Human palaeontology and prehistory (Palaeopopulations, palaeogenetics, migrations)

After Last Glacial Maximum: The third migration

Après le Dernier Maximum Glaciaire : la troisième migration

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A B S T R A C T

A critical analysis of "Real World" data concerning the genetic origins of people, archaeology and palaeoclimatic conditions, demonstrates possibilities of population migration for third time in ancient history, from East to West after Last Glacial Maximum (LGM), which gave the foundations of modern human civilization.

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R É S U M É

Une analyse critique des données du *Real World* relatives aux origines génétiques des hommes, l'archéologie et les conditions climatiques démontre les possibilités d'une troisième migration de population dans l'histoire ancienne de l'humanité de l'est vers l'ouest, après le Dernier Maximum Glaciaire (DMG), troisième migration qui a donné les fondements de la civilisation humaine moderne.

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1. Introduction

Does archaeological antiquity present evidences of foundation of civilization in South Asia starting between 45,000 and 28,500 years ago? Refined stone blades, stone architecture, beads, red ochre paint, ostrich shell jewellery, and religious shrines make the characteristics of an earliest culture before any substantial modern human existence in the West (Petraglia et al., 2005).

Between 35,000 and 25,000 years ago, archaeological findings of the Upper Palaeolithic period in Europe also shows some aspects of prehistoric culture at a site called Aurignac in the Haute Garonne region of France hence, the name the Aurignacian culture.

The Venus of Hohle Fels, found in a cave at Schelklingen in Baden-Württemberg in southern Germany, is supposed to be from this culture.

Two major climatic conditions were the most consequential for establishing demographic affiliation with present people in Eurasia, the Ice age around 70,000 years ago and the Last Glacial Maximum (LGM) around 20,000 years ago.

Palaeoclimate determines circumstances for antediluvian relocations and demographic diffusion of mtDNA genes, leading eventually the Out-of-Africa migration, during short openings avowed by deviations in sea levels and climatic settings (Forster, 2003).

The interdisciplinary investigation presented here is without Out-of-Africa extrapolation. From the view point of present Real World Genetic, palaeoclimatological and archaeological data, it is found, in fact, that the ancestors of ancient tribes and nomads of northwestern regions of South Asia wandered into West, central Asia and further west for the third time in prehistory, between 15,000 and 5,000 years ago, carrying cultural foundations of farming and languages.

2. Eurasian demography and Last Ice Age

Since many decades, the prevalence of archaeological investigations was concentrated and still continuing on the European continent to understand many aspects of Last Ice Age. This has been the subject of multiple field studies. Subjects like Würm glaciation, eco-cultural niche modeling, human diversity in Europe, Neanderthal and Modern Humans, climate variability off the western Iberia, hominin evolutionary ecology, Palaeolithic radiocarbon chronology, Devensian Late-glacial environmental changes in Britain, Hiatus or continuity, Paleolithic and Mesolithic, refugial debate, postglacial recolonization, Upper Palaeolithic settlement of Iberia, western Europe in Dryas I, a quarter-century of research on the Solutrean, genetic legacy of Paleolithic *Homo sapiens* in Europe, Younger Dryas climate in Europe, warming phases, the radiocarbon evidence for the human recolonisation, Upper Paleolithic Solutrean culture, caves, palimpsests and dwelling spaces, and many other features (Banksa et al., 2008; Bocquet-Appel and Demars, 2000; Caramelli et al., 2003; Charles, 1996; Davies and Gollop, 2003; De Abreu et al., 2003; Foley, 2002; Gamble et al., 2004; Bailey and Galanidou, 2009; Pettitt et al., 2003; Renssen and Isarin, 2001; Richards et al., 2000; Semino et al., 2000; Smith, 1964; Straus, 2000a, 2000b; Straus et al., 2000; Street et al., 2001; Terberger and Street, 2002; Toroni et al., 2001; Van Andel, 2002; Walker et al., 2003; Weniger, 1990; Willis and Whittaker, 2000). However, the persistent debate continues about human survivors during whole of Last Ice Age and search for possible genetic association with the present European population.

Explorations of postglacial population expansion in Europe and archaeology gave foundations of new subject called "Archaeogenetics" (Renfrew, 2001; Richards and Macaulay, 2000). Questioning genetic structure, whether there were farming migrants or cultural diffusion or even both, after last glaciation and comparison of early genetic
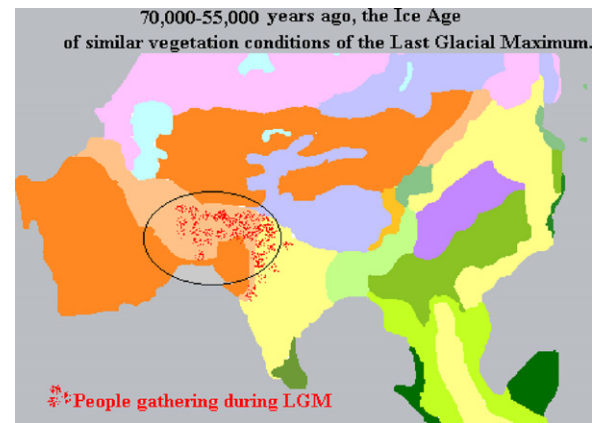

