clinching evidence from existent human DNAs

2.1 The R1a Controversy

Eurocentricism in the studies:

The Y-chromosomal DNA haplogroup R1a was identified by a marker M17. This Y-DNA R1a or M17 is widespread in the living population of Eurasia—from India to Europe through Central Asia. This finding prompted many authors to link it with the Indo-European migration. Wells (2001) claimed that the humans made their first settlement in Central Asia, and that the M17 was born in Central Asia from where it reached India with the Aryan invaders in about 1500 BC. “This pattern of high diversity is consistent with an early settlement of Central Asia by anatomically modern humans, perhaps 40,000–50,000 years ago (see below), followed by subsequent migrations into Europe, America, and India,” (Wells 2001: 10247)

By 2006, another identifying mutation M198 was identified by the scientists for the same DNA, and the particular DNA was given the new name R1a1-M198 (or, R1a1-M17). This is now its preferred name. Regueiro (2006) claimed that the DNA R1a1-M198 had originated in the Kurgan culture of the steppe from where it migrated into India. He noted, “This finding

supports the inferred migration of the Indo-Iranians during the period 3,000 to 1,000 B.C. as proposed by Mallory” (Regueiro 2006:140). However such views were based on the Aryan Invasion Theory; and there was no supporting evidence regarding the direction of migration.

2.2 Later Evidence favouring Indian origin of R1a1

Later on, voluminous DNA evidence emerged which proved that the place of origin of this DNA was India and that it had later migrated into Central Asia, from there to Volga-Ural region and from there to East and then Central Europe. Yet, ironically, in general the authors till date ignore the recent evidence and say that this DNA originated in Ukraine from where migrated to Central Asia, India and Europe. Stephen Oppenheimer too holds this view privately as communicated to me in a meeting held at Lalit Hotel in Delhi.

Several researchers pointed out on the basis of the further analysis that this male lineage of DNA known as R1a1 had not arrived from outside but was indigenous of India (Sahoo 2006; Sengupta 2006; Sharma 2009). These researches also noted the formidable presence of this DNA (R1a1) in the Dravidian speaking South Indians as well as the Austro-Asiatic speaking tribal groups.

Underhill (2010) further examined this DNA and found that the oldest haplotypes of the DNA was present in India and it expanded from India (Indus Valley region) to Central Asia and then to Europe as well as Mongolia (Underhill 2010:Fig.1). He was able to identify two branches within this lineage with the help of two markers. One branch identified by the marker M434 was distributed in West Asia and it also migrated into Arabia. The other branch was identified by the marker M458 and it was restricted to Europe with a particularly high concentration in East Europe like Ukraine. However not a single person belonging to this branch could be found in India or Iran. Thus Underhill ruled out any migration from Ukraine or from the adjoining steppe to India or to any other part of Asia. **“Importantly, the virtual absence of M458 chromosomes outside Europe speaks against substantial patrilineal gene flow from East Europe to Asia, including to India, at least since the mid-Holocene.”** (Underhill 2010:Abstract)

Pamjav (2012) was able to find finer details about the branches of the R1a1 lineage. He noted that the M458, earlier identified by Underhill, and another branch Z280 were found in Europe, whereas the branch Z93 had split from the main trunk in India. Thus it became clear that the main trunk M198, gave birth to branch Z93 in India from where it spread to Uzbekistan and Mongolia, as well as to Southeast Asia (Pamjav 2012:2). Some members of this Indian branch Z93 also reached up to Hungary independently of any Roma migration (*ibid*: 3). This means Indians certainly migrated to Mongolia, Central Asia and Hungary after the birth of this branch. And of course they could have migrated before the birth of this lineage in the earlier eras.

The European branches of R1a1 namely M458 and Z280 originated while the main trunk was passing through the Caucasus region and the steppe (Pamjav 2012:Abstract). Then the whole group of people moved forward into Europe through the North Black Sea region. Hence we get M458 and also Z280 in the steppe, East Europe and Central Europe but not in India or Iran. “Inner and Central Asia seem to be the overlap zones for the R1a1-Z280 and R1a1-Z93 chromosomes as both forms were observed at low frequencies.” (*ibid*:3)

This is because the Indian branch Z93 also migrated into Central Asia along with its parent main trunk M198. But the European branches found in Central Asia and the steppe never came to India. It is big evidence which clarifies the direction of human movement. Hence the Indian branch can be found today in Mongolia, Central Asia and even in Hungary today. But the European branches (M458 and Z280) cannot be found in India. This finding irrefutably fixes the direction of migration as to be from India to Europe, and leaves no room to any further argument in the matter.

Underhill (2015) further worked on this lineage and found that the R1a1 has several branches which can be grouped into two. One set of branches are found in India and Central Asia, where as the other set of branches are found in Europe. Of the European samples of R1a, 96% belonged to Z282, and 98.4% of Indian and Central Asian lineages belonged to the lineage Z93. Underhill (2015) found that one branch M558 originated in Volga-Ural area and migrated with the group further west into East Europe. The branch M458 broke off after that. Only after these, the branches M282 and M284 originated.

The Indian branch Z93 is quite common today in South Siberia, Altai region of Russia, Kyrgyzstan and Iran. The further branches of Z93 lineage are 1. Z2124 found in Pashtun Afghanistan, Caucasus and Iran; 2. M750 in India, Pakistan, Afghanistan and Himalayas; 3. M560 in Burushaski, Hazara, and Iranian Azeri (Underhill 2015:11).

Underhill in his latest work proposed the place of origin of R1a in Iran (2015:11-12). However it is only conjectural in nature and cannot be accepted on several accounts. This conclusion does not take into the account of the R1a lineages present in the Indian tribes and Dravidian speakers. They were not included by Underhill (2015) in his consideration. The study also did not include the study of R1a present in several eastern regions of India like Bihar, UP, as well as R1a present in Myanmar, Thailand, and Indonesia etc. The Y-DNAs R1 (M173) and R* (M207) are found in large numbers in Bali (Indonesia) today, and they have migrated there from India (Karafet 2005:Table 1). In fact at least 12% of Balinese male lineages were found to be of Indian origins in this study. These R1 DNAs are ancestral to R1a1. Kusuma (2015) found that R1a lineage has reached Madagascar (Malagasy) also when people of Indonesia migrated to this island. Such findings only prove that R1a1 originated in India and not in Iran.

More truth is revealed by the recovery of the R1a1 samples from the archaeological samples of human remains. One R1a1a has been found from 5100 BC Spain at Els Trocs site (Haak 2015). This

is a descendant of R1a1a. This could have migrated there with the goat-pastoralist migration which took place from India to Southwest Europe through Ganj Dareh (Iran) about that time (*vide infra*). One R1a1 has been found from Oleni Ostrov (Northwest Russia) dated 6,400 BC (Mesolithic Culture; Haak 2015). Before these there was no R1a1 lineage in Europe. Apart from these two examples, the R1a1 did not migrate to Europe in large numbers during the Neolithic period. Its general migration from India and Iran to Central Asia and Europe took place mainly during the Copper, Bronze and the Iron Ages, which was also the time of rise and fall of the Indus Valley Civilization. This shows that this lineage got established in the Indus Valley just before its rise in about fifth millennium BC.

The Tarim Basin mummies recovered from Xinjiang in Central Asia had all males in the R1a1 (M198A) lineage (Li 2010), which is Indian. The date was late Bronze Age to Iron Age. Since the lineage was not present in Europe in such large frequency before this time, its arrival could have been only from India or Iran. The high frequency may be because of the founder effect. Other evidence also shows migration during that period from India/ Iran. Li (2015) further clarified that the Tarim Basin mummies carried Indian maternal DNAs in good frequency.

2.3 The Indian Y DNA L

The Indian male lineage Y-DNA L, which is younger in age than the R1a1 lineage, seems to have established in the Indus Valley just after the peak of R1a1a lineage (Sengupta 2006). From Indus Valley it migrated to Turkey through Iran, to Hindu Kush, Kashmir and Pamir and from there to Central Asia along the Oxus River (see Fig. below). It also migrated to UP, Central India and Nepal, and also to South India. Its branch L1a has been recently recovered from four skeletons from Armenian site (Bird's Eye Cave) dating 4100 BC to 3700 BC (Lazaridis 2016). This migration could have been the one migration from India to Ararat province of Armenia as has been mentioned in the *Baudhayana Shrauta Sutra* (Priyadarshi 2014:119; Kazanas 2012:224; Lal 2007). This text belongs to the *Yajurveda* group of texts which has been dated 5500 to 2500 BC by Priyadarshi (2014), and also mentions migrations from India to Iran and Afghanistan at that time. It is possibly the time when Chalcolithic Indians migrated to Armenia and then further north in the Caucasus to establish the archaeological Maikop Culture in the north Caucasus which has many of the features of India and Indo-European civilization.

Fig. The male lineage Y-DNA haplogroup L distribution. The dark point marked +25 is the location of the Jammu and Kashmir Neolithic (3000-1000 BC), where many people from the Indus Valley must have migrated following the arrival of the drier period.

2.4. Other Indian Y DNAs

The Y-DNA Q1a3 has been found in the several ancient human remains recovered from the Lake Baikal region (Russian Siberia) dating between 5500 BC and 1700 BC (Moussa 2016). This DNA

originated in India (Sharma 2007), and its presence in Lake Baikal region indicates human migration from India to Siberia during the Neolithic and Bronze Ages.

Another Indian Y-DNA is F* and its early branches which are frequently found in the Neolithic Europe as well as are present in modern Europe (Sengupta 2006:211; Haak 2015; Szecsenyi-Nagy 2015). The presence of the Indian Y-DNA F*, Q*, R2 and their branches in the Neolithic and extant populations of steppe (Malyarchuk 2011) and Europe is another evidence of Indian migration to the steppe and Europe.

2.4. Indian mtDNA M in Europe

India-specific mitochondrial DNA M5 is widely distributed in Europe, particularly in Romania, Hungary, Slavonia, Poland, Ukraine and Russia, often reaching 3% to 5% of the populations. It is also well distributed in Iran and Iraq. The workers have generally ignored this finding, and considered it a result of later migrations during historical periods. Palanichamy (2014) noted that the general mtDNA pool of Mesopotamia is composed of DNAs of South Indian and northwest Indian origin (Palanichamy 2014:Abstract). The fact was substantiated by finding of Indian mtDNA from ancient Mesopotamian human specimen (Witas 2013; Palanichamy 2014). They found Indian mtDNAs M4b1, M49, M65 and M61 in ancient Mesopotamian samples. There are many more Indian mtDNAs present in extant European as well as the ancient European, Central Asian and Middle Eastern samples, however listing them all here is beyond the scope of this work.

3. Environment, Ecology and Farming

- The Likely Places and Times of the Origins of Farming and pastoralism in this part of Eurasian Archaeology

Before 10,000 BC too farming and pastoralism had been experimented at several places in the world at the warmer wetter epochs of climates for the respective region. However, they either ended up as failed experiments or had to eclipse during the subsequent episodes of dry cold spells of glaciations, and the people in general had to return back to the hunter-gatherer mode of subsistence. Yet it is very much plausible that at the warmer latitudes of the world, the earlier evolved, i.e. the Pre-Holocene practices of experiments of animal-herding/ domestication might have survived and continued into the Holocene era.

The putative locations for such continuity of culture to have taken place through the late glacial into the Holocene include Tropical Africa, Tropical India and South-East Asian landmass (which was a single piece of land then due to low sea-level of the times). In fact such continuities in pastoral practices dating back to the Last Glacial Period have been noticed in Central India (G.R. Sharma 1980) and in Afghanistan at Aq Kupruk Neolithic (Perkins 1972; Allchin and Allchin 1982:97; Meadow 1989:25-26, Table 2; Possehl 2002:24). Rissman noted that India had for the ages in her past, all the wild species of animals and plants required for domestication and the development of farming like cattle, buffalo, elephant, horse, camel, sheep, goat, pig, dog and fowl. He strongly and convincingly argues on archaeological and biological grounds that these were domesticated locally in India during the Indian Mesolithic and Neolithic (1989:15).

This assumption that the Indian Neolithic farming culture had evolved locally from the Late Ice Age Mesolithic and associated earlier domestication experiments is supported by many facts and by many arguments. Bellwood and Oxenham find that the population where the Neolithic evolves *in situ* (i.e. develops locally) take much longer time to grow and to saturate the carrying capacity of the area, whereas the areas where the Neolithic culture arrives in a package as an import from outside show very rapid population expansion (2008).

This is clearly visible at Mehrgarh where we get the sequentially evolving skeletons of domesticates over time, from the wild to the fully domesticated forms, over a period of more than one millennium (Meadow 1981, 1984, 1989, 1993a, 1993b, 1998; Fuller 2006:26; Priyadarshi 2014:339-41). On the other hand such sequences of evolving skeletons towards domestication are absent from the sheep and goat remains recovered from the early Neolithic of the Levant, Anatolia and Zagros (Zeder 2005:126). Clearly this is a sign of import of the Neolithic culture to West Asia from somewhere else at about 7700 BC to 7400 BC (uncalibrated dates 8600 BP and 8300 BP respectively).

Kivisild (2005) found the theory of the West Asian evolution of farming culture unacceptable because farming suddenly appears there in West Asia as a complete “readymade package of culture” as if delivered from somewhere else. He considers India as the most likely source of such package (2005:S18). James and Petraglia too argue by the analysis of the archaeological evidence from India that the source of the West Asian Neolithic cultures was India (James and Petraglia 2005:S46).

Dennel (2005) too supports Petraglia's arguments. Thus there is a body of evidence strongly suggesting the evolution of the West Asian Neolithic by import from India.

Bar-Yosef (2007) rejects the possibility of the West Asian origin of the farming culture. He attributes the new successful technologies observed in the Eurasian Upper Palaeolithic to the "social processes and the economic innovations" by the Middle Palaeolithic of "some particular region" from where it spread as a package to West Asia and to the rest of the world (2007:3-18). Although he is unable to suggest India as the likely source of such innovations, and guesses Africa as such likely source, we can safely infer now, in light of the newer findings from the archaeology of India and the views of the other authors expressed above, that such Neolithic arrivals to the Fertile Crescent had taken place from India at that time of the Holocene (Priyadarshi 2011:30, 2014:339-41). However it was not like a just one wave-front, but was like a continuous process of trickling of arrivals of people and cultural innovations up to the Iron Age.

- Ecological Considerations

When we talk of evolution of farming, we generally mean the development of farming as a continuous process following the end of the Late Glacial peak at about 9,500 B.C. or say roughly 10,000 B.C. Hawks noted that it is at this time that the rate of the human population growth became fastest—at the end of the last glacial period and the following warmer post-glacial period (Hawks 2007). The rapid population growth forced man to adopt farming and other related technology.

The transformation from hunter-gatherer mode of subsistence to farming was the result of the specific climatic changes necessitating the changes in the mode of subsistence for man. The alterations in the available niche in different micro-ecosystems forced man to change food habits, and to invent and/or adopt new technologies. The complete picture of the climatic change *vis-à-vis* biotic changes (plants and animal species living in the area) taking place in the ecosystem is important for the proper understanding of the transformation from hunter-gatherer to farmer lifestyle.

The herbivores (like deer, cattle, horse, sheep, goat, elephant, rhinoceros, vegetarian humans; also called primary consumers) in any ecosystem have always almost ten times larger population (actually bio-mass) than the hunter (lion, tiger, wolf, hunter humans; secondary consumers). Hence as soon as a human population changes from hunter to farmer there is a population explosion as the population carrying capacity of the same location rises enormously owing to the change in the consumer status of man from secondary to primary level (Pimentel and Pimentel 2003; Priyadarshi 2011:137-143). A ten times population growth is expected even without farming if man leaves hunter's meat diet and adopts vegetarian diet in any given place. Farming, by providing a greater yield from the same land, produces a much larger population growth.

This population rise from farming provides the essential input or ingredient for migration which is the large population in the tropical ecosystems. The large population leads to stress and disorder which causes human migration out. The larger is the number of microstates (or, humans in our case) in any macrostate (given geographical ecosystem), the greater is the entropy or disorder—a conclusion which comes from the Laws of Thermodynamics applied to population ecology (Schneider and Kay 1992; also see Georgescu-Roegen 1971). And migration becomes a compulsion because of the intra-specific competition and stress, as per the laws of thermodynamics applied to ecology (see Priyadarshi 2011:139).

- Our study shows that the Tamil Nadu had a good climate between 9,000 BC and 5500 BC which was better than Northwest India (*vide infra*), and therefore there must have been a population growth in South India. This population expansion must have led to a population migration to the north India between 6000 and 5000 BC. This is perhaps the reason how we get islands of the Dravidian languages in the north India like Brahui (Balochistan of Pakistan), Kurukh languages viz. Oraon and Kisan (Orissa, Chhattisgarh, Jharkhand Bengal and Bangladesh), Dhangar language in Nepal and Bhutan, Mal Paharia (Malto) language in West Bengal and North Bangladesh-Assam region, Gondi (Maharashtra, Madhya Pradesh, Chhattisgarh, Orissa), Khond (Orissa and Andhra Pradesh) and Kui, Kuvi, Pengo and Manda (Orissa).

Possibly these people of the Dravidian speaking South arrived in the north India to settle amongst the Neolithic farmers of the north, which were particularly concentrated in Assam, Bengal, Uttar Pradesh, Jharkhand and Central India. The Dravidian linguistic migration seems to be more prominent along the east coast of India reaching up to Bengal, Nepal and Bhutan. This too correlates well with the fact that between 9000 BC and 5500 BC, the Bay of Bengal monsoon was much stronger than the extremely weak western coastal Arabian Sea monsoon (*vide infra*). The northern (winter) monsoon supplying Nepal, Assam and Bhutan too had been strong. Hence there is a migration of the Dravidian speakers from Bengal into Bhutan, Assam and Nepal. This is the most parsimonious explanation for the presence of the Dravidian languages in the far north and northeast of the sub-continent.