Fig. 1. The period 70,000–55,000 years ago, the Ice Age was similar to LGM. 70,000–55,000 years ago, the previous ice age was about similar vegetation conditions as of the Last Glacial Maximum, 24,000 years ago (Adams et al., 1999). The black lines and red spots are by the author.
Fig. 1. Carte de la période entre 70 000 et 55 000 ans : le précédent âge glaciaire avait des conditions de végétation similaires à celles du Dernier Maximum Glaciaire, il y a 24 000 ans (Adams et al., 1999). Les lignes noires et les points rouges sont de l'auteur.

information, assumed to have arrived during Upper Paleolithic (Cavalli-Sforza et al., 1994).

The demographic transition has direct effect from topographic and vegetative nature of the regions. The following analysis comprises the description of vegetation of LGM epoch, based on palaeoclimatological research.

Eurasia during LGM, the map in Fig. 1., shows that large area of extreme desert conditions existed across central Asia (dark red), surrounded by semi-desert (light red), under conditions much colder than the present-day (the red spots in black line circle on the map are only indicating an area around Indus region where people could have arrived from west and northern regions).

In South Asia, rainforest (darkest green) retreated and was replaced by grasslands (yellow) and monsoon forests and woodlands (lime-green). Scrub and open woodland (lightest green) probably existed in presently moist forest climates of Bangladesh and SW China.

In the Northwest of India, the only exception is Kashmir, which was (possibly) rather moister with steppic vegetation, perhaps fitting in with the pattern of moister conditions also seen in northern Iran (Adams and Faure, 1997).

Discovery of nature by humans is most parsimoniously described. Even before LGM, some groups in South-Southeast Asia had discovered the abundant variety of Nature. Between 50 and 20,000 years ago, there were few groups, perhaps, who discovered literally a "Natural Paradise" in regions of Kashmir, northern India, and many other parts of South Asia. Even birds and animal life must have introduced to children the fruits of nature.

Archaeological investigations confirmed the farming and plant domestication in South Asia by indigenous peoples (Fuller, 2003, 2006a,b). "...*agriculture began between 16 and 20 times world wide, but it could be a few more than this. I have posited a minimum of 3 centers of plant domestication in South Asia (Middle Ganges, Gujarat, South India), but*
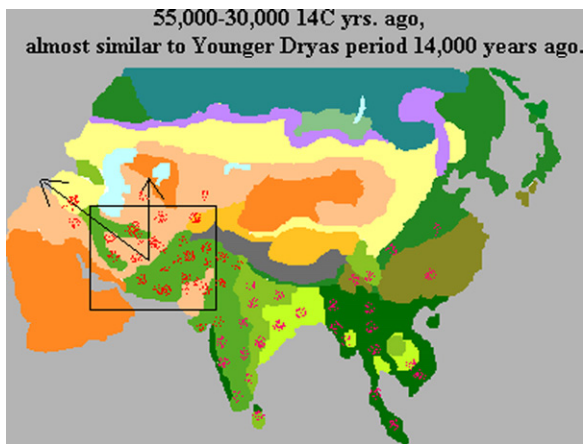
Fig. 2. The period 50,000 to 30,000 years ago. Map based on http://www.esd.ornl.gov/projects/qen/euras(1_gif). The black lines and red spots (scattered population) are by the author.

Fig. 2. Carte de la période entre 55 000 et 30 000 ans, période presque similaire au Dryas récent, il y a 14 000 ans. Les lignes noires et les points rouges sont de l'auteur. Carte d'Adams d'après http://www.esd.ornl.gov./projects/qen/euras(1_gif.fr).

Fig. 3. Map from Adams et al., 1999: where did people go during Last Glacial Maximum? The black line circle is by the author.

Fig. 3. Carte d'Adams et al., 1999 : où les humains d'Asie centrale à l'aridité extrême, ont-ils été pendant le Dernier Maximum Glaciaire ? La ligne noire est de l'auteur.

this could in fact be 5 (plus Orissa, plus upper Yamuna/upper Ravi)" (Fuller's comment).

The LGM map of Fig. 2 shows grasslands in South Asia, woodlands, forest with tropical monsoon areas in northeastern India, South India and all over Southeast Asia. Eurasia, 55,000–30,000 yrs, was nearly under the same climatic conditions as at the time of Younger Dryas period 14,000 years ago.

It seems history of population migration repeated itself for the same reasons.

Between 70,000 BP and 50,000 BP, modern humans did not move towards west because of Ice Age. Continuous extreme cold and aridity made the Fertile Crescent passage inhabitable. Humans stayed for 30 thousand years, since their arrival 80,000 years ago, in Indus region and South Asia, before moving west (Oppenheimer, 2005).

The first migration took place 50,000 years ago when humid and temperate changes, made the Persian-Asia Minor landscape livable. People reached regions of Turkey, the Levant, finally to Bulgaria and Southern Europe.