The mtDNA of the southern Indian locations have ultimately spread all over India and have even migrated to Europe during the Iron Age. One such example is the mtDNA hg M5* and M5a, found in the Dravidian speaking tribes of Andhra Pradesh and Karnataka the Koya and Chenchu (Sun 2006: Table 2; Kivisild 2003). This mtDNA most probably originated in South India (Sun 2006; Kivisild 2003; Edwin 2002). This is today found in Brahui (Pakistan; Hartmann 2, number 28), Nepal (Fornarino 2009), Iran (Metspalu 2004; Derenko 2013), Russia (Malyarchuk 2002, 2006, 2008), China (Xinjiang-Kazakhstan; Kong 2010:516), Romania, Slovaks and other Slavs and Polish (Malyarchuk 2008) populations outside India.

This DNA can be found today in the people of Iran, Romania and the Slavs of East Europe as well as in the Roma (Gypsy) populations of Europe (M5a in study by Malyarchuk 2008). The mtDNA M35 of the same tribes too are widespread in the Indo-European speaking East Europe (Malyarchuk 2008). Clearly many of the South Indians, who migrated to north and further out of India during later periods, had already undergone language change into Indo-European speakers.

The migration of the mtDNA M5 took place to Central Asia during the Bronze Age along with the Indo-European migration. This is evidenced from the fact that the ancient mtDNA M5 has been recovered from the Bronze Age remains of humans from the Xiaohe Cemetery in the Tarim Basin of the Xinjiang province of Chinese Central Asia dating 2000 to 1500 BC (Li 2015). Other lineages recovered from the Tarim Basin include U7 and U5 mtDNAs (Li 2015: Abstract), which have now been confirmed to be of Indian origin because of their absence of the European samples dating before 6000 BC.

In Southern Europe the frequency of the LP Gene frequency is less (Romero 2011). This gene which is present today in North and Central Europe up to 70 to 90% frequency was found absent from the pre-Neolithic and the Neolithic farmers of Europe (Kruttli 2014:Abstract; Gamba 2014; Burger 2007). In fact more recently Allentoft (2015) found that the LP Gene was not present in Europe even during the Bronze Age (3000-1000 BC). In fact it reached its present frequency at about 1200 AD (Kruttli 2014). Clearly the gene migrated later to Europe, and had Natural Selection applied to it. This LP Gene originated in India (possibly South India) as a random mutation, without any biological advantage to the individual inheriting it in the very beginning.

4. Evidence Supporting India as Source of West Asian Farming

- Zagros (West Iran) from where the West Asian Farming evolved

Zeder found in her archaeological study in Syria, that the gazelle hunting was the predominant mode of subsistence for thousands of years before 7308 BC (8300 BP uncalibrated). However the first goat appears there at Abu Hureyra in 7730 BC (8600 BP uncalibrated) which had much resemblance with Dareh Ganj (Zagros, Iran) culling practices. It can be inferred that it had arrived

in Syria from Dareh Ganj (Iran). Within the next 400 years, goat became the main food of the archaeological site at Abu Hureyra (Syria) completely replacing the gazelle hunting:

“However, it is also possible that the abrupt increase of goats in the Southern Levant at about 8600 BP uncalibrated marks the introduction of managed but morphologically unchanged goats from somewhere else. The first appearance of goats in the assemblage from Abu Hureyra in the northern Levant (most securely dated to about 8600 BP uncalibrated) is accompanied by demographic data that suggest a similar culling strategy to that detected at Ganj Dareh (Legge 1996, Legge and Rowley-Conwy 2000). Goats dominate in the assemblage from the site after about 8300 BP uncalibrated, reversing a many millennia emphasis on hunted gazelle.” (Zeder 2005:142)

Thus the West Asian (Levant and Anatolia) pastoral culture was not local innovation, but had arrived there from West Iran. This leads us to the next question whether the West Iranians and the West Asian (Levant and Anatolia) people were the same people, or the people of West Iran had arrived from somewhere else.

A new technique, the ancient DNA (aDNA) technique is throwing much direct light on the matter. Recently the full genome of a human skeleton (female) from 7900 BC from Ganj Dareh was successfully recovered. Its study examined this DNA and found that these people who were the architects of the Zagros Neolithic were not from Anatolia nor the Levant, or from Europe, steppe or the Caucasus, but were from a southern and eastern location (Gallego-Llorente 2016:Abstract). This cultural package brought to Zagros was later adopted by the Anatolians and the people of the Levant (Israel, Lebanon, Jordan, Syria), who brought the culture to the further west into Southeast Europe and Romania.

On the basis of the DNA recovered it was concluded that the people of Zagros (West Iran) were not the same as the people of West Asia (**Gallego-Llorente 2016**). In fact, the farmers of Levant, those of Anatolia and those of Iran were three distinct genetic populations (Lazaridis 2016). Gallego-Llorente and the team of scholars concluded in the Abstract of their aDNA-based article that the people **“of the Central Zagros were somewhat isolated from other populations of the Fertile Crescent. Runs of homozygosity are of a similar length to those from Neolithic farmers, and shorter than those of Caucasus and Western Hunter-Gatherers, suggesting that the inhabitants of Ganj Dareh did not undergo the large population bottleneck suffered by their northern neighbours. While some degree of cultural diffusion between Anatolia, Western Iran and other neighbouring regions is possible, the genetic dissimilarity between early Anatolian farmers and the inhabitants of Ganj Dareh supports a model in which Neolithic societies in these areas were distinct.”** These authors also suggested that the population had arrived to Zagros from somewhere further south and east: **“It is possible that the ancestors of the Anatolian and Ganj Dareh farmers spent the LGM in areas further south or east”** (Gallego-Llorente 2016:4).

The agricultural package of the Ganj Dareh site too matched the northwest Indian agricultural package found at the Mehrgarh. “The site has been directly dated to 9650–9950 cal BP7, and shows intense occupation over two to three centuries. The economy of the population was that of pastoralists with an emphasis on goat herding. Archaeobotanical evidence is limited but the evidence present is for **two-row barley with no evidence for wheat, rye or other domesticates**.” (Gallego-Llorente 2016:2) This finding too is consistent with the transfer from the Mehrgarh agricultural package (Jarrige 2008).

We have already seen that archaeologies of Afghanistan and Central India exhibit the oldest evidence of goat-domestication in the world, and that too since before the Holocene period (vide supra). The wild presence of the goat in Afghanistan and Pakistan adds substance to Priyadarshi’s claim that the goat was first domesticated in northwest India and Afghanistan (Priyadarshi 2014:342-346; Sultana 2003:420-421). Priyadarshi (2014) found on the basis of the information from the genetic studies that the goat was domesticated for the first time in India-Pakistan. In another study, Priyadarshi found on the basis of available DNA research that the sheep too had been domesticated for the first time in India-Pakistan (Priyadarshi 2013:206-211).

- From where the Zagros Neolithic people came? Ancient Zagros DNA X2.

It became clear from the ancient DNA that the West Asian farmers of Levant (Syria etc) were not the same people genetically who were doing farming and goat domestication at the Zagros site (Gallego-Llorente 2016; Lazaridis 2016). Gallego-Llorente tried to find the source of the Zagros farmers in light of the fact that the Zagros region had become uninhabitable during the late glacial peak, and its farmers must have come from somewhere outside.

The ancient DNA recovered from the single female skeleton (named GD13a) from Neolithic Ganj Dareh (Zagros, west Iran) belongs to the mtDNA haplogroup X2 which is a sister of X1; and both X1 and X2 descended from X haplogroup. Today, the X2, along with X1 is well distributed in Europe, and had been till late considered European or Western Eurasian mtDNA, although wrongly. Many geneticists had claimed that the haplogroup X had originated in Europe about 20,000 years back (Kivisild *et al* 1999; Quintana-Murci *et al* 2004; Reidla *et al* 2003; Shlush *et al* 2008; Richards *et al* 2000). These claims had been made on the basis of the presence of this DNA in the modern European population. However the recent studies of the ancient DNAs from Europe revealed that this DNA was not present in Europe before 6000 BC.

Les Groube on the basis of his ecological study declared that any migration would not have been possible from the Fertile Crescent to South or East, because these areas would have been already filled with expanding humans (1996:105). Hence on purely ecological grounds also we know that the people of the Fertile Crescent could move only into Europe or to the steppe.

In South Europe, which was warmer, the earliest sample of X mtDNA has been found from northern Greece at Revenia dating about 6300 BC (Hofmanova 2016). It belonged to the X2b branch. Just at this time we get another sample of mtDNA X of X2m branch from Barcin in West Anatolia (Turkey). Hence we can say that the farmers of the Zagros were gradually moving west through Turkey into Southern Europe via Greece at about 6300 BC.

The mtDNA X (which has two branches X1 and X2) reached Central Europe as a part of the “Neolithic DNA package”, and its earliest presence in Central Europe occurs in the LBK (Linear-Pottery Culture), only about 5600 BC (Brandt 2013:260). This culture most probably arrived to Central Europe from the north Black Sea locations.

However from the south, the Starcevo Cultural grows from the Balkans and expands to Central Europe about the same time. From Starcevo cultural sites in Hungary several people with mtDNA X (belonging to X2 lineage) have been found dating 5615 BC (mean of the radiocarbon date range 5660-5570 BC; Szecsenyi-Nagy 2015).

[Figure showing migration of farming and people from Southeast Europe after having arrived there from Asia through Anatolia. Courtesy: Szecsenyi-Nagy 2015]

Clearly, we can say from the available evidence that the people (and their DNA lineages like X2) were reaching Europe from the Zagros by two routes—one through Anatolia, Bosphorus and Romania and the Balkans, and the other through Caucasus, north Black Sea steppe and then to Central Europe, effectively changing the DNA-landscape of the regions they were sweeping. The migration into Europe from north Black Sea, South Siberia and Central Asia has been attested in the ancient DNA studies by Haak (2015).

- Modern Distribution of X2 and the likely place of origin of X2 lineage

The mtDNA X2 which migrated into Europe with the Neolithic (vide supra) is present in European population till date. However it has been replaced in West Asia by arrival of newer people over time with different DNAs. Hence, the X2 mtDNA is not now that common in the Levant in the general Arab Muslim population. However, it is found in good percentage in the relict minority population Druze living in Israel, Jordan, Lebanon and Syria. The Druze, particularly the ones living in the secluded Galilee area of Israel have maintained an isolated existence, and thus have been able to retain the old genetic material (Shlush 2008). It is to be noted that this community follows a unique system of religious belief which resembles the Hindu beliefs in many ways. These people believe in the series of rebirths ultimately leading the soul to merge in the cosmic reality (Khuri 2004; Dwairy

2006). It is possible that the Druze are the relic descendants of the goat-keeping farmers who reached the Levant from the Zagros bringing the Neolithic practices.

In South Asia, which we consider to be the likely source of the Zagros farmers (*vide supra*), the mtDNA X2 is found today in the Hazara, Baloch and Makarani relict tribes of Pakistan and Afghanistan. Hazara is a relict tribe of Afghanistan. A recent DNA study has shown that the Tajik and the Pashtun speaking people of Afghanistan arrived somewhat later to Afghanistan from India during the early Holocene (Haber 2012:3), and that the Hazara had been in Afghanistan from much older days. This finding contradicts the common folk notion that the Hazaras arrived there with Genghiz Khan's army from Mongolia.

The Hazara which constitute about 20 per cent population of Afghanistan today and speak Dari (an Indo-Iranian) language are in fact the oldest inhabitants of the Afghan country since the late glacial period. Majority of the Pashtun-speaking males of Afghanistan (51%) have the R1a1a-M17 Y-chromosomal DNA from South Asia. However the frequency of R1a1a-M17 is only 6.6% among the Hazara males. It has been shown recently by Poznic (2016) that the population of the arriving people with technological advantage expands much faster, and that it greatly decimates or replaces the population percentage, particularly of the males, of the original people of the locality (Poznic 2016:6) :

“Using either mutation rate estimate, the lineage expansions seem to have followed innovations that may have elicited increased variance in male reproductive success, innovations such as metallurgy, wheeled transport, or social stratification and organized warfare. In each case, privileged male lineages could undergo preferential amplification for generations. We find that rapid expansions are not confined to extraordinary circumstances and that the Y chromosome resulting from these rapid expansions can predominate on a continental scale and do so in some of the populations most studied by medical geneticists. Inferences incorporating demography may benefit from taking these male–female differences into account.”

This has been the case of the Hazaras vis-à-vis the Pashtun speaking Afghanistani people. The R1a1a-M17, which constitutes the 51% of Pashtun male lineages, was found to have originated in India, expanded in Gujarat and the Indus Valley and then migrated through Afghanistan to Central Asia, Steppe and thence to North Europe (Underhill 2010; Sahoo 2006; Sengupta 2006; Sharma 2009; *vide supra*). It gave three important branches en route to Europe. Out of these the one R1a-Z93 expanded in the Indus Valley during the late Bronze Age (Poznic 2016:5). It reached the steppe and then to Europe mainly during the Bronze Age. It has been recovered in large numbers from the Late Bronze Age and Iron Age human remains from Central Asia (Tarim Basin) and Europe, but with a much smaller frequencies before that time.

Some authors continued to express doubt over the Indian origin of the R1a1a. However, this particular branch R1a-Z93 which expanded in the Indus Valley is also found in the Malaysian

Indians (of Dravidian speaking South Indian ethnicity), as well as the Roma (Gypsy) from Hungary, but not in the other Hungarian population (Pamjav 2012). On this basis Pamjav concluded that this lineage is of Indian origin. This body of genetic evidence only proves that the Pashtun of Afghanistan reached their modern homes from Indus Valley/ North India and largely reduced the percentage of the native Hazara who had been the original people of Afghanistan and who had earlier migrated with the early farming and goat-herding to Zagros at the advent of the Holocene.

One particular branch X2d of the X2 lineage is found in the Roma-Gypsy population of Europe and in none else (Martinez-Cruz 2015). Its other early branch X2a is found in the American tribes only, who possibly migrated to North America crossing the Bering Strait Land-bridge after expanding through Central Asia, Altai and Siberia just before the end of the last glacial period (Fagundes 2008; Reidla 2003).

“Principal Component Analysis” is a technique applied to the statistics generated from the study of the genome or the complete DNA. This was done for this Ganj Dareh DNA too. It was found that the genome recovered from the Ganj Dareh lady was related largely to the Balochi, Makrani and Brahui populations of modern Pakistan (Gallego-Llorente 2016). This fact again supports the Indian origin of the Zagros farmers.

- Domestication of animals: DNA findings

There is another method of knowing about the evolution of the farming and domestication processes. This is DNA study of the domesticated animals and plants vis-à-vis their wild relatives present today. As a general rule, the genetic diversity is highest at the original place of domestication, because many lineages have survived there. But at a place where the domesticated animal has been brought later on, the genetic diversity is less, because only selected individuals of the breed can be transported, not all members. Zeder noted that the genetic diversity of the Indian goats and sheep is much higher than that of the Middle Eastern goat and sheep populations (2005).

Zeder (2005) puts it in the following words: “The geographic location of origin can be inferred from the geographic distribution of certain alleles or lineages as follows. In all livestock species, including goats, cattle, buffalo, pigs and sheep, a divergent DNA lineage occurs *only* in Southern and Eastern Asia. This suggests a possible centre of animal domestication in Southern or Eastern Asia” (p. 300). This fact suggests India (and also China) as the most likely place for domestication of most of these animals.

Mitochondrial DNA variation is an index of the age of a lineage in any area. Zeder wrote “In goats, however, mtDNA variation is not higher in the Fertile Crescent region compared to most other continental region” (2005:300). That means in simple words that the Fertile Crescent was not an

early centre of goat (and by implication) domestication”, something which the other scholars have dared not pronounce so far.

5. Climate Change and its impact on Civilization

- It is only lately that the Holocene climate change has been understood accurately.

Priyadarshi (2014) gave the detailed sequence of climate change in India and Central Asia during the Holocene. His details match with the general trends of climate change described by Berzenkova (2015) for the Baltic region. Borzenkova found, “The Holocene climate history showed three stages of natural climate oscillations in the Baltic Sea region: short-term cold episodes related to deglaciation during a stable positive temperature trend (11,000–8000 cal year BP); a warm and stable climate with air temperature 1.0–3.5 °C above modern levels (8000–4500 cal year BP), a decreasing temperature trend; and increased climatic instability (last 5000–4500 years).” (Abstract).

Priyadarshi’s study divides the Indian Holocene in three periods, 8000-6000 BC dry a bit cold Indus-Sarasvati region, 6000-5500 BC transition period, 5500-3500 BC wet warm period, 3500-1000 BC dryness increases, becomes very bad after 1900 BC (Priyadarshi 2014, 2015). The same periods behave differently in three different monsoonal regions of India. Thus when Indus is dry, Mehrgarh, Afghanistan and Kashmir are having a wet period. This is because of three different sources of monsoon for different parts of India.

- Indian Climate: The Three Monsoonal Systems

The Indian Territory receives monsoonal rains or precipitation from three different monsoonal systems. First is the northern ‘Winter Monsoon’ which comes from Siberia and Arctic and supplies the much needed snow to the Himalayan glaciers. It also provides the rains in the winter months to Afghanistan, Punjab, Himachal, Uttarakhand, Nepal, North Bihar, North UP, Arunachal and Assam. This monsoon provides rains/ snowfall to Caucasus, Turkey, Kurdistan, North Iran, Central Asia, Tibet etc.

The second monsoon system comes from the Bay of Bengal and supplies rains to most of the Peninsular India (particularly Andhra Pradesh, Karnataka and Tamil Nadu), Bengal, Meghalaya, Bihar, U.P. and much of Central India. When strong, it provides rains up to East Haryana, East Rajasthan, and West UP.

The third monsoonal system in India is the Arabian Sea monsoon which supplies the western coastal peninsular India, Gujarat, Sind, Pakistan, Iran, Arabia and East Africa. When strong it reaches Afghanistan and southern Central Asia also.

The relative strengths of the three have varied during the Holocene. In general, when the Bay of Bengal Monsoon is strong, the winter monsoon is strong too, but the Arabian Sea monsoon is weak. However when the Arabian Sea monsoon became strong, the winter monsoon became weaker and the Bay of Bengal monsoon became very weak causing decline of the farming cultures over East and South India.

- Early Holocene Climate 8000-6250 BC

The Tardiglacial (the last 1000 years of the last glacial) was the cold dry period when no farming was possible. Hunting-gathering and to some extent animal husbandry were the only means of subsistence. Northwest India was a cold desert then. The waters were all trapped in the glaciers, and the rivers of the region had scanty waters flowing in them. This, the Late Glacial phase of the Late Pleistocene, ended about 11,500 years BP or roughly about 9,500 BC, after which the period till date is known as the Holocene (Mayewski 2004).

Earlier there was no scientific data or accurate information about the Holocene climate changes. Hence different authors wrote differently on the basis of their assumptions. Thus Misra wrote: "The end of the Pleistocene Ice Age, around 10,000 years ago, saw a sharp increase in rainfall, which stimulated the growth of both plant and animal life and consequently of human population." (V.N. Misra 2001:525,498). A.K. Gupta also wrote the same (2004:56). However these inferences were not correct. Several geologists were able to show that the rainfall had actually decreased in the western coastal regions during the Early Holocene (Sarkar 2000; Thamban 2001; Staubwasser and Weiss 2006).

The reconstructions of the ancient climates have been done mainly in Europe and North America. Climates behaved varying in different regions of Europe (Davis 2003; Mayewski 2004; Magny 2013:2044). Results become different even by the change of method. Out of the several methods used, the one applying the study of the fossil pollens seem to be the most accurate, because it monitors the end result of the climates *i.e.* the plant life of the region for a particular time.

- Study of Indian Pollen Data for climatic reconstruction

The pioneer work on Holocene climate change in India was done by Gurdeep Singh which postulated a wet period between 8000 BC and 7500 BC and also 3000 BC and 1800 BC (1971, 1974). However this finding was not correct. He had studied pollens from Sambar, Didwana,

Lunkaransar and Pushkar lakes. The results he obtained have not been supported by later works like that of Enzel (1999) done on the fossil pollens recovered from Lunkaransar Lake (Shinde 2001, 2008:78, 2006:66-7).

In fact the different lakes had different micro-climates at any time in the past, because they were having different combinations of the three monsoons as the locations differed. While fossil pollens from Lunkaransar (near Bikaner) located in western Rajasthan reflect more the past climate of Indus-Sarasvati, those from Sambar located to the north and east reflect the climate of Uttar Pradesh (which is fed by the Bay of Bengal monsoon) and also the winter monsoon fed regions (like the Himalayan regions).

Gurdeep Singh went wrong because he tried to formulate single unified conclusions on the basis of those lakes which essentially represented different monsoonal zones. Shinde (2001) describes, for the Sambar Lake, a wet phase for the period 3800 BC to 2200 BC, which obviously is not true for the Indus Valley region. This conclusion from the Sambar Lake can be applicable to western Uttar Pradesh and Haryana, and not to Mohenjo-Daro or Harappa.

Shinde (2008:79) notes the unreliability of these earlier works in the following words, “Firstly all the earlier studies were carried out only in the north and western parts of Rajasthan and all the data collected for climate reconstruction was from the dried salt lakes in Rajasthan. Such inadequate data cannot be used for drawing meaningful conclusions. The data from lakes do not reveal general climate of the region but provide only limited information such as climatic history of the lake and its catchment areas.”

- Early Holocene Climate

The later evidence from archaeo-botany, particularly one from palynology, supports a dry cool Early Holocene in the southern part of the Indus Valley region (Priyadarshi 2014) in the Early Holocene. The rainfall increased certainly immediately after the glacial period, yet it did so in the northern and the central regions of Asia where much of the things had been frozen during much part of the year before the Holocene. Mehrgarh was integrated more with Central Asian monsoon. Hence it had a better rainfall during early Holocene.

Although some warm centuries did occur during the first two millennia of the Holocene, on the whole it was a cool period. The climate of the Mediterranean region was cool during 9,700 BC to 5000 BC (Magny 2013:2044). Mayewski (2004:249-250) found that the period between 7000 BC and 6000 BC was quite cool globally and particularly so in the tropics. Bjune (2004:218) found that Dalmatladdo was dry and cool at 7500 BC. Thus Priyadarshi's finding that the 8000 BC-6000 BC period in northwest India was dry and cool is consistent with these reports and can be accepted as the working formula (Priyadarshi 2014, 2015)

The glaciers were melting fast, hence the Himalayan rivers were all flooded and had very fast currents (Giosan 2012). As the consequence the sea level was rising. But these rivers were of no use to agriculture. “Wild, untamed rivers once slashed through the heart of the Indus plains. They were so unpredictable and dangerous that no city could take root on their banks.” (Nuwer 2012). However farming was adopted on those flood-plains away from the river currents and which were known to be safer by the people by general experience (Giosan 2012).

“The presence of Harappan and even earlier settlements within these incised valleys (vide infra) also argues for major incision predating the Harappan. During Harappan times, the alluvial landscape in Punjab offered suitable terrain for floodwater farming within incised valleys and important protection against large floods on interfluvies.” (Giosan 2012:e1689)

Immediately following the end of the Last Glacial period, the winter monsoon which also supplies Central Asia, steppe and Europe became strong. Thus we get evolution of early Neolithic activities in the northern parts of Pakistan (Mehrgarh and further north) as well as in Ladakh, Tibet and Afghanistan between 8000 and 6000 BC (Jarrige 2008; Miehle 2009; Ganjoo and Ota 2012).

The region just to the north of Mehrgarh was wet from the winter monsoon, and that to the south was drier because of the inadequate Arabian Sea monsoon during this period. Thus Mehrgarh depicts flora and fauna of the wet type as well as the dry type, because it was located at the junction of the dry and wet regions of northwest India for that period.

However the presence of the domestic water buffalo and also elephant at Mehrgarh is an indicator of the good rains received from the northern winter monsoons. Mehrgarh is not in the natural habitat range of the wild water buffalo. Hence the presence of this animal at Mehrgarh makes it obvious that the buffaloes had been domesticated somewhere else in east India and then brought to Mehrgarh.

Between 8000 and 6000 BC, the Arabian Sea monsoon was weak. Hence the Indus Valley proper was devoid of much rain and was a mix of desert and grassland, as well as open forests with scanty shrubs and xerophyte trees. Hence we find that the Indus Valley Civilization (Lothal, Mohenjo-Daro and Harappa) did not take off during this period.

The Bay of Bengal Monsoon was strong between 8000 and 6000. Hence the Neolithic activity flourished in Central India including Lahuradewa, Koldihwa, Mahadaha and Mahagara.

During this period, the southern part of the land surrounding Indus and Sarasvati river basins was devoid of much rain, and stayed dependant on the river water system which also supplied the playas

through the underground water streams. The playas (or, *saras* in Sanskrit) were the source of water for the people, animals and plants who inhabited the Indus-Sarasvati region before 6000 BC. The rivers were getting huge amount of waters from melting glaciers. Hence they had torrential flows, which would often cause floods, and would slash the banks and cause avulsions. This was quite unsuitable for any large human settlement coming up over their banks. Thus we can say why Mehrgarh was located not on the bank of any river but quite away from that: “Wild, untamed rivers once slashed through the heart of the Indus plains. They were so unpredictable and dangerous that no city could take root on their banks.” (Giosan’s interview cited by Nuwer 2012).

The human population expansion taking place between 8000 and 6000 BC in the region from Mehrgarh to Afghanistan was eventually forced to migrate to Iran reaching Zagros, and also into Central Asia through the Hindu Kush passes. The northern regions of Iran and Iraq and the Fertile Crescent being supplied by the winter monsoon rains were having good rains between 8000 and 6000 BC as it was a period of strong winter rains. Hence migration out from Mehrgarh and Afghanistan was directed west to these regions. They did not expand towards the south to Sind and Rajasthan, because Sind and Rajasthan were devoid of much rain fall due to weak Arabian Sea monsoon.

- The 8.2 Kilo-year cooling event of 6250 BC—a brief freezing

At 8,200 BP i.e. about 6,250 BC, there was an extra-ordinary dip in temperature, and this event has been named the 8.2 Kilo-year Event (Staubwasser and Weiss 2006:1). Many people died and many habitation sites were abandoned. This climatic event caused severe reduction in the farming communities in West Asia (Weninger 2006).

There was a severe global freeze just like the glacial period lasting for 60 years, and the total length of cooling was spread over about 150 years. This freeze killed most of the people in the temperate regions. The populations of North Europe, Central Asia and the steppe were decimated, and whoever survived in these regions, hunting only was their subsistence.

Tropical regions too were affected and a decline in the number of human habitation is noted in the archaeology of Indus-Sarasvati region and West Asia. But humanity survived adequately in India, parts of Iran, Southern Europe and SE Asia. As soon as the climate improved about 6,000 BC, the population of northwest India quickly picked up, and so did the populations of the different regions of Iran.

The effects of 8.2 Kilo Event on India have not been ascertained so far in the archaeological studies. We can expect breach in the continuity at many sites, and abandonment of many other Neolithic sites in northwest India. In the new radiocarbon dates for Bhirrana given by Dikshit and Mani

(2013:50), the cultural continuity of the period I ends abruptly about 6500 BC. Then we get the onset of the Period II (Transitional Period, 6025-5045 BC). This period is marked by new settlements which correspond to the resettlements taking place following the 8.2 Kilo Cold Event. Clearly there is a break or decline of civilization for about 450 years. Following this cold epoch, when population re-expanded, a better climate ensued in the Indus Valley and Gujarat region as Arabian Sea monsoon started picking up. People migrated to Gujarat and we find new settlements in Gujarat just following 6250 BC event (Dikshit 2013:136). This was again because of the climate change. Most probably people from Central India and South India must have migrated to Gujarat and the Indus Valley region immediately after the improvement of climate.

- The Climate Change after 6000 BC in India and consequent migrations

By 6000 BC, a newer, warmer climate arrived which provided better availability of food in the Indus Sarasvati region in particular and Eurasia in general. Thus the human population expanded again in different parts of Eurasia. By 5500 BC, the western monsoon *i.e.* the Arabian Sea monsoon became very strong, and it remained so for two millennia. It brought rains to western coastal India, Maharashtra, Gujarat, Sind, Rajasthan, Haryana and Punjab. Under better rainfall, the Thar of Rajasthan became a grassland and open forest from its previous desert condition, and its playas started showing lake full stages (Deotare 2004). There is evidence of much nomadic human activity in the Thar at this time.

The Bay of Bengal monsoon or the eastern monsoon became very weak following 5500 BC. This led to a decline in the Neolithic civilizations of Bihar, Uttar Pradesh and Central India. South India being largely supplied by Bay of Bengal monsoon, became dry. The northern winter monsoon too lost some strength leading to some decline in Kashmir, Ladakh and Mehrgarh.

At this time Central Asia and the steppe show increase in the warmth and climatic recovery from the devastating effects of the 8.2 Kilo-Event (Kremenetski 1997:403). The steppe and Central Asia witness population growth. People arrive in Central Asia from many directions including India, Caucasus, Tibet and eastern Siberia. This demography is reflected in the ancient DNAs recovered from Kazakhstan which show significant numbers of India specific DNA types *e.g.* mtDNA M* and M4 (Lalueza-Fox 2004:944, 945; also *vide supra*).

It is likely owing to this sixth millennium BC Neolithic Indo-Kazakh migration, and perhaps also to the Bronze and Iron Age Indo-Kazakh migrations that the Kazakh population till date carries up to 5% Indian specific DNAs (*ibid*:945). The India specific mtDNAs also reached Eastern Europe, where they are found in a frequency up to 3% in Russians, Poles, Slovak and Romanian populations today (Malyarchuk 2002:Table 1 and 2; Malyarchuk 2008:228, 230).

The mtDNA U*, U5 and U5a mtDNAs found from the ancient human remains of Kazakhstan might have too arrived here about this time. This particular mtDNA U5a was earlier assumed to be of European origin, because of its presence in Europe. However it is now found that it entered Europe from Iran during the early Holocene between 8600 BC and 6000 BC. The U5a moved into Egypt and Caucasus also. When the Neolithic related migration moved into Europe after 6000 BC, the U5a again moved in with the marching farmers (*ibid*:944).

Thus we see that after 6000 BC, the re-growing northwest Indian population gave rise to migration from India to Iran and Iraq first, and from Iran and Iraq to Caucasus and Central Asia respectively, and from these latter two into the steppe up to Ukraine. From Ukraine, the further migration went even further west into Europe. This was like a relay-race. Hence most of the people who ultimately reached Europe were not those who had started migration from northwest India. The largest number of those who reached Europe with the Neolithic can be traced to Iran where they had arrived and settled during Early Holocene or in the Late Pleistocene.

- The Reorganization of settlements after 6000 BC in northwest India

Another major geological event took place at about the same time. The Sarasvati River lost two of her strong glacial tributaries. Yamuna turned to East and after joining the Chambal system ultimately joined the Ganga. And the Sutlej left Sarasvati about 6500 BC to join the Indus River. Yet, as the Arabian Sea monsoon became very strong by 5500 BC, the Sarasvati maintained her profile of a large river, although it had become dependent on the monsoons.

When the population regrowth started with improving climate, the settlements started to increase in number. The flow of Sarasvati had lost its slashing power and its banks had become safely habitable by now. A large number of villages and occupations develop on the Sarasvati (Ghaggar-Hakra) River. It may be noted that the monsoon was extremely strong between 5500 and 4500 BC, and it caused almost annual floods due to rains in the lower reaches of the Indus-Sarasvati system. Therefore settlements now developed in the north-east part of this geographical region, and as the monsoon became less powerful after 4000 BC, cities developed to the further south in the Indus Valley proper. After 1900 BC when the Indus-Sarasvati became dry again, the human population moves to east towards UP which had monsoon supply from Bay of Bengal as well as from northern winter monsoon.

[Figure Settlements on morphological units of the western Indo-Gangetic plain (see Fig. 2 for color conventions and legend). (A) Early and Mature Harappan sites, with names of some major urban centers: D ¼ Dholavira; M ¼ Mohenjo-Daro; G ¼ Ganweriwala; H ¼ Harappa; K ¼ Kalibangan; R ¼

Rakhigarhi. (B) Late Harappan (red) and Painted Gray Ware (white) sites. Courtesy Giosan]

- Correlation of Climate and Culture in Holocene India

When the grasslands disappeared and forests covered the northwest India region during the Mid-Holocene's wet-warm period, many grassland-animals of the arid climates which had formed the food of the hunters of the past also disappeared. This was caused by the attendant loss of the habitat for these cursorial (running) grazing animals. Such animals which disappeared after the Early Holocene from northwest India would include antelopes, horse, some other equids, camel, giraffe, bison etc. It has been concluded that the North American horse also became extinct due to growth of forests due to climate change in the early Holocene (Guthrie 2003). By analogy, it can be assumed that the wild horse in general became extinct due to growth of forests in this part of India. Yet there is evidence that the mountain adapted horses survived in the Himalayas and some horse probably managed to survive in the Thar which had become a grassland during the Mid-Holocene period.

At the same time the farming became much easier because of the increased rainfall and warmth. Thus the subsistence shifted from hunting to farming. Besides this, the carnivorous food-chain can support much less number of individuals in any given area. The increasing population (of humans) causing the increased requirement of food forced man to cultivate the plants for food and bring itself down to the herbivore level in the pyramid of food. Owing to more humid climate, rice could now be cultivated in the Ghaggar-Hakra region too, whereas we get rice cultivation only in Central India before this time (Shinde 2008:122). Barley and wheat were too now grown in the Ghaggar-Hakra region (*ibid*).

The pressure from environmental change (extrinsic cause) and the dynamics of human populations, particularly the pressure from population growth (intrinsic cause) are the principal factors why hunters and gatherers turned to agriculture (MacDonald 2003:518). Added to it, the farming made life easy, and thus it became very economical in terms of thermodynamic energy-economics in comparison to the hunter-gatherer way of life (A.K. Gupta 2004:55).

Yet availability of the appropriate natural factors like rain, temperature and the availability of the domesticable animal and plant species must constitute a pre-requisite for any such transformation of humans from hunters to farmers to take place. The herding and domestication could be done only to some selected species of animals and plants and not to all. South Asia was gifted with such species in the wild and when need forced, the South Asians were able to domesticate these animals (sheep, goat, cow, buffalo) and the plants like wheat, rice, barley, pulses and vegetables (Rissman 1989:15).

- Northern Monsoon regions in early Holocene: Plant and Animal Life

The type of climate which we get in between 8000 BC and 6000 BC in NW India could sustain semi-arid ecosystems like savannah, Sahel, grasslands, steppes and semi-desert, having grasses, scrubs and scattered xerophyte trees. However contrasting this picture, humidity and forest-cover were present in the Himalayas during this same period, and to some extent in the adjoining plains too, as the result of the good winter monsoon which came from Central Asia during winter months. One of such moister regions adjoining the Hindu Kush range was Mehrgarh (Costantini 2008), where buffalo too could live during the Early Holocene (J-F Jarrige 2008:143). In fact Mehrgarh was located at the transitional zone between the dry and wet climates. From the wetter northern side they had nilgai (*Boselaphus tragocamelus*), *Cervus* (a large deer species), swamp deer, boar (*Sus scrofa*), elephant and water buffalo (*bubalus arnee*). From the drier plains located to the south they had *Equus hemionus* and blackbuck (*Antelope cervicapra*) for game. From the hills they had wild sheep (*Ovis orientalis*) and wild goats (*Capra aegragrus*) for domestication and game (Jarrige 2008:143; Costantini 2008:168). On the other hand Himachal Pradesh, Jammu and Ladakh within the Himalayas were very humid between 8000 and 6000 BC (Trivedi and Chauhan 2008, 2009; Ganjoo 2004). Humidity in this region during the Early Holocene was in continuity with the humid geography of Central Asia.

The wild animal fauna for the dry-cold ecosystems of western India of Early Holocene would have included lion, wild horse, equids, wild camel, giraffe and ostrich (Mathpal 1984; 1985; Sali 1985, 1989; Wakankar 1985). Sali noted that the ostrich eggshells were present in the Late Upper Palaeolithic but absent from the Mesolithic layer at Patne (Maharashtra, near Goa and Belgaum). At Patne, the 'Late Upper Palaeolithic' means Early Holocene and the Mesolithic period at Patne represents Mid-Holocene of that region of Maharashtra and Karnataka. Thus we can say that the Early Holocene was arid in Maharashtra and the Mid-Holocene was wet forest there.

The animals which cannot survive in dry and cold grasslands and deserts, and live in wet climates include buffalo, tiger, rhinoceros, beaver, crocodile, crow, python etc. Wakankar (1985:176), while working in the Patne region noted that the Mesolithic culture (Mid-Holocene) was represented by fowl (chicken), bison, tiger and rhinoceros in that region (Maharashtra). This means that Maharashtra was wet during mid-Holocene, and this gave rise to the Mesolithic culture at that time. In fact buffalo occurs in the western Indian archaeology in the Mid-Holocene, and not before that.

When the Early Holocene arrived, grasslands appeared in north India. The team of archaeologists studying the Early Holocene period at Lahuradewa concluded, "The area around Lahuradewa was largely a grassland with only a few thickets of trees and shrubs, at least since the beginning of Holocene. The proportion of trees and grasses, however, changed with the increase and decrease in rainfall during the fluctuating climatic conditions, in the times to follow." (Tewari 2008:357).

Saraswat and Srivastava (2000) too found seeds and fruits of several species of grasses at Damdama (Pratapgarh) during the Early Holocene. Thus the north Indian heartland the Uttar Pradesh was a mix of steppe and open forest during the Early Holocene. Similar grasslands with open scattered forest trees must have prevailed in the Central Indian Vindhyan region and further south. Since the rainfall in the Indus –Sarasvati region from the Arabian Sea monsoon was the least at that time, we can guess that this region too was semi-desert and grassland type arid ecosystem.

Adjoining the Indus-Sarasvati region in Rajasthan is the Lake Lunkaransar near Bikaner. Its fossil pollen deposits have been examined. In Lunkaransar, the lake levels were shallow and fluctuating during the Early Holocene. This indicates scanty rainfall which was coming with the winter monsoon. However, the lake level rose abruptly at 6300 C14 BP or 5250 calBC. This we can take as the onset of the strong Arabian Sea monsoon leading to the mid-Holocene wet period for the Indus-Sarasvati region. The lake completely desiccated around 4800 C14 BP or 3570 calBC (Enzel 1999). This point of time must be considered the beginning of the drier climate for the region when the Arabian Sea monsoon became weak as the result of shifting to the Bay of Bengal.

This picture of the climate is consistent with G.R. Sharma's (1980) finding of the horse bones from the end of the early Holocene Central India dated 6570-4530 BC. The same bones were re-examined by D.K. Chakrabarti who gave a date earlier than about 5000 BC (1999). Clearly the grassland was the natural habitat of wild horse, and no one so far has denied the existence of the wild horses in this region during the Early Holocene. It is important to understand that scientifically the *sivalensis* and the *namadicus* described in Indian archaeology were just the local breeds of the same caballus species which existed elsewhere in the world then and today. Another fact not known to many is that the steppe horse Przewalskii belonged to a different species than the domestic caballus horse and had nothing to do with the horse domestication at any stage in history (Ridgeway:1905:425; Jansen 2002; Bowling 2003; Wade 2009; Cai 2009:481; Achilli 2011).

However the Indus-Sarasvati steppe was certainly drier than the Ganga Valley region's steppe during the Early Holocene. This we can say because no *Ficus* species grew in northwest Indian plains before 3000 BC (Thiebault 1988), while *Ficus glomerata* or *gular* (Hindi) grew in Damdama site in Pratapgarh from the Early Holocene days (Saraswat and Srivastava 2000:24). Similarly, the wild rice (*nivara*), which requires more water, grew then at Pratapgarh in the Early Holocene (*ibid*), however it did not grow in northwest India during the same period.

6. Central Asian Climate

- Central Asian Climate Better than India during early Holocene.

In fact the climate of the western Himalayas varied in the same pattern as the Central

Asian climate, both being fed by the winter monsoon. Because the climates of Central Asia and the steppe were much more humid than northwest India during the Early Holocene, it was a better place for living. This caused the northwest Indians to migrate through Central India reaching up to East Europe along the northern Caspian and northern Black Sea regions during Early Holocene. This migration was particularly marked just following the 8.2 Kilo event of 6200 BC. This migration has been detected by the study of ancient human DNAs recovered from Central Asia, the steppe and Europe.

The Early Holocene the steppe had a much better climate compared to northwest India.

Blyakharchuk found, “The increased moisture and temperature in the steppe was associated with the Atlantic storm systems as well as with insolation-enhanced Asian monsoon.” (Blyakharchuk 2007). He noted that the climate was moist up to 3000 BC, however it started becoming drier slowly over the next 3000 years. Clearly the region underwent afforestation making it unfit for the survival of horse which needs open fields.

- Climate change in Late Holocene

Apart from this, there is evidence of intense human induced grazing pressure in the steppe which started in the Iron Age leading to permanent deforestation at about 1000 BC in Karginskaya (Blyakharchuk 2007:529). Many regions within Central Asia converted back to steppe even earlier just after 2000 BC due to degradation by intense human activities (Zhou 2008, cited by Chen F. 2009:3). Such human activities might have resulted from the people arriving into Central Asia from the deserted and desolate Indus Valley. In fact the Himalayas which too were moist with plenty of rains just like Central Asia following 1900 BC, gave refuge to the escaping Indus Valley people. So did the Ganga Valley. “Between 3,900 and 3,000 y ago, there was a proliferation of smaller, village-type settlements (2–4, 6, 18), especially in the Himalayan foothills and the western part of the Ganges basin along the Yamuna River and on the Yamuna-Ganga interfluvium (Fig. 3B).” (Giosan:1 early web version). The northern steppes had converted into forest during the Early Holocene. Many areas in them converted back to steppe ecosystem earlier by 5,000 BC (Zhao 2009:249; Jiang 2006).

- The wet and warm period of Indus-Sarasvati: Mid-Holocene

Following the Early Holocene we get a transitional period and after this, we get the Mid-Holocene period from 5,500 BC to 3000 BC in northwest India. This period is very wet and warm. The Bay of Bengal monsoon shifted to the Arabian Sea (Thamban 2001, 2007; Sarkar 2000; Staubwasser and Weiss 2006), and the region from Arabia, Mesopotamia, Iran and northwest India enjoyed a wet climate over more than two thousand years. The temperature rose world over and this period has

been called the Mid-Holocene Temperature Maximum or Optimum. The warmest time was between 5000 and 4000 BC.

It must be anticipated that the torrential rains plagued this region more than was required for settled life. Annual floods from the monsoonal rains must have been the rule for a large part of the period. This is possibly the reason of the Indus Valley Civilization not taking off until drier period with lesser rainfall arrived. Decrease in rainfall has been linked with the development of the Indus Valley Civilization in several recent studies (Shinde 2008:79; Giosan). Thus at 5000 BC the strong western monsoon for northwest India was good for the growth of forests but not suitable, because of floods, for the Indus Valley region to have supported a stable civilization.

In the Indus Sarasvati region, if one moved westward the rains became less. Yet the Ghagghar region of Haryana, which indeed had lesser rains than the Indus Valley region could not develop high civilization during the early periods. The human settlement in the Ghagghar-Hakra geography is later than that of Aq Kupruk of Afghanistan (Possehl 2002:24) and Mehrgarh period 1 (Jarrige 2008). The habitation was delayed in Sarasvati basin until the tributaries of Sarasvati parted from her to join the Indus and Ganga rivers, relieving the land from the devastating and dangerous floods, perpetually coming from the Sarasvati river which had been gorged with waters from several mighty tributaries like Sutlej, Yamuna etc. It has been found by the geologists that the Sutlej left Sarasvati at about 6500 BC (Clift 2012; Giosan 2012:e1690; Valdiya 2013).

Northwest India changed into a forest during Mid-Holocene. There were water logged areas and swamps in the region because of excessive rains. The Thar Desert largely got replaced by grasslands and open forests. It had a green carpet cover over most of the places at about 3000 BC (Deotare 2004; Meher-Homi and Gupta 1999:221). Because of geo-tectonic movements, the Sarasvati River had lost her connection with the Himalayan glaciers at about 6,500 BC, and had become a rain-fed river (Giosan). The rains in the northwest were very strong after 5,500 BC and the river remained big in spite of losing her supply from the Himalayas in the Mid-Holocene Period. The Sarasvati river started becoming weaker after 3,000 BC, when the monsoon started shifting from the Arabian Sea back to the Bay of Bengal, and became quite weak by 2500 BC drying completely by 1900 BC (Giosan).

The climate of the Mid-Holocene northwest India is the type in which rice, wheat, barley and vegetables would grow well. Agriculture would be successful. Forest trees which can grow well in such climates include the *Ficus* species, grape-vine (*Vitis*), poplar, date (*Phoenix*) etc. Although this climate was appropriate for mango (*Mangifera*), mango did not grow in the region then because it had not arrived there from East India (Assam and Burma) by that time. Mango arrived in this region sometime about 2600-2200 BC at Farmana when the onset of the draught had about set in and soon the tree would become unfit to grow in the region because of increasing aridity becoming absent again (Kashyap and Weber 2013:178; Kashyap and Weber 2010).

Tiger which hunts from behind the trees in the dense forests singly would be successful in such environment. The swamps would harbour crocodiles. Wild horse, wild camel, giraffe and ostrich would become extinct, because these animals could survive predation by dint of their fast speed only which was not possible in dense forests. In the forests, they lose speed and become easy prey to the large carnivores. The pythons hanging from the trees would trap and strangle their prey. As the Thar Desert turned into grassland, human arrival and habitation and nomadic and pastoral activities could take place.

- The Drying of the Indus Valley Civilization

The time about 4,200 BP (or, 2250 BC) was a very dry time. It has been named the 4.2 Kilo event. It is at this time that the region would face draughts and famines. We find archaeological evidence of the sudden decline in Hakra Wares sites in Sarasvati Delta, Cholistan and Kot Diji areas and other regions in India, and also in Levant in West Asia corresponding to this 4.2 Kilo event draught (Possehl 1997, also 2002:63; Staubwasser and Weiss 2006). These would lead to death and disease, and then desertion of the region. People would be forced to abandon the region and to move out to east and north in search of subsistence. Central Asia's climate was much better than the Indus-Sarasvati region at about 2200 BC.

Deotare noted that at about 5000 BC, hunter-gatherer people arrived in the Bap-Malar area, District Jodhpur (Rajasthan), and established their camps (Deotare 2004:404). *Prosopis cineraria*, *Acacia sp.*, *Capparis sp.*, *Tamarix sp.*, *Mimosa rubicaulis*, *Ziziphus sp.*, *Calligonum polygonoides*, *Syzygium cumini* and sedges grew in the Thar during this period, when the rainfall there was 500 mm more than what it is today (Meher-Homi:221). This must have been caused by improvement in the ecological condition of the Thar region owing to the increased rainfall in the region by 5000 BC. Hence the Thar must have converted into a savannah or grassland in which hunter-gatherers could subsist. The grassland ecosystem is suitable for the hunter-gatherer subsistence and pastoral nomads. In the Thar we get the evidence of nomadic existence too (Deotare 2004:404; 2004b:Abstract).

The Himalayan regions became drier during the Mid-Holocene because of the weakening of the winter monsoon. In Nainital the organic matter became low and carbon contents high—indicating change in climate towards dry conditions (Asha Gupta 2005:44). Thus we find that climate changes were taking place in the direction reverse to that in the Indus region in the western Himalayan regions like Jammu Uttarakhand and Himachal Pradesh during the Mid-Holocene.

Thereafter, in Late Holocene at Nainital, the organic matter became high again with low carbonate contents, reflecting restoration of humid climate in the region. Contrasting this the Indus-Sarasvati region became dry during the same period of Late Holocene (Asha Gupta 2005:44). Thus the western Himalayas had two wet or favourable periods—one during the Early Holocene and the other in the Late Holocene. This is precisely the reason for a late take off of the Neolithic revolution

in the Himalayan regions like Gufkral and Burzahom where the Neolithic revolution took off about 3000 calBC and not earlier (Upinder Singh:114, 111).

- It is obvious that the western Himalayan region (Jammu and Himachal Pradesh) were part of the Central Asian rain-system, and they went more along the changes in climate taking place in Central Asia. The fossil pollen studies from Central Asia, South Siberia, Northern and Western China and other steppe zones have shown that the steppes became wet and converted into forests in the Early Holocene (8000-6000 BC). Jiang (2006) found that the inner Mongolian steppe changed into birch-pine (*Betula/Pinus*) forest at 10,500-7,200 BC period, and evolved into woodland with these two trees dominating at 7,200-4,700 BC period. But the same regions reverted back to the steppe status after 4,700 BC.

Conversion back from forest to the dry steppe and desert ecosystems took place at different times in the different regions of the Inner Asia. Many areas remained forest till as late as 2000 BC. This is because many regions of Inner Asia had other sources of rains in addition to the Siberian winter monsoon. Atlantic and Mediterranean winds supplied rains to the westerly regions of the steppe including even up to the Kazakh steppe. The southwestern Siberian steppe and the Kazakh steppe became birch forest about 5800 BC and converted into *Pinus* forest between 3800 and 4000 BC. The *Pinus* forest continued in the region up to 1000 BC (Tarasov 1997, 2012; Maman 2013). Then the climate degradation brought about by human interference led to clearing of the forests in which feral and domestic horse could arrive from outside and live.

The eastwardly regions received rains from the Chinese monsoon too. At Yolin Am steppe (Southern Mongolia), it was found that it was a forest between c. 3600 BC and 2000 BC, and *Betula* (birch) and *Salix* (willow) trees dominated (Miehe 2007:156, Table 1). At Bosten Hu, which is located in the Chinese Central Asian province Xinjiang, a lake became established around 6000 BC, and the moisture in the weather of that area increased after 4000 BC.

Contrasting the Indus Valley which became dry in the Late Holocene, there was a wet climate from Mid- to even the Late Holocene period in Bosten Hu (Huang 2008). This site was located not too much away from our route of migration through Central Asia. During the late Holocene period, we can say, when the Indus-Sarasvati was drying, there were regions in Central Asia which were wet and flourishing, and the famous steppe (of Kazakhstan and Ukraine) was in fact a forest during most of the Holocene period.

Certainly the steppe and Central Asia regions had better-than-Indus-Valley climate during the second millennium BC. Another author van Geel noted that between 3000 BC and 1500 AD, the North Mongolia region witnessed transformation into forest and there was a lake level rise (2004, cited in Table 5, Tchebakova *et al* 2009).

It is because of the dry climate that the barley was the only cereal in Early Holocene Mehrgarh. Wheat requires water, and rice requires much more water. Both, the rice and wheat, were absent from Mehrgarh Period 1. However after 5000 BC, we get both the rice and the wheat in the Hakra-Ghagghar region. This is the result of climate change.

In general, however, after 3000 BC, more and more of Central Asia converted into steppe and desert with the passing time (Zhao 2009; Zhao 2008 cited in F. Chen Editorial 2009:1). There was an abrupt change to arid climate at about 2500 BC (4.2 Kilo Event) in many regions of China (Zhao 2009: Abstract; Chen, W. 2009). Miehe *et al* noted in their study of the succession of ecologies in the Gobi desert, that birch and willow pollens and charcoal were present in the soil layers before 3000 BC (calibrated radiocarbon date), however birch became extinct from that site after that time (Miehe 2007:163; 156 Table 1).

Trees of the more humid climate like willow, juniper, oak, pine grew in the Kachi plain earlier at least since the seventh millennium BC. This type of flora lasted up to 4000 BC (Costantini 2008); and could have well continued for some centuries more in the fourth millennium (J.-F. Jarrige, 2008). But after 3000 BC willow did not grow in the northwest Indian plains. The tree grew during the *Rig-Vedic* period and has been mentioned by the name *vetasa* (*Rig-Veda*: 4.58.5; Priyadarshi 2014:173-187). However the date 1500 BC, which has been claimed to be the date of the arrival and subsequent settlement of the Aryans, northwest India was climatically quite hot and dry and no ‘wet climate’ tree could have survived there. Hence the received date of arrival as 1500 BC, that of the *Rig-Veda* as 1200 BC and that of the humid climate text *Yajur-Veda* 1000 BC, needs to be revised.

The type of vegetation changed everywhere during the Holocene. The western coasts of the Black sea, where we get forest today, were steppe lands up to 5000 BC (Wright 2003:133). East of the Black Sea in the Caucasus region, the climate changed from the steppe to the woodland at 3000 BC (*ibid*: 133-4), and in the Maykop region the climate changed to moist at about 3500 BC. In the Altai region at the junction of Kazakhstan, Russia, Mongolia and China, the steppe changed into conifer forest at about 6,000 BC (*ibid*: 134). The “western steppe” to the north of the Black Sea was unforested until a much later date than all these.

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7.1. Indian DNAs from Archaeological Remains of Europe: Evidence of Indo-European Migration

The Starcevo male sample from Hungary, immediate pre-Neolithic dating 5565 BC (mean age) had H2 (Y-DNA), which is characteristically Indian (Haak 2015: Extended Data Table 2; Szecsenyi-Nagy 2015). The only likely possibility is its arrival from India through Iran and Armenia where these are found today. It is also found in Sardinia today (Szecsenyi-Nagy 2015:4-5). The same Y-DNA H2 was found from Spain too (El Portalón cave at Sierra de Atapuerca) dating quite later

between about 3500 and 5500 BC (Gunther 2015), indicating some Indian migration from India to Hungary, and later from Hungary to Spain.

The Central Asian farmers brought the farming culture to Central Europe following 5500 BC, and are known to us as the LBK (Linear Pottery Culture) people of Neolithic Central Europe. However the migration was not easy or smooth. The newcomers were hunted and cannibalized by the older population of Europe. These professional hunters attacked the colonies of the arriving farmers, took them captive, brought them to their villages and consumed them as delicious food after properly slaughtering them. The hunters looted the pottery of the farmers too, as it was a novelty to them. Such events took place between 5300 and 4900 BC (Boulestin *et al*, 2009; Orschiedt and Haidle 2006). Ultimately the hunter-gatherers were eliminated soon, not by the earlier claimed “elite-dominance” but by sheer competition and the survival of the fittest technology. This finding disproved the earlier claims of Colin Renfrew, Peter Bellwood etc. that language change occurred by elite dominance in Europe.

The mtDNA data from the Central European hunter-gatherers comprise exclusively some U lineages (U, U4, U5, and U8) and not even U2e, U3, T and many other lineages found today in Europe, whereas the LBK (*i.e.* Central Europe after 5500 BC) is characterized by a distinct haplogroup (DNA lineages) profile including N1a, T2, K, J, HV, V, W, and X which are entirely different from the ones found previously. These latter haplogroups can be denoted as a mitochondrial “Neolithic package” and comprise around 79.4% of the diversity in the LBK, whereas the older Europe’s hunter-gatherer lineages are rare (2.9%) in this culture (Brandt 2013:260).

Out of these newer ones, the N1a, T2 and HV most probably originated in Iran. We cannot say anything about the origin of the other Neolithic lineages of the list at the moment, which will only become clear with more research. In addition to these eight lineages, the Carpathian Basin *i.e.* the region to the south of the Danube River in Romania and Hungary exhibits some more Neolithic DNAs which are not found in the northwardly located LBK culture. These are T1, H, U2, U3, U4 and U5a (Szecsenyi-Nagi 2015:3.). Out of these T1 is Iranian and U2 is Indian. U3 is common in the Roma/Gypsy and is possibly a western Indian lineage of the Iron Age, now not so commonly found in India.

Fig. Picture suggesting likely place of origin of mtDNA T in South Iran and then its migration into the steppe and Arabia. Courtesy Fernandes 2015, PLoS1.

Significantly enough, we find that the Iranian N1a appears in the Neolithic Central Europe (LBK culture) in good numbers (20%) only for a short time and then disappears. It is very rare in the modern European population—only about 0.2% (Lee 2012:577; Palanichamy 2010:2). This could mean only one of the two possibilities *viz.*: one, that the Neolithic people had arrived from a place

which later did not contribute to the migrations to the steppe/ Europe any more, and two, that the N1a frequency was superseded in the home region by growth of later lineages there and later N1a became less in frequency in the source area itself. Considering the two scenarios, India and Iran either could have been the source of the Neolithic LBK's N1a DNA.

They took two routes. From Indus, Afghanistan and East Iran, people reached by the route along the Oxus river, while from the west Iran and Iraq people migrated by the Caucasian route to the steppe. From West Asia people also took sea route in the Mediterranean to reach Italy and Greece; and some took the Bosphorus route from Anatolian to reach the Balkans and Romania.

This migration entered Europe between 5500 and 5000 BC. Thereafter, people migrated from the steppe to north Europe. North Europe had a scanty hunter gatherer dark-skinned population, which were cannibals also. This population finally gave way to the light skinned people coming from Iran and Iraq through the steppe.

References:

Achilli, A. *et al*, 2011, Mitochondrial genomes from modern horses reveal the major haplogroups that underwent domestication, *PNAS*, Early Ed. 1111637109.

Albert, M.J. *et al*, 1980, Vitamin B₁₂ synthesis by human small intestinal bacteria, *Nature* 283:781-782.

Allchin, B. and Allchin, R., 1982, *Rise of Civilization in India and Pakistan*, Cambridge University Press.

Allentoft, M.E. *et al*, 2015, Population Genomics of Bronze Age Eurasia, *Nature*, 522:167-172.

Bag, A.K., 2015, Early System of *Naksatras*, Calendar and Antiquity of Vedic & Harappan Traditions, *Indian Journal of History of Science*, 50.1 (2015) 1-25.

Bala, Saroj and Mishra, K., 2012, *Historicity of Vedic and Ramayan Eras*, Vision India Publications, Delhi.

Bar-Yosef, Ofer; The Archaeological Framework of the Upper Paleolithic Revolution, *Diogenes* 2007, 54(2): 3-18.

Basu Mallick C, Iliescu FM, Mo'Is M, Hill S, Tamang R, et al. (2013) The Light Skin Allele of SLC24A5 in South Asians and Europeans Shares Identity by Descent. *PLoS Genet* 9(11): e1003912. doi:10.1371/journal.pgen.1003912

Bellwood, Peter and Oxenham, Marc, 2008, “The expansion of farming societies and the role of Neolithic Demographic Transition”, in Jean-Pierre, Bocquete-Appel and Ofer Bar-Yosef (Eds.), *The Neolithic Demographic Transition and its Consequences*, Springer, Netherlands.

Berezina, Galina *et al*, 2011, The analysis of the genetic structure of the Kazakh population as estimated from mitochondrial DNA polymorphism, Medical and Health Science Journal, 6:2-6.

Bjune, A.E. *et al*, 2004, Holocene vegetation and climate history on a continental–oceanic transect in northern Fennoscandia based on pollen and plant macrofossils, *Boreas* 33:211-223.

Blyakharchuk, T.A. *et al*, 2007, Late Glacial and Holocene vegetational history of the Altai Mountains (southwestern Tuva Republic, Siberia), *Palaeogeography, Palaeoclimatology, Palaeoecology*, 245:518–534.

Borzenkova, Irena *et al*, 2015/ 2016, “Climate Change During the Holocene (Past 12,000 Years)” in Bolle, Hans-Jurgen *et al* (Eds.), *Second Assessment of Climate Change for the Baltic Sea Basin, Regional Climate Studies*, Springer.

Boulestein, Bruno *et al*, 2009, Mass cannibalism in the Linear Pottery Culture at Herxheim (Palatinate, Germany), *Antiquity*, 83(322): 968-982.

Boulesten, Bruno *et al*, 2009, Mass cannibalism in the Linear Pottery Culture at Herxheim (Palatinate, Germany), *Antiquity*, 83: 968–982.

Bowling, A.T. *et al*, 2003, Genetic variation in Przewalski’s horses, with special focus on the last wild caught mare, 231 Orlitza III, *Cytogenet Genome Res*, 101: 226–234.

Bramanti, B. *et al*, 2009, Genetic discontinuity between local hunter-gatherers and Central Europe’s first farmers, *Science* 326:137.

Brandt, Guido *et al*, 2013, Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Genetic Diversity, *Science*, 342:257-261.

Broushaki, Fernaz *et al*, 2016, Early Neolithic genomes from the eastern Fertile Crescent, *Science*, 353(6298):499-503.

- Burger, J. *et al*, 2007, Absence of the lactase-persistence-associated allele in early Neolithic Europeans, *PNAS*, 104(10):3736-3741.
- Burrow, T., 2001 (reprint), *The Sanskrit Language*, Delhi, Motilal Banarsidass Publ.
- Cai, D. *et al*, 2009, Ancient DNA provides new insights into the origin of the Chinese domestic horse, *Journal of Archaeological Science* 36:835–842.
- Canfield, V.A. *et al*, 2013, Molecular Phylogeography of a Human Autosomal Skin Color Locus Under Natural Selection, *G3 Genes Genomes Genetics*, 3:2059-2067.
- Chakrabarti, D.K., 1999, *India: An Archaeological History*, N Delhi, OUP.
- Chen, F. *et al*, 2009, Holocene climate variability in Arid Asia: Nature and mechanism (Editorial), *Quaternary International*, 194:1-5.
- Chen, W., Wang, W.M., Dai, X.R., 2009, Holocene vegetation history with implication of human impact in the lake Chaohu area, Anhui Province, East China, *Vegetation History and Archaeobotany*, 18:137e146.
- Clift, P.D. *et al*, 2012, U-Pb zircon dating evidence for a Pleistocene Saraswati River and capture of the Yamuna River, *Geology*, 40:211-214; DOI 10.1130/G32840.1.
- Comas, David *et al*, 2004, Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages, *European Journal of Human Genetics*, 12:495–504.
- Costantini, L. and Costantini, L.B., “Prehistory of Agro-biodiversity”, in *The Archaeology of Agro-Biodiversity*, A Food and Agriculture Organization document on the net. accessed 12 September, 2014.
- Costantini, Lorenzo, 2008, The first farmers in western Pakistan: the evidence of the Neolithic Agro-Pastoral settlement of the Mehrgarh, *Pragdhara*, 18:166-178.

Curry, Andrew *et al*, 2013, Archaeology: The milk revolution When a single genetic mutation first let ancient Europeans drink milk, it set the stage for a continental upheaval, *Nature*, 500(7460):20-22.

- Davis, B.A.S. *et al*, 2003, The temperature of Europe during the Holocene reconstructed from pollen data, *Quaternary Science Reviews*, 22:1701-1716.
- Dennel, Robin, 2005, “Comments”, in James, H.A.V and Petraglia, M.D., 2005, Modern human Origins and the Evolution of Behaviour in the Later Pleistocene Record of South Asia, *Current Anthropology*, Supplement.
- Dennel, Robin; in “Comments” on James, Hannah and Petraglia, Michael, 2005, *Current Anthropology* Volume 46, Supplement, December 2005, by The Wenner-Gren Foundation for Anthropological Research, p. 18.

Deotare, B.C. *et al*, 2004, Palaeoenvironmental history of Bap-Malar and Kanod playas of western Rajasthan, Thar desert, *Proc. of Ind. Acad. Sci (Earth Planet. Sci.)*, 113(3):403-425.

Der Sarkissian, C. *et al*, 2013, Ancient DNA Reveals Prehistoric Gene-Flow from Siberia in the Complex Human Population History of North East Europe, *PLoS Genet*, 9(2): e1003296.
doi:10.1371/journal.pgen.1003296.

Derenko, M. *et al*, 2013, Complete Mitochondrial DNA Diversity in Iranians. *PLoS ONE* 8(11): e80673. doi:10.1371/journal.pone.0080673

Dikshit, K.N. and Mani, B.R., 2013, The origin of Indian civilization buried under the sands of 'Lost' River Saraswati, *Dialogue*, 15(1):47-59.

Dikshit, K.N., 2013, Origin of Early Harappan Cultures in the Sarasvati Valley: Recent Archaeological Evidence and Radiometric Dates, *J. Ind. Ocean. Arch.*, 9:87-141.

Dixit, S. and Bera, S.K., 2012, Holocene climatic fluctuations from Lower Brahmaputra flood plain of Assam, northeast India, *J. Earth Syst. Sci.*, 121(1):135–147, publ Indian Academy of Sciences

Dogette, H., 1991, "Sorghum history in relation to Ethiopia", in Engels, J.M.M. *et al* (Eds.), *Plant Genetic Resources of Ethiopia*, Cambridge University Press.

doi:10.1371/journal.pone.0034288

Dulik, M.C. *et al*, 2011, Y-Chromosome Variation in Altaian Kazakhs Reveals a Common Paternal Gene Pool for Kazakhs and the Influence of Mongolian Expansions, *PLoS ONE*, 6(3): e17548.
doi:10.1371/journal.pone.0017548

Dwairy, M., 2006, The psychosocial function of reincarnation among Druze in Israel, *Cult Med Psychiatry*, 30(1):29-53.

Dwairy, M., 2006, The psychosocial function of reincarnation among Druze in Israel, 30(1):29-53.

Dymoc, W., Warden, C.J.H. and Hooper, D., 1892, *Pharmacographia Indica: A history of the principal drugs of vegetable origin met with in British India*, Part V, Kegan Paul, Trench Trubner and Co. Ltd, London.

Edwin, Deepa *et al*, 2002, Mitochondrial DNA diversity among five tribal populations of southern India, *Current Science*, 83(2):158-162.

Edwin, Deepa *et al*, 2002, Mitochondrial DNA diversity among five tribal populations of southern India, *Current Science*, July, 83(2):158.

- Engels, J.M.M. and Hawkes, J.G., 1991, “The Ethiopian gene centre and its genetic diversity”, in Engels, J.M.M., Hawks, J.G. and Worede, M. (Eds.), *Plant Genetic Resources of Ethiopia*, Cambridge University Press, pp. 23-41.
- Enzel, Y. *et al*, 1999, High- Resolution Holocene environmental changes in the Thar Desert, Northwestern India. *Science* 284:125-128.
- Fagundes, N.J.R. *et al*, 2008, A Reevaluation of the Native American MtDNA Genome Diversity and Its Bearing on the Models of Early Colonization of Beringia. *PLoS ONE* 3(9): e3157. doi:10.1371/journal.pone.0003157.
- Fernandez, H. *et al*, 2006, Divergent mtDNA lineages of goats in an Early Neolithic site, far from the initial domestication areas, *PNAS*, 103(42): 15375–15379.
- Fornarino, S. *et al*, 2009, Mitochondrial and Y-chromosome diversity of the Tharus (Nepal): a reservoir of genetic variation, *BMC Evolutionary Biology* 2009, 9:154 doi:10.1186/1471-2148-9-154.
- Fu, Q. *et al*, 2016, The Genetic history of Ice-Age Europe, *Nature*, *Nature* **534**: 200–205.
- Fuller, D.Q. 2006, Agricultural Origins and Frontiers in South Asia: A Working Synthesis, *J World Prehist*, 20:1–86.
- Fuller, D.Q. and Boivin, N., 2009, Crops, cattle and commensals across the Indian Ocean Current and Potential Archaeobiological Evidence, *Etudes Ocean indien*, 42-43:2-24.
- Fuller, D.Q., 2003, Further evidence on the prehistory of sesame, *Asian Agri- History*, 7(2):127-137.
- Gallego-Llorente, Marcos *et al* 2016, The genetics of an early Neolithic pastoralist from Zagros, Iran, bioRxiv. Online publication.
- Gamba, Christina *et al*, 2014, Genome flux and stasis in a five millennium transect of European prehistory, *Nature Communications*, 2014, Online publication.
- Ganjoo, R.K. and Ota, S.B., 2012, Mountain environment and early human adaptation in NW Himalaya, India: A case study of Siwalik Hill Range and Leh valley, *Quaternary International* 269 (2012) 31-37.
- Ganjoo, R.K., 2007, Multi-proxy evidences of climate change from middle Miocene to Holocene in NW Himalaya, Paper presented at Conference on Milankovitch cycles over the past 5 million years, The Abu Salem International Centre for Theoretical Physics.
- Georgescu-Roegen, Nicholas, *The Entropy Law and the Economic Process*, Harvard University Press, Cambridge, Mass., 1971.
- Giosan, L. *et al*, 2012, Fluvial landscapes of the Harappan civilization, *PNAS* 109(26): E1688-E1694.
- Groube, Les; “The impact of disease upon the emergence of agriculture”, in *The Origins and Spread of Agriculture and Pastoralism in Eurasia*, Ed. Harris, D.R., Routledge, 1996, p. 105.
- Gunther, Torsten *et al*, 2015, Ancient genomes link early farmers from Atapuerca in Spain to modern-day Basques, *PNAS*, 112(38): 11917–11922.

Gupta, A.K., 2004, Origin of agriculture and domestication of plants and animals linked to early Holocene climate amelioration, *Current Science*, 87(1):54-59.

Gupta, Asha, 2005, "Climate Assessment of Himalaya—Multidisciplinary approach", paper presented in *Challenges in Indian Palaeobiology : Current status, Recent developments and Future directions, Abstract Volume—Diamond Jubilee National Conference, 15-16 November 2005, BSIP, Lucknow*.

Guthrie, R.D. *et al*, 2003, Rapid body size decline in Alaskan Pleistocene horses before extinction, *Nature* 426:169-171.

Haak, Wolfgang *et al*, 2015, Massive migration from the steppe is a source for Indo-European languages in Europe, *Nature* 522:207–211.

Haber, M. *et al*, 2012, Afghanistan's Ethnic Groups Share a Y-Chromosomal Heritage Structured by Historical Events, *PLoS ONE*, 7(3):e34288,

Hafmanova, Z., 2015, Early farmers from across Europe directly descended from Neolithic Aegeans, Advance Online publication, Biorxiv,

Hartmann 2 DNA, EU597563 (Brahui, Pakistan HGDP00005) Hartmann Haplogroup M5 06-APR-2008; A73G T199C A263G 315.1C T489C G709A A750G A1438G G1888A A2706G C3107N C3921T T4454C A4769G G4991A C7028T A8158G A8701G A8860G T9540C A10398G C10400T G10685A T10873C G11719A T12477C C12705T G14323A C14766T T14783C G15043A T15262C G15301A A15326G G16129A C16223T T16519C. Accessed data online 15 January, 2017.

Hawks, John, 2007, Recent acceleration of human adaptive evolution, *Proceedings of National Academy of Science of USA*, 104(52):20753-20758.

Hervella, M. *et al*, 2015, Ancient DNA from South-East Europe Reveals Different Events during Early and Middle Neolithic Influencing the European Genetic Heritage. *PLoS ONE* 10(6): e0128810. doi:10.1371/journal.pone.0128810

Hervella, M. *et al*, 2015, Ancient DNA from South-East Europe Reveals Different Events during Early and Middle Neolithic Influencing the European Genetic Heritage. *PLoS ONE* 10(6): e0128810. doi:10.1371/journal.pone.0128810

Hofmanova, Zuzana *et al* 2016, Early farmers from across Europe directly descended from Neolithic Aegeans, *PNAS*, 113(25):6886-91. Advance online publication 25 Nov 2015 on bioRxiv accessed 1 January 2017.

Huang, X.Z. *et al*, 2008, Dry late-glacial and early Holocene climate in arid central Asia indicated by lithological and palynological evidence from Bosten Lake, China. *Quaternary International* 194:19–27.

James, H.A.V and Petraglia, M.D., 2005, Modern human Origins and the Evolution of Behaviour in the Later Pleistocene Record of South Asia, *Current Anthropology*, Supplement, published by Wenner- Gren Foundation for Anthropological Research.

James, Hannah V. A and Petraglia, Michael D., 2005, Modern Human Origins and the Evolution of Behavior in the Later Pleistocene Record of South Asia, *Current Anthropology* Volume 46, Supplement, December 2005, by The Wenner-Gren Foundation for Anthropological Research.

- Jansen, T. *et al*, 2002, Mitochondrial DNA and the origins of the domestic horse, *PNAS*, 99(16):10905-10910.
- Jarrige, J.-F., 2008, Mehrgarh Neolithic, *Pragdhara* 18:135-154.
- Jiang, W.Y. *et al*, 2006, Reconstruction of climate and vegetation changes of the lake Bayanchagan (Inner Mongolia): Holocene variability of the East Asian monsoon, *Quaternary Research*, 65:411–420.
- Kadowaki, S. *et al*, 2016, Mitochondrial DNA Analysis of Ancient Domestic Goats in the Southern Caucasus: A Preliminary Result from Neolithic Settlements at Göytepe and Hacı Elamxanlı Tepe, *International Journal of Osteoarchaeology*, May 2016; John Wiley and Sons. Online advance publication.
- Karafet, T.M. *et al*, 2005, Balinese Y-Chromosome Perspective on the Peopling of Indonesia: Genetic Contributions from Pre-Neolithic Hunter-Gatherers, Austronesian Farmers, and Indian Traders, *Human Biology*, 77(1):93-114.
- Kashyap, Arunima and Weber, Steve, 2010, Harappan plant use revealed by starch grains from Farmana, India, *Antiquity* 84(326). Available: <http://antiquity.ac.uk/projgall/kashyap326/>. Accessed 24 June 2014.
- Kashyap, Arunima and Weber, Steve, 2013, “Starch grain analysis and experiments provide insight into Harappan cooking practices”, in Abraham, S.A. *et al* (Eds.), *Connections and Complexity: New approaches to the archaeology of South Asia*, Left Coast Press.
- Kazanas, N., 2012, Vedic and Avestan, *Vedic Venues*, 1:183-229.
- Khuri, Fuad I., 2004, *Being a Druze*, Druze Heritage Foundation.

Khusri, Faud I., *Being a Druze*, Druze Heritage Foundation, 2004.

- Kivisild, T. *et al*, 1999, Deep Common Ancestry of Indian and Western-Eurasian Mitochondrial DNA Lineages, *Current Biology*, 9:1331-1334.
- Kivisild, T. *et al*, 2005, Comments to Jamaes and Petraglia,'s “Modern Human Origins and the Evolution of Behavior in the Later Pleistocene Record of South Asia”, *Current Anthropology* Volume 46, Supplement, December 2005, by The Wenner-Gren Foundation for Anthropological Research. P. S 18.
- Kivisild, T. *et al*, The genetic heritage of the earliest settlers persists both in Indian tribal and caste populations, *Am J Hum Genet* 2003, 72 (2) : 313-32.
- Kong, Qing-Peng, 2010, Large-Scale mtDNA Screening Reveals a Surprising Matrilineal Complexity in East Asia and Its Implications to the Peopling of the Region, *Mol. Biol. Evol.*, 28(1):513–522. 2011 doi:10.1093/molbev/msq219.
- Kremenetski, C.V. *et al*, 1997, Postglacial Development of Kazakhstan Pine Forests, *Géographie physique et Quaternaire*, vol. 51, n° 3, 1997, p. 391-404.

- Kruttli, A. *et al*, 2014, Ancient DNA Analysis Reveals High Frequency of European Lactase Persistence Allele (T-13910) in Medieval Central Europe, *PLoS ONE* 9(1): e86251. doi:10.1371/journal.pone.0086251
- Kusuma, P. *et al*, 2015, Mitochondrial DNA and the Y chromosome suggest the settlement of Madagascar by Indonesian sea nomad populations, *BMC Genomics*, 16:191.
- Lal, B.B., 2009, Emigration of some Vedic people from Sarasvati river basin to western Asia ca. 2nd millennium BCE, Paper presented at the Conference of the Indian Archaeological society, Allahabad University 2009, also published in *Puratatva* 2009.
- Lalueza-Fox, C. *et al*, 2004, Unravelling migrations in the steppe: mitochondrial DNA sequences from ancient Central Asians, *Proc. R. Soc. Lond. B*, 271:941–947.
- Lancelotti, C., Tengberg, M. and Thiebault, S., 2013, “Vegetation and wood exploitation at Harappa, Punjab (Pakistan): Preliminary results of the charcoal analysis”, in Dambledon, F. (Ed.), *Proceedings of the Fourth International Meeting of Anthracology, Brussels, 8-13 September 2008*, Archaeopress, Oxford.
- Lazaridis, Iosif *et al*, 2016, Genomic insights into the origin of farming in the ancient Near East, *Nature*, advance web publication, doi:10.1038/nature19310.
- Li, Chinxiang, 2010, Evidence that a West-East admixed population lived in the Tarim Basin as early as the early Bronze Age, *BMC Biology*, 8:15.
- Li, Chinxiang, 2015, Analysis of ancient human mitochondrial DNA from the Xiaohe cemetery: insights into prehistoric population movements in the Tarim Basin, China, *BMC Genetics*, 16:78.
- MacDonald, G. M., 2003, *Biogeography: Space, Time, and Life*, John Wiley, New York.
- Madella, M. and Fuller, D.Q., 2006, Palaeoecology and the Harappan Civilisation of South Asia: a reconsideration, *Quaternary Science Reviews*, 25:1283–1301.
- Magny, M. *et al*, 2013, North–south palaeohydrological contrasts in the central Mediterranean during the Holocene: tentative synthesis and working hypotheses, *Clim past*, 9:2043–2071.
- Malyarchuk, B. *et al*, 2011, Ancient links between Siberians and Native Americans revealed by subtyping the Y chromosome haplogroup Q1a, *Journal of Human Genetics*, 56:583–588.
- Malyarchuk, B.A. *et al*, 2002, Mitochondrial DNA variability in Poles and Russians, *Ann. Hum. Genet.* (2002), 66, 261–283.
- Malyarchuk, B.A. *et al*, 2008, Mitochondrial DNA Variability in Slovaks, with Application to the Roma Origin, *Annals of Human Genetics*, 72:228–240
- Malyarchuk, B.A., 2006, Mitochondrial DNA Diversity in the Polish Roma, *Annals of Human Genetics* 70(Pt 2):195–206 .
- Maman, S. *et al*, 2013, *Mid-Holocene stabilization of the Karakum and Kyzylkum sand seas, central Asia – evidence from OSL ages* , EGU General Assembly 2013, held 7–12 April, 2013 in Vienna, Austria, id. EGU2013-2533.

Martinez-Cruz, B. *et al*, 2016, Origins, admixture and founder lineages in European Roma, *European Journal of Human Genetics*, 24(6):937-43.

Mathpal, Y., 1984, *Prehistoric Rock Paintings of Bhimbetka, Central India*, Abhinav Publications.

Mathpal, Y., 1985, "The hunter-Gatherer way of life depicted in the Mesolithic Rock Paintings of Central India", in Misra, V.N. and Bellwood, P.S. (Eds.), *Recent Advances in Indo-Pacific Prehistory: Proceedings of the International Symposium Held at Poona, December 19-21, 1978*, BRILL.

Mayewski, P.A. *et al*, 2004, Holocene climate variability, *Quaternary Research*, 62: 243–255.

McIntosh, Jane R., 2008, *Ancient Indus Valley: New Perspectives*, ABC-CLIO, Understanding Ancient Civilizations Series.

Meadow, R.H., 1981, "Notes on the Faunal Remains from Mehrgarh, with a focus on cattle (*Bos.*)", in Allchin, B. (Ed.), *South Asian Archaeology*, pp. 34-40.

Meadow, R.H., 1984, "Animal domestication in the Middle East: A view from the eastern margin", in Clutton-Brock, J. and Grigson, C. (Eds.), *Animals and Archaeology: 3. Early herders and their flocks*, British Archaeological Reports, International Series, No. 202, Oxford, pp. 309-337.

Meadow, R.H., 1989, "Pre-historic wild sheep and sheep domestication on the eastern margins of the Middle East", in Crabtree, P.J. *et al* (Eds.), *Early Animal Domestication and its Cultural Context: Dedicated to the Memory of Dexter Perkins, Jr. and Patricia Dali*, University of Pennsylvania Museum of Archaeology.

Meadow, R.H., 1993a, "Animal Domestication in the *Middle East*: A Revised View from the Eastern Margin" in Possehl G.L. (Ed.), *Harappa Civilization*, Oxford & IBH, New Delhi, pp. 295-320.

Meadow, R.H., 1993b, Continuity and change in the agriculture of the Greater Indus Valley, *International Association for the Study of the Cultures of Central Asia: Information Bulletin* 19:63-77.

Meadow, R.H., 1998, Pre- and proto-historic Agricultural and pastoral transformation in northwestern South Asia, *Review of Archaeology*, 19(2):12-21.

Meher-Homi, V.M. and Gupta, H.P., 1999, A Critical Appraisal of Vegetation and Climate Changes during Quaternary in the Indian Region, *PINS*, 565(5):205-44.

Metspalu, M. *et al*, "Most of the extant mtDNA boundaries in South and Southwest Asia were likely shaped during the initial settlement of Eurasia by anatomically modern humans" in *BMC Genetics* 2004, **5**: 26 doi:1186/1471-2156-5-26.

Miehe, G. *et al* 2009, How old is pastoralism in Tibet? An ecological approach to the making of a Tibetan landscape, *Palaeogeography, Palaeoclimatology, Palaeoecology* 276:130–147.

- Miehe, G. *et al*, 2007, Mountain forest islands and Holocene environmental changes in Central Asia: A case study from the southern Gobi Altay, Mongolia, *Palaeogeography, Palaeoclimatology, Palaeoecology*, 250:150–166.
- Misra, V.D., 2008, “Beginning of agriculture in the Vindhya (North-Central India)” in Gopal, L. (Ed.), *History of Agriculture in India, Up to C. 1200 A.D.*, Concept Publishing Company.
- Misra, V.N., 2001, Pre-historic human colonization of India, *J Biosc*, 26(4) supplement:491-532.
- Mitchell, P., 2005, *African Connections: Archaeological Perspectives on Africa and the Wider World*, Rowman Altamira.
- Moussa, N.M., 2016, Y-chromosomal DNA analysed for four prehistoric cemeteries from Cis-Baikal, Siberia, *Journal of Archaeological Science*, Online version, 15 November, 2016.
- Norton, H.L. *et al*, 2007, Genetic Evidence for the Convergent Evolution of Light Skin in Europeans and East Asians, *Mol. Biol. Evol.*, 24(3):710–722. 2007
- Nuwer, R., 2012, An Ancient Civilization, Upended by Climate Change, *The New York Times*, May 29, accessed 14 March 2014.
- Olade, I. and Lalueza-Fox, C., 2015, Modern humans’ paleogenomics and the new evidences on the European prehistory *STAR* 2015; 1(1): STAR20152054892315Y.0000000002.
- Olalde, Inigo *et al*, 2014, Derived immune and ancestral pigmentation alleles in a 7000-year-old Mesolithic European, *Nature*, 507:225-228.
- Orschiedt, J. 2008, Violence on the living, violence on the dead: the human remains from the LBK site of Herxheim, Germany, in R. Schulting & L. Fibiger (ed.) *Neolithic violence in a European perspective*: 16-17, Preprint of the School of Archaeology, University of Oxford conference, 14-15 March 2008.
- Orschiedt, J. and Haidle, M.N., 2007, “The LBK enclosure at Herxheim: theatre of war or ritual centre? References from osteoarchaeological investigations”, in Pollard, T. and Banks, I. (Eds.) *War and sacrifice. Studies in the archaeology of conflict*, pp. 153-67, Leiden, Brill.
- Palanichamy, M. G. *et al*, 2014, Tamil Merchant in Ancient Mesopotamia, *PLoS ONE*, 9(10): e109331. doi:10.1371/journal.pone.0109331
- Pamjav, Horolma *et al*, 2012, Brief communication: New Y-chromosome binary markers improve phylogenetic resolution within haplogroup R1a1, *Am. J. Phys. Anthropol.*, 149: 611–615. doi: 10.1002/ajpa.22167
- Parpola, Asko and Carpelan, Christina, 2005, The cultural counterparts to Proto-Indo-European, Proto-Uralic and Proto-Aryan: matching the dispersal and contact patterns in the linguistic and archaeological record, in Bryant, F. and Patton, L.L. (Eds.), *The Indo-Aryan Controversy: Evidence and Inference in Indian History*, pp. 107-142.
- Perkins, D., Jr., 1972, “The fauna of the Aq Kupruk caves: A brief note”, in Dupree, L., *Transactions of the American Philosophical Society*, 62(4):73.
- Pimentel, D. and Pimentel, M., 2003, Sustainability of meat-based and plant-based diets and the Environment, *American Journal of Clinical Nutrition*, 78(suppl):660S–3S.

- Possehl, G. et al, 1989, Harappan Civilization and Rojdi, BRILL Archive.
- Possehl, G.L., 2002, *The Indus Civilization*, Rowman Altamira.
- Poznic, G.D. et al, 2016, Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences, *Nature Genetics* 48:593–599.
- Priyadarshi, P. 2014, *In Quest of the Dates of the Vedas*, Partridge Publishing, India.
- Priyadarshi, P., 2011, *The First Civilization of the World*, Siddhartha Publications, Delhi.
- Priyadarshi, P., 2013, Some Domestic Animals of the Indo-European Homeland and their dispersal, *Vedic Venues*, 2:200-247.
- Priyadarshi, P., 2015, Dating of the Vedas and the Indo-European Migration, *Vedic Venues*, 3:134-224.
- Quintana-Murci, L. et al, 2004, Where West Meets East: The Complex mtDNA Landscape of the Southwest and Central Asian Corridor. *American Journal of Human Genetics* 74:827-845.
- Regueiro, M. et al, 2006, Iran: Tricontinental Nexus for Y-Chromosome Driven Migration, *Human Heredity*, 61:132-143.
- Reidla, M. et al, 2003, Origin and Diffusion of mtDNA Haplogroup X, *American Journal of Human Genetics* 73:1178-1190.
- Richards, M. et al, 2000, Tracing European Founder Lineages in the Near Eastern mtDNA Pool, *American Journal of Human Genetics* 67:1251-1276.
- Ridgeway, W., 1905, *The Origin and Influence of the Thoroughbred Horse*, CUP Archives, Cambridge.
- Rissman, P., 1989, “The status of research on animal domestication in India and its cultural context”, in Crabtree, P.J. et al (Eds.), *Early Animal Domestication and Its Cultural Context: Dedicated to the Memory of Dexter Perkins, Jr. and Patricia Daly*, UPenn Museum of Archaeology.
- Romero, I.G. et al, 2011, Herders of Indian and European cattle share their predominant allele for lactase persistence, *Molecular Biology and Evolution*, Advance Access Published August 11, 2011.
- Sahoo, Sanghmitra et al, 2006, A prehistory of Indian Y chromosomes: Evaluating demic diffusion scenarios, *PNAS*, 103(4): 843-848.
- Sali, S.A., 1985, “The Upper Palaeolithic Culture at Patna, District Jalgaon, Maharashtra”, in Misra, V.N. and Bellwood, Peter (Eds.), *Recent Advances in Indo-Pacific Pre-history: Proceedings of the International Symposium*, BRILL, pp. 137-146.
- Sali, S.A., 1989, *The Upper Palaeolithic and Mesolithic cultures of Maharashtra*, Deccan College Post-Graduate and Research Institute, Pune.
- Saraswat, K.S. and Srivastava, C., 2000, “Ancient plant economy of pre- and proto- historic sites in northern and western India”, *Annual Report 1999-2000*, Birbal Sahani Institute of Palaeobotany, Lucknow.
- Sarkar, A. et al, 2000, High resolution Holocene monsoon record from the eastern Arabian Sea, *Earth and Planetary Science, Letters*, 177:209–218.

- Schneider, E. & Kay, J., 1992, Life as a manifestation of the second law of thermodynamics, *Mathematical and Computer Modelling*, 19(6-8):25-48.
- Sengupta, S. *et al*, 2006, Polarity and Temporality of High-Resolution Y-Chromosome Distributions in India Identify Both Indigenous and Exogenous Expansions and Reveal Minor Genetic Influence of Central Asian Pastoralists, *American Journal of Human Genetics*, 78(2): 202–221.
- Sharma, Chhaya and Srivastava, Chanchala, 2000, “Studies of lake sediments in Rajasthan desert proxy climate signals”, *Annual-Report 1999-2000, Birbal Sahni Institute of Palaeobotany, Lucknow*, p. 23.
- Sharma, G.R., 1980, *Beginning of Agriculture: From Hunting and Food-gathering to Domestication of Plants and Animals—Epipalaeolithic to Neolithic: Excavations at Chopani Mando, Mahadaha and Mahagara*, Abinash Publications.
- Sharma, S. *et al*, 2007, A novel subgroup Q5 of human Y-chromosomal haplogroup Q in India, *BMC Evolutionary Biology* 2007, 7:232 doi:10.1186/1471-2148-7-232.
- Sharma, S. *et al*, 2009, The Indian origin of paternal haplogroup R1a1* substantiates the autochthonous origin of Brahmins and the caste system, *Journal of Human Genetics*, 54: 47–55.
- Shinde, V. *et al*, 2006, Basic issues in Harappan archaeology: Some thoughts, *Ancient Asia*, 1:63-72.
- Shinde, V. *et al*, 2008, “Exploration in the Ghaggar Basin and excavations at Girawad, Farmana (Rohtak District) and Mitathal (Bhiwani District), Haryana, India” in Osada, T. and Uesugi, A. (Eds.), *Linguistics, Archaeology and the Human Past, Occasional Paper 3*, Indus Project, Research Institute for Humanity and Nature, Kyoto, Japan; Also published later as: *Current Studies on the Indus Civilization*, Manohar, 2010.
- Shinde, V. *et al*, 2008, “Exploration in the Ghaggar Basin and excavations at Girawad, Farmana (Rohtak District) and Mitathal (Bhiwani District), Haryana, India”, in Oshada, Toshiki and Uesugi, Akinori (Eds.), *Occasional Paper 3, Linguistics, Archaeology and the Human Past*, Indus Project Research Institute for Humanity and Nature Kyoto, Japan.
- Shinde, V., Yasuda, Y. and Possehl, G.L., 2001, Climatic conditions and the rise and fall of the Harappan Civilization of South Asia, *Monsoon* 3:92-94.
- Shlush, L. *et al*, 2008, The Druze: A Population Genetic Refugium of the Near East, *PLoS ONE*, 3(5): e2105. doi:10.1371/journal.pone.0002105
- Singh, G. *et al*, 1974, Late quaternary history of vegetation and climate of the Rajasthan Desert, India .
- Singh, Gurdeep, 1971, The Indus Valley culture seen in context of post-glacial climate and ecological studies in northwest India, *Archaeology and Physical Anthropology in Oceania*, 6(2):177-189.
- Singh, Upinder, 2008, *A History of Ancient and Early Medieval India: From the Stone Age to the 12th century*, Pearson Education India.
- Staubwasser, M. and Weiss, H., 2006, Holocene climate and cultural evolution in late prehistoric–early historic West Asia, *Quaternary Research*, 66, Advance web publication..

Sultana, S. *et al*, 2003, Mitochondrial DNA diversity of Pakistani goats, *Animal Genetics*, 34:417–421.

Sun, Chang *et al*, 2005, The Dazzling Array of Basal Branches in the mtDNA Macrohaplogroup M from India as Inferred from Complete Genomes. *Mol Biol Evol*, 23(3): 683-690. doi: 10.1093/molbev/msj078

Surugue, Lea, 2016, Ancient DNA reveals how farming emerged independently in different Neolithic populations, Science News item in *International Business Times*, July 25, 2016. Accessed 8 January 2017.

Szecsényi-Nagy (Sze'cse'nyi), A. *et al*, 2015, Tracing the genetic origin of Europe's first farmers reveals insights into their social organization. *Proc. R. Soc. B* 282: 20150339

Tarasov, P.E. *et al*, 1997, A continuous Late Glacial and Holocene record of vegetation changes in Kazakhstan, 136(1-4):281-292.

Tarasov, P.E. *et al*, 2012, "Environmental Change in Temperate Grasslands and Steppe", in Matthews, J.A. (Ed.), *The SAGE Handbook of Environmental Change: Volume 2, Human Impacts and Responses*, SAGE, pp. 215-244.

Tarlykov, P.V. *et al*, 2013, Mitochondrial and Y-chromosomal profile of the Kazakh population from East Kazakhstan, *Croat Med Journal*, 54(1):17-24.

Tarlykov, P.V., 2013, Mitochondrial and Y-chromosomal profile of the Kazakh population from East Kazakhstan, *Croat Med J.* 2013;54:17-24, doi: 10.3325/cmj.2013.54.17.

Tchebakova, N.M. *et al* 2009, Reconstruction and prediction of climate and vegetation change in the Holocene in the Altai–Sayan mountains, Central Asia, *Environ. Res., Letter* 4.

Tewari, Rakesh *et al*, 2008, Early Farming at Lahuradewa, *Pragdhara*, 18:347-373.

Thamban, M. *et al*, 2001 Glacial to Holocene fluctuations in hydrography and productivity along the southwestern continental margin of India, *Palaeogeography Palaeoclimatology Palaeoecology*, 165:113–127.

Thamban, M. *et al*, 2007, Indian Summer Monsoon Variability during the Holocene as Recorded in Sediments of the Arabian Sea: Timing and Implications, *Journal of Oceanography*, 63:1009-020.

- Thiebault, S., 1988, Palaeoenvironment and ancient vegetation of Baluchistan based on charcoal analysis of archaeological sites, *Proc. Ind. National Science Academy*, 54A(3):501-509.
- Trivedi, A. and Chauhan, M.S., 2008, Pollen proxy records of Holocene Vegetation and climate change from Mansar Lake, Jammu region, India, *Current Science*, 95(9):1347-1354.
- Trivedi, A. and Chauhan, M.S., 2009, Holocene Vegetation and Climate Fluctuations in Northwest Himalaya, Based on Pollen Evidence from Surinsar Lake, Jammu Region, India, *Journal of Geological Society of India*, 74:402-412.
- Underhill, P. *et al*, 2009/2010, Separating the post-Glacial coancestry of European and Asian Y-chromosomes within haplogroup R1a, *European Journal of Human Genetics* 2009, 4 November, advance internet publication; later published *EJHG* 2010, 18:479-484.
- Underhill, P. *et al*, 2015, The phylogenetic and geographic structure of Y-chromosome haplogroup R1a, *European Journal of Human Genetics*, 23:124–131.
- Valdiya, K.S., 2013, The River Saraswati was a Himalayan-born river, *Current Science*, 104(1):42-54.
- Vishnu-Mittre, 1978, Palaeoecology of the Rajasthan desert during the last 10,000 years, *The Palaeobotanist*, 25:549-558.
- Wade, C.M. *et al*, 2009, Genome sequence, comparative analysis, and population genetics of the domestic horse, *Science*, 326: 865–867.
- Wakankar, V.S., 1985, “Bhimbetka: The stone tool industries and rock paintings”, in Misra, V.N. and Bellwood, Peter (Eds.), *Recent Advances in Indo-Pacific Pre-history :Proceedings of the International Symposium*, BRILL, pp. 175-6.
- Wells, R.S. *et al*, 2001, The Eurasian Heartland: A continental perspective on Y-chromosome diversity, *PNAS*, 98: 10244-10249.
- Weninger, B., *et al*, 2006, Climate Forcing due to the 8200 cal BP event observed at Early Neolithic sites in the Eastern Mediterranean, *Quaternary Research*, 66(3):401-420.
- Witas, H.W. *et al*, 2013, mtDNA from the Early Bronze Age to the Roman Period Suggests a Genetic Link between the Indian Subcontinent and Mesopotamian Cradle of Civilization, *PLoS ONE*, 8(9): e73682. doi:10.1371/journal.pone.0073682.
- Witzel, M., 2003, *Linguistic Evidence for Cultural Exchange in Prehistoric Western Central Asia, Sino-Platonic Papers*, 129:48-56.
- Wright, H.E. *et al*, 2003, “Late-Glacial and Early-Holocene Dry Climates from the Balkans Peninsula to Southern Siberia” in Tonkov, S. (Ed.), *Aspects of Palynology and Palaeoecology*, Pensoft Publishers, Sofia, Moscow, pp. 127-136.
- Yasuda, Y. and Tabata, H., 1988, Vegetation and Climatic Changes in Nepal Himalayas II. A preliminary study of the Holocene vegetational history in the Lake Rara National Park area West Nepal, *Proceedings of Indian National Science Academy*, 54A(4):538-548.
- Yonebayashi, C., Minaki, M., 1997, Late Quaternary vegetation and climatic history of eastern Nepal, *Journal of Biogeography*, 24(6):837-843.

Zeder, Melinda, 2005, "A view from the Zagros: New perspectives on livestock domestication in the Fertile Crescent", in Vigne, J.D. *et al* (Eds.), *First Steps of Animal Domestication: New Archaeological Approaches*, Oxbow Books, Oxford.

Zhao, Y. *et al*, 2009, Vegetation response to Holocene climate change in monsoon-influenced region of China, *Earth Science Review*, 97:242-256.

Zolfagharifard, Ellie, 2014, Light skin in Europeans stems from ONE 10,000-year-old ancestor who lived between India and the Middle East, claims study, News, *Mailonline*, 7 January, 2014, accessed 8 January 2017.

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Categories ancient DNA, archaeobotany, history, Uncategorized

Vedic Indian Migration to Sumer: DNA evidence

February 5, 2015 //

4

Vedic Indians in Iraq in 5000 BC and The rise of Sumerian Civilization
by P Priyadaarshi

Sumer was located in South Iraq where the rivers Tigris and Euphrates produce marshland in the region just before the delta. In the sixth millennium BC, the region was dry and hot yet usually got flooded by the end of the harvesting season from the water coming down both the rivers. The catchment area of the Tigris and Euphrates rivers were fed by the winter monsoon, usually leaving snow on the mountains to melt at spring season. Hence the floods came just about the end of the winter or beginning of the summer, when barley was due to be harvested. This flood destroyed the crops. This had kept the region in perpetual economic darkness, until some new technology appropriate to the climate arrived here.

Before 5500 BC, the people were hunter-gatherers in this fish, bird and small game rich region. Thereafter people from the east came with newer ideas and technologies. Uruk was one of the oldest cities of Sumer, which suddenly emerged about 4000 BC (radiocarbon-14 date; Crawford 2004:23). [Crawford, Harriet, 2004, *Sumer and Sumerians*, CUP, Cambridge.].

There is evidence that the Sumerian Civilization took off at this time with the help of an agro-pastoral economy which had arrived from India and which relied heavily on the domestic water-buffaloes for the cultivation of rice in the marshy lands and water logged areas. Aquatic breeds of rice grow well in the water-logged lands of the marshes, and they are harvested in autumn, i.e.

much before the winter monsoon. Water-buffaloes are happy to live in the marshes and their bulls pull the ploughs and the carts well.



Figure: A modern Marsh Arab Village

(Source: upload.wikimedia.org/wikipedia/commons/c/c1/Village_of_the_Marsh_Arabs.jpeg)

Indian Buffalo in Sumer

While the linguistic comparisons had not thrown any light on this Indo-Sumerian connection, recent DNA studies have clarified a lot. The three viz. the buffalo, the cattle and rice had migrated to Sumer from northwest India between 5000 BC and 4000 BC, giving rise to a new economy which led the region into the earliest phase of urbanization and subsequently larger state formation.

Marshall identified the water-buffalo in many Sumerian pictographs and texts, and also the Indian wild bull *Bos gaurus* in a tablet (No. 312) excavated from Jemdet Nasr near Kish (Marshall 1996:453). These tablets also clarified that the Sumerians used horse at least since 2600 BC as has been depicted in the pictograms (anšu-kur, the mountain-ass, or 'Iranian ass'; because mountain = Zagros of Iran in Sumer). Sir John Marshall mentions that the water-buffalo disappeared from Sumer at about 2300 BC, during the period of the King Sargon of Akkad (Marshall 1996:453). This can be expected because there had been a general trend of aridity in the third millennium reaching its peak at 2200 BC (4.2 Kilo Event). Water buffaloes cannot survive dry hot climates.

It is known by now that the water-buffalo was domesticated in India in the eastern part of the country which was kept wetter by the Bay of Bengal monsoon and the winter monsoon during the Early Holocene (Satish Kumar 2007; Pal 2008:275; Thomas 1995:31-2; Groves 2006). In fact there is "evidence that both river and swamp buffaloes decent from one domestication event, probably in the Indian subcontinent." (Kierstein 2004). It is at the very earliest Neolithic period that the water-buffalo had reached Mehrgarh as domestic animal (Possehl 202:27; J.F. Jarrige 2008:143; Costantini 2008:168). In northwest India, Mehrgarh received most of its rains from northern monsoon called the winter monsoon, which was strong then and hence the buffaloes could thrive at Mehrgarh as evident from the archaeology. In fact the Mehrgarh region was wet enough to support not only the water-buffalo, but also elephant, rhinoceros, swamp-deer and wild pig which prefer to live in the wetlands (Costantini 2008:168).

However at the Early Holocene, areas to the south of Kachi plain in NW India, and southern Iran received only scarce rains from the extremely weak southwest monsoon, which was not good enough for the survival of this water-adapted animal in this area. However subsequent to 5500 BC, when the south-western or the Arabian Sea monsoon built up strong, the southern Indus-Sarasvati region and the western coast of India started getting good rains from the improved south-western monsoon, the buffalo-pastorals arrived in the southern Indus Valley region too. From 5500 calBC

onwards we get bones of the hunted water-buffalo from Bagor in southern Rajasthan (Possehl 2002:32), and then the buffalo continues in the Harappan culture becoming very important in the Mature Harappa (Possehl 2002:63).

Archaeological evidence of water buffalo from Harappa region comes in the form of buffalo-horn motif of deities and depiction of this animal in the seals. We get such motifs from a pot recovered from Kot Diji dating to Early Harappan-mature Harappan transition (Possehl 2002:73), and from a broken terracotta cake recovered from Kalibangan dating to mature Harappa period. A Period II pot from Lewan depicts the horns of the water-buffalo (Possehl 2002:142-145). Rojdi too had domesticated buffalo (Possehl 2002:83). Buffalo bones have been found from the Ahar-Banas site of Rajasthan (McIntosh 2008:124).

But when and why the Indian buffalo-farmers migrated to South Iraq's province of Sumer is the real question. The time between 5000 BC and 4000 BC was full of torrential rains for West India region fed by the southwest monsoon. The sea level had reached higher than today's at about 5000 BC leading to the sluggish drainage of the rivers (Kumaran:22pdf). This was causing massive flooding and death on annual basis forcing the people of the region to migrate to the further west in search of lesser flooded lands.

The dominant presence of the Indian water buffalo in the Sumerian culture is enough evidence to say that the Indian farmer-pastoralists had led the transformation of this society by elite-dominance. Yet there is no evidence of the language change having taken place by this elite-dominance.

Vedic Influence

However the Sumerian divinity is entirely Vedic, with the gods and goddesses even conserving the Vedic Indo-European names (Whittaker 2009:127-140). Even where the name has been changed the story has stayed the same. In the Sumerian, Kur is the 'serpent' and it also means the 'mountain', which has stolen all waters in its mouth. The same word kur also means the 'land'. The serpent was killed by the warrior god to release the waters (Kramer 1961:76-80). This myth is clearly the Rig-Vedic myth of the demon Vṛtra who has stolen the waters within it lying over the mountain range, and is killed by the God Indra to release the trapped waters. This has been considered the metaphoric reminiscence of the Himalayan glacial having stolen the nature's waters and causing draught like conditions during the terminal part of the glacier period (Priyadarshi 2014b; RV 1.32.1-11; 4.28.1; 4.19.1-8; Bhagwan Singh 1987; also see Kazanas 2009). There have been also suggestions that the Sumerian script and astronomy too had been imported from India (Priyadarshi 2007).

[https://books.google.co.in/books?id=VKS_C45BSOAC&pg=PA127&lpg=PA127&dq="Milking+the+udder+of+heaven:"&source=bl&ots=uMom4-Y2nQ&sig=KhA8WZMOVY5q9-G9jk7KagHQqMk&hl=en&sa=X&ei=k5XTVIjrOoOXuATy4IHIAQ&ved=0CB8Q6AEwAA#v=onepage&q=%22Milking%20the%20udder%20of%20heaven%3A%22&f=false](https://books.google.co.in/books?id=VKS_C45BSOAC&pg=PA127&lpg=PA127&dq=)

Also: <http://www.sacred-texts.com/ane/sum/sum08.htm>

Indian Rice in Sumer

The cultivation of rice in the marshes of southern Iraq, which revolutionized the whole region about 4000 BC has been generally bypassed by the modern historiographers. However more and more people are now becoming aware that the Marsh Arabs which inhabit these marshes have been cultivating rice in Iraq since the rise of Sumer (Vinding 2004:326):

"They traditionally constructed artificial islands, made of layers of reed and mud, on which they constructed their homes using woven reeds. They fed the sprouting reeds to their water buffalo and

they used the dung of the water buffaloes for the fuel. They depended on fishing and hunting and they planted rice and tended date palms along the edges of the marshes.” (ibid).



(Source: <http://imgc.allpostersimages.com/images/P-473-488-90/21/2179/E9TCD00Z/posters/marsh-arab-village-iraq-middle-east.jpg>)

This same is true even today of many of the marsh-dwellers of Bihar and Bengal's Gangetic marshes. Not only that the ancient Mesopotamian buffaloes depicted in the seals have their native home in India.



(Bubalus arnee which lives in the wild in India and is the source for the domestic river as well as the swamp buffaloes)

The ancient Sumerian buffaloes as in seal are in fact from this stock. This has been demonstrated genetically too :



Although there has been linguistic identification of 'rice' from Assyrian cuneiform texts (Thompson 1939), the conclusive evidence of the presence of the Indian rice in Iraq comes from DNA studies. A recent DNA study of the Iraqi rice has clarified that there is exact match of some Iraqi rice DNAs with the Indian rice DNAs proving the migration of the Indian domestic rice to South Iraq. "Also, the SSR marker (RM1) results confirmed that Amber and Daawat were very closely related, which means that the origin of Amber might be come from Indian ancestors the same as Daawat variety." (Younan 2012). Agrama found in a worldwide sampling that 68% of the Iraqi rice was of the eastern Indian sub-species of rice named *Oryza sativa* aus. The rest was mainly aromatic which too originated in northwest Indian Himalayas (Agrama 2010:252). The eastern Indian rice *O. s. aus* grows best in marshes and water-logged areas. xxxx

It has become clear from the DNA studies that India was home of two important sub-species of cultivated rice and one wild semi-cultivated wild breed of rice. These are *Oriza sativa indica* and *O. s. aus* and the *Oriza sativa nivara* respectively (q.v.). It is no more held now that the Indian rice has come from China and the earliest rice-cultivating Pottery Neolithic sites of the world have been found in the Ganga Valley. From the Ganga Valley its cultivation reached northwest India (Hakra-Ghagghar) by 5000 BC or 5500 BC when the weather of NW India became humid enough (Tewari 2008; Shinde; Priyadarshi 2014a, 2014b).

But the Arabian Sea monsoon was very strong up to at least 4000 BC and it is likely that the Indus Valley, particularly the western part of it, was full of perennial floods for about 1000 years or more between about 5000 BC and 4000 BC. It has been even known that the Indus Valley Civilization started growing faster only after the rains had decreased and somewhat safer and drier climate had arrived by 4000 BC in the region. "Harappan urbanism emerged on the face of a prolonged trend towards declining rainfall", notes Madella and Fuller (2006:Abstract). Giosan also wrote: "adaptation to aridity contributed to social complexity and urbanization" (2012:E1693). Thus the early humid flooded phase was not conducive to high civilization formation, and thus it promoted westward migration of people in search of drier better places to keep their livestock and do farming.

It is during this flood time that many of the Indian farmers and pastoralists from the Indus-Sarasvati region migrated westward to the places like Sumer along with their caravans of buffaloes, cows, bulls, goats and rice to avoid being eliminated by the devastating floods. Sir John Marshall examined the Sumerian seals and tablets. He was able to identify the Indian bison (*Bos gaurus*) and the Indian water-buffalo depicted on the tablets at Jamdet Nasr (Marshall:453).

Recently a DNA study of the Marsh Arabs, that inhabit the Sumerian region today, was done for the purpose of identifying the Indian connection, if any, of this population of South Iraq. The Marsh Arabs are considered to have arrived there from somewhere else, and some legends suggest India. The DNA study of the Marsh Arabs residing today in the former Sumer region showed that majority of the ethnic group carries the Semitic specific male DNA, yet up to almost 8% can be traced to India. Indian lineages found in the Marsh Arabs included: L-M20xM76 (0.7%); Q-M242 (2.8%); R1-M269 (2.8%) and R2-M124 (1.4%): all together adding up to 7.7% (Al-Zahery 2011:13pdf; also p. 3pdf, Fig. 2). In an earlier study, Al-Zahery had demonstrated the presence of mtDNA U7 in Iraq, which is a marker of past Indian migration to Iraq (Al-Zahery 2003:10pdf).

It may be noted that the R1a-M17 is an Indian Y-DNA haplogroup (Underhill 2010), which is absent from the Marsh Arab DNAs, yet is present up to 8.4% in the Iraqi population (Al-Zahery 2011: Fig 2). In our examination it was inferred that the R1a migration had taken place out from Pakistan in response to the cold-dry weather of the 8.2 Kilo event (6.2 BC). This migration took place along the northern Iran which was wetter then due to good winter monsoon, and reached

North Iraq, but did not reach South Iraq. Hence the R1a is absent from the Sumerian region (South Iraq) yet present in the northern Iraq.

In addition to these there is the presence of J2*-M172 at the frequency of 3.5% in the Marsh Arab population. This male DNA lineage originated in the Uttar Pradesh in North India (Sahoo 2006; Priyadarshi 2010). It was associated with the earliest Holocene migration of the Mesolithic/ Neolithic interface era (say about 10,000 BC) out of India which came out with the *Mus musculus domesticus* species of mouse along the Iranian coast, and on reaching South Iraq split into two, one going north to Iraq and Kurdistan and the other reaching the Levant went further into the Mediterranean islands, Italy and the Balkans (Priyadarshi 2012). The association of J2-M172 with the spread of Neolithic (farming-culture) in the regions with good rainfall in Iraq, and also in the southern Europe, is well attested. "While J2-M172 has been linked to the development and expansion of agriculture in the wetter northern zone and is also considered the Y-chromosome marker for the spread of farming into South East Europe" (Al-Zaheri 2011:10pdf).

Thus we can see that about 8% of the male Marsh Arab population consists of DNAs of Indian origin. When these Indians went there, they were rich with the wealth of cattle and buffalo. They had the bags of rice seeds and the art of cultivating rice. From the female lineage or the mitochondrial DNA side, we find a larger migration from India to Sumer having taken place. Today it is represented in the Marsh Arab population by the presence of the mtDNA U7, R2 and M (Al-Zaheri 2011:12). One particular sample was found to have mtDNA of the type M33a2a (GenBank accession number: JN540042), which is found in the Uttar Pradesh state of India (ibid). Thus the migrations from India were not male exclusive, but they consisted more of the females. This is understandable, because women play a greater role in paddy cultivation as well as buffalo keeping. Once the Sumer civilization took off with the help of Indian water-buffaloes and rice cultivation in the South Iraq's marshes, males of some Semitic tribes arrived to live in the area, and married in this community. They could outnumber the original population. This can be noted today by the 72.8% frequency of Hg J-Page08 in the Marsh Arab population in the male lineage side (Y-chromosomal DNA). The scientific examination reveals that this population (J-Page08) expanded in the region at 4.8 years ago, or about 2,800 BC (Al-Zawahri: Table 2 on page 11). They had arrived there from the northwest (Al-Zaheri 2011:Fig 6). We know from the history that a powerful wave of the Semitic speaking people known as the Akkadian arrived in the region and settled just to the north of the Sumerian marshland establishing an empire about the middle of the third millennium. The Hg J-Page08 male DNA could have been the dominant lineage of the Akkadians. Hence we can say that the Semitic arrival, although male alone, was later than the Indian arrival to the region and it outnumbered the original Sumerians genetically and wiped them out linguistically.

See also:

http://www.amazon.com/Quest-Dates-Vedas-Comprehensive-Indo-European/dp/1482834251/ref=sr_1_1?ie=UTF8&qid=1423152727&sr=8-1&keywords=in+quest+of+the+dates+of+the+vedas

Tags buffalo, DNA, flood, India, J2b, kur, marsh arab, R1a, R2, rice, Rig Veda, Serpent, sumer, U7, uruk, Vedic

Categories archaeology, history

In Quest of the Dates of the Vedas: Preface

September 29, 2014 //

In Quest of the Dates of the Vedas:

A comprehensive study of the Vedic and the Indo-European flora, fauna and climate over the last 10,000 years in light of the information emerging from the disciplines of archaeology, archaeobotany, geology, genetics and linguistics

by Premendra Priyadarshi

Partridge

Preface

There has been a perpetual debate about the dates of the Vedas and the origin of the Indo-European speaking people. “Paradigms, especially old ones, die harder than Bruce Willis.” said James Adovasio.[1] There have been explosively new findings in archaeology and genetics, and also in the field of linguistics, having the capacity to rewrite an entirely different history of mankind. But the history as stated in the books and preserved in the minds of the authors has not changed the least.

There is a lot of information in the Vedas which pose the time limits for each of the four Vedic *Samhitas*. The *Rig-Veda* does not have wheat, rice, millets, lentil, date-palm (*Phoenix*). These appear in the *Yajur-Veda*. From archaeology, we know that wheat and rice both were well cultivated in the Ghaghar-Hakra culture in the fifth millennium BC (Shinde). Thus *Rig-Veda* must be before that time. Lentil was domesticated in West Asia, but it arrived in India in the Bronze Age. Its absence from the *Rig-Veda* and presence in the *Yajur-Veda* speaks a lot about the dates of the two texts. Date-palm arrived in the region in the mid sixth millennium (Costantini). Its absence from the *Rig-Veda* fixes the date of this text to before the sixth millennium BC.

The finger millet, which came from Africa to India in the late second millennium BC (Fuller) is absent from all the Vedas, clearly indicating that all the Vedas had been edited finally before this time. Contrasting this, the foxtail millet (*priyangu*), which arrived in India from China during the early Bronze Age has been mentioned in the *Yajur-Veda*, and not mentioned in the *Rig-Veda*. This finding would fix the date of the *Rig-Veda* before the Bronze Age and that of the *Yajur-Veda* contemporary with the Bronze Age.

The *Yajur-Veda* corresponds to the wet and warm mid-Holocene (5,500-2500 BC). And this is the reason why we generally get mention of those animals in the *Yajur-Veda* which lived only in the wet and warm climates, but cannot live in cold dry climates. Such animals are crocodile, tortoise, beaver, rhinoceros etc which are completely absent from the *Rig-Veda*. Rhinoceros, beaver and crocodile become absent again in the *Atharva-Veda* indicating change to the dry climate, and placing the *Atharva-Veda* after 1900 BC. However the domestic animals are present in all the periods indicating early domestication of the cow, buffalo, camel and horse.

The period of the *Sama-Veda* comes to 6000-5,500 BC, which was the transition period between cold-dry Early Holocene and the wet and warm mid-Holocene. The *Rig-Veda* gets placed in the cold and dry Early Holocene (8000-6000 BC) when the Sarasvati was connected with the Himalayan glaciers.

The DNA of the humans have revealed that once evolved in East Africa, man used the Arabian southern coast as a land-bridge to reach India and then all further human expansion and dispersal took place from there. This has been proved again and again that this was the sole route out of Africa. That the man came out from Africa through the Sinai land-bridge has been ruled out by an infinite number of DNA studies. Yet most of the authors, including even many of the geneticists refer to the out of Africa route as through Sinai to Middle East, and then trifurcating the way one leading to Europe, other to Central Asia and the third to Iran!

The human DNA studies have not been covered in this book, because I have already dwelt on that topic in my previous book *The First Civilization of the World*. Nor have I discussed here in this book the DNA studies of most of the domestic animals and plants, as they too have been discussed and analyzed in my earlier book as well as some of my journal articles. The conclusion of these DNA studies is that domestic mouse (*Mus musculus*), black rat (*Rattus rattus*), Shrew, cow (*Bos indicus*), pig, buffalo, sheep and goat were domesticated first in India, and then they migrated to the rest of the world. Some of these have been mentioned in this book.

The most powerful blow to the Aryan Invasion Theory came not from the study of the human DNA but from the studies of the horse DNA. The theory had rested on the hypothesis that the steppe was the home of the wild caballus horse Przewalskii, which was domesticated there and with the help of this domesticated horse the countries to the west (Europe) and to the south (India, Iran) were conquered by the Aryans of the steppe. However the DNA examinations of the horses have contradicted this view. They have revealed that the Przewalskii was not a member of the caballus horse species at all, but it was an independent species with two chromosomes more than the true horse—*Equus caballus* (or *Equus ferus f. caballus*). Other studies came out with the conclusion that the DNAs recovered from the archaeological remains of the domestic horse found in Central Asia and western steppe were all of the horses originating in China or anywhere else but not in the steppe itself. Frachetti demonstrated that the domestic horse and riding became features of Central Asian nomads in the Common Era, and not before that. Levine clarified that the horse bones recovered from the steppe and Central Asia belonged to the hunted horses, not the domestic horses.

There is enough evidence generated in literature about origin of the light race horses from the Indian *Sivalensis* (q.v.). Nearly all of such evidence had been generated by the benevolent generation of the English and other Western scholarship which lived before the Second World War. Current generation of scholars, whether Indian or Western, is more interested in popularity and important positions, and concern for the truth has become uncommon. Thus, whenever DNAs of the domestic horses (or even sheep, goat and camel) of the world have been compared, the Indian samples have been left out.

As such, there is no sound evidence of the origin of the domestic horse from the steppe. Thompson found that either the European wild horse Tarpan or the Mongolian wild horse Przewalskii was the ancestor of the heavier built daft type horse of Europe, and that the lighter race horses of the south like the Arabian horse originated from the *Sivalensis*. By this time it has become clear that the Tarpan was the ancestor of the European daft horse, not the Przewalskii.

The DNA studies of the living as well as the archaeological horses found that there were centres of local horse domestication in Europe older than the supposed presence of the domestic horse in the steppe. Another development was the collapse of David Anthony's Dereivka horse of 4200 BC. The

claim was retracted by the author himself after the radiocarbon dating of the Dereivka horse's skull proved him wrong.

The reason why there was a sharp decline in the number of horses after 6000 BC in India is climatic. The mid-Holocene wet climate converted the Indus-Sarasvati region from grassland to a dense forest region making it inhospitable to the wild horse and camel, as well as the ostrich and giraffe. Hence the Indian wild horse *Sivalensis* became extinct from the wild existence soon after 6000 BC. The regional wild horses either died or migrated to the Thar region in India and also to Iran and South Central Asia (Turkmenistan, Tajikistan). Some of the light Indian horses which had adapted to the high altitudes of the Himalayas too survived this period. But over the time their mares were captured and assimilated into the domestic stock, and they too became extinct from the wild.

During 6000 BC to 2000 BC, and even after that, the Indus-Sarasvati region had only domestic horses, which dwindled greatly in number because of the Vedic ritualistic slaughter of the horse. This is the why we get so less horse bones in the Indus Valley Civilization. But Kazanas pointed out in his lecture delivered in the Patna University in April 2013 that the horse bones do not increase in Indian archaeology even up to 800 BC; and there is no archaeological evidence of any increase in the number of the horse bones in Indian archaeology at about 1500 BC or any time in the second millennium BC. The animal got strongly associated with the burial-ritual and its graphic depiction probably became a taboo. This could be one of the reasons for its not having been depicted in the Indus seals.

When the DNA studies ruled out any human migration from Europe, Central Asia or West Asia to have arrived into India between 8,000 BC and 1000 BC, it was expected that the Aryan Invasion hypothesis would be retracted. However, it did not happen. The argument was changed from "invasion" to "language-conversion". The languages of North India and Iran were changed under the powerful rule of a handful of invading Aryans who have not left any mark of their genes on India, yet were able to convert the whole of North India into Indo-European speaking within a couple of centuries, at a time when there was no mass media, a very low literacy rate and very restrictive travelling conditions. This is a very far-fetched imagination. This type of language change did not happen in north India during the 600 years of rule by the Persian speaking elite Muslims in India. Nor did it happen in Europe during the period of the Roman Empire or in Spain during the long Arab rule in the country.

Often self-contradictory stands have been taken by people when it comes to the history of India. Thus, Peter Bellwood wrote that the elite-dominance leading to language change cannot operate over a very large population. However when the issue related with India, he supported the hypothesis that the Aryans from Turkey arrived into India with farming, and changed the language of the northern part of India under their dominating farming skills.

There was the need to produce a robust multi-disciplinary work to clarify the confusions, false beliefs and wrong impressions prevailing in the field of Indo-European history. For the purpose, I persuaded and talked with a large number of learned people in India. Failing in my effort, I decided to do the team work alone. By this I mean, I had to myself study the basics of all the disciplines involved and make in-depth examination of the available facts, arguments and possibilities.

The whole philology of the animal and plants having bearing on the homeland issue has been re-examined in this book. It has been established in this book on the basis of philological examination

that lion, tiger, mongoose, camel, crab, oyster, conch-snails, carp (fish), snakes (including even the python), frog, tortoise, chameleon and lizard lived in the original home of the Indo-Europeans. These animals are characteristically Indian or southern in distribution and presence of the Indo-European name for these animals proves that the Indo-Europeans lived at a place where these animals were found.

The Lachs Theory of Thieme (1951) has been examined here and it has been found that words *lachs* etc for “salmon” are actually words from the substrate language of Europe and Central Asia and the cognates are distributed up to Japanese and even North Amerindian languages. Hence, these words are certainly not Indo-European, and the Lachs Theory should not have been launched in the first place. Thus the Lachs Theory can be discarded now onwards in the Indo-European studies.

That the plants mulberry, opium, *Calotropis*, lotus, *Acacia* and rose-apple (Indian plum) grew in the homeland has been made evident by the philological survey done in this book. These are typically Indian plants. However there are some European plants which have been claimed by Witzel and the other authors to have been part of the philologically deciphered Indo-European flora. The examination of such claims reveals that there was gross manipulation of facts for achieving such conclusions. The sections on beech and oak demonstrate how scholars have concocted and lied. However attempt has been made in this book to identify the Vedic names of those plants and animals which existed in India in the Early Holocene dry and cold climate but became extinct once the region became wetter and warmer, and are not found in India today except some of them in the Himalayas.

I have tried not to repeat the arguments of the earlier authors like Nicholas Kazanas, B.B. Lal, S.P. Gupta and Koenraad Elst. However if anything in the argument needed to be explored further that has been done. The fundamental bases of some of the arguments of Parpola, Witzel, Thieme etc have been examined and found to be wrong. Copper toy-chariots have been found from the Indus Valley Civilization (Mackay, Vats), although denied by these authors. There is enormous genetic and cultural evidence of dispersal of Indians in all direction during the Bronze Age, which cannot be accounted for by the hypotheses of the AIT authors.

Although the language used in the Vedas is nearly the same, the content covers information of periods separated by thousands of years. Obviously it will have to be accepted that the same contents were given new language as the time changed. Thus the texts were regularly edited for the language change taking place with time within the northwest India's Indo-European linguistic stock. However it is possible that no further editing has been done after 1300 BC, the date of the last of all the Vedas (*Atharva-Veda*).

It is easier and better to accept that the language of the texts were changed with time, rather than to say that the two thirds of such a large and populous sub-continent as India changed its language at 1500-1300 BC. Both are assumptions, but which one could have happened more easily is the deciding point—language change of the entire population or the gradual language editing of the sacred texts as time passed. After all it was an oral tradition in which the language changes take place even without being discernible to the speakers.

In this entire book the word “Veda” has been used to imply the respective *samhita* portions of the four Vedas only. The flora, fauna and climate of the four Vedas are all entirely different from each other as if they describe or pertain to four entirely different periods of time. Such information needed to be correlated with that available from the recent studies in archaeo-biology and geology.

Geology has recently clarified that the Sarasvati River lost her connection with the Himalayan glaciers at about 8900 BP or about 6950 BC. This problem can be only resolved if we date the *Rig-Veda* to about 6000 to 8000 BC. That was the time when no tiger lived in that region although the lion lived because it was a grassland ecosystem. Consistent with this information we find that there is no mention of the tiger in the *Rig-Veda*. Historians have ignored the Vedic texts completely while writing about the history of the Vedic period. The *Rig-Veda* depicts all three modes of life, hunter-gatherer, pastoral and farming. This pertains to the dawn of the Neolithic period.

The reports of the presence or absence of the pollens of the various trees have come out in the last ten years in many scientific journals. They have been thoroughly exhausted here to provide a picture of the different trees or types of ecosystems present during the various eras of the Holocene in India, Iran, Central Asia, the steppe and North and South Europe. This picture explains why some names of certain plants and animals survived in either North Europe or South Europe but not in both.

The survival of the names of the plants and animals depended on the presences of such animals or plants throughout the route of migration as well as at the source and the destination. Such climatic conditions were present in which millennium has been determined in this book on the basis of the recent palynological reports. That gives us the precise date of migration to any particular country or region. This method has been utilized for the first time in this book.

Attempt has been made to identify the some of the animals and plants mentioned in the *Rig-Veda* or in the later Vedas but which no more exist in India. Or if at all they exist, they exist in the high reaches of the Himalayas and have slipped out of the popular memory. Such plants include the *soma*, *suparṇā*, *kadru*, *kuṣṭha*, *devadāru* etc. Such identifications will help the medical field as many of such plants have been mentioned in the Vedas as the cure of some serious diseases like tuberculosis.

Although I believe that the word Aryan has been abused too much, and the phrase ‘original Indo-European speakers’ should be used instead, yet I have used it often because of its brevity and handyness. I do suppose that that was an original language for all mankind, and its relic evidence is printed on all the languages of the world (Bengston and Ruhlen). Thus the family tree of the languages will also emerge parallel to the DNA family trees. Matrilineal trees (mtDNA) would reflect more exactly the language tree. There was a language which was ancestral to all the Indo-European languages, although it was not the same as the suggested PIE forms, but in many ways similar. It cannot be the same because of the limitations of the human minds to visualize the truth. But this language did not come in isolation from the heaven, and it resembled the other languages in its neighbourhood, like the Proto-Munda, Proto-Dravidian etc. In this book, the word Veda has been used to denote the respective *Samhita* portions only.

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[1] My friend Stephen Oppenheimer had once cited this, and I owe this quote to him.

<http://www.amazon.com/Quest-Dates-Vedas-Comprehensive-Indo-European/dp/1482834251>

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