The second migration 40,000 years ago is suggested from Northwest India, through western Kashmir then to central Asia. From central Asia, people moved westward from the Urals to western Russia arriving in the Czech Republic and Germany (Oppenheimer, 2003, 2005).

Comparable events of migrations took place for the third time in history, having relatively same rationale of extreme climatic circumstances, all through LGM and after.

During Younger Dryas, around 15,000 yrs, the whole of South Asia, the region of Northwest India and western region covering Iran appear to have developed considerable vegetation and again this region was occupied by large number of people, in diverse tribal groups. The scenario is analogous to the events of 50,000 to 30,000 years ago.

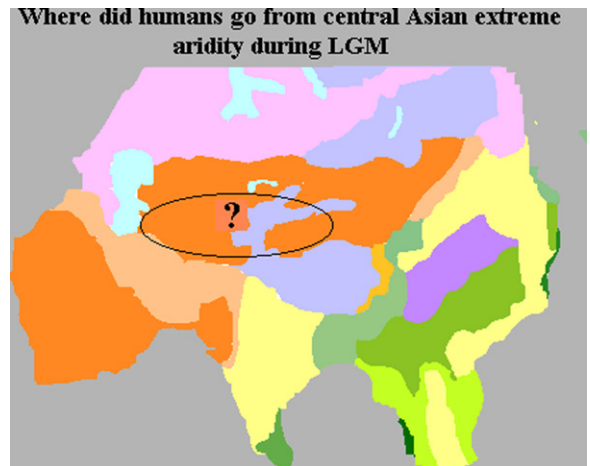The LGM vegetation shows grasslands in India, woodlands and forest with tropical monsoon areas in northeastern India, South India and all over Southeast Asia. In the northwest of India, the only exception is Kashmir, which was (possibly) rather moister with steppic vegetation, perhaps fitting in with the pattern of moister conditions also seen in northern Iran (Adams and Faure, 1997).

There is no clear data of central Asia under extreme aridity during LGM. This raises most important question concerning human genetic history. Where did people go during that calamity (Fig. 3)?

A scenario depicted by some that previously populated by Upper Palaeolithic game hunters in vast central Asia, was completely deserted during LGM, except, perhaps few survived in one refuge, in southern Siberia. There appears to be a general agreement about genetic time scale of Europeans, having three quarters of their ancestors came between 15,000 and 7,500 years ago (Fig. 4). Another hypothesis predicted a contribution from Ice-Age refuge in the Basque region of southwestern Europe (Oppenheimer, 2006).

> *"In northern and central Europe, the record is perhaps detailed enough to suggest a complete or almost complete depopulation during the Younger Dryas".* (Adams and Otte, in press).

Almost 90% of Europeans are of the periods between Late Pleistocene and Early Holocene is the unambiguous consanguinity, validating the third migration of people from east, presented in this paper. The remaining 10% are statistical representations of age estimation, corresponding Upper Palaeolithic period, derived from the Out-of-Africa theory.

Recent results questioned the re-peopling of Europe by the example of the M173 Y-chromosomal haplotype in Basques and the British. The Paleolithic ancestry common to European populations does not support Basques as the focus of major population expansions (Alonso et al., 2005).
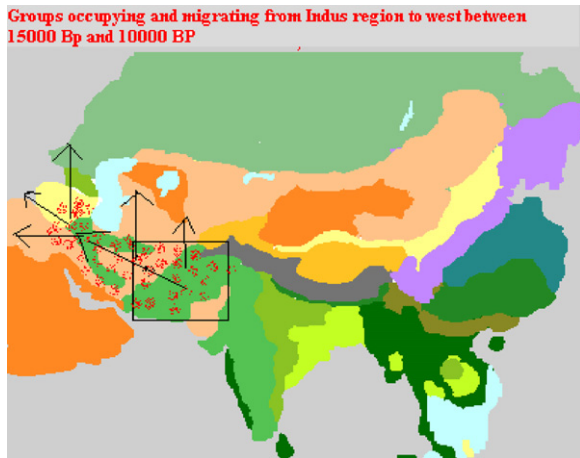
Fig. 4. Map which shows group occupying and migrating from Indus-Persian region to west between 15,000 and 10,000 BP. Map based on Pr Adam's http://www.esd.ornl.gov/projects/gen/euras(1_gif). The black lines and red spots are by the author.

Fig. 4. Carte d'occupation et de migration de groupes de l'Indus et de Perse vers l'ouest entre 15 000 et 10 000 BP. Les lignes noires et les points rouges sont de l'auteur. Carte d'Adams d'après http://www.esd.oml.ov/projects/qen/eurast(1_gif.fr).

3. Genetics

The majority reconstructions of human population genetic history are based on Modern DNA samples (especially the non-recombining mtDNA and Y chromosome loci or gene trees).

One of the well-acknowledged disconcerting aspect in human population genetic history is that the age estimates are assumed on numerous invalid hypotheses involving large number of mutations in historical human constitution. However, that uncertain information is taken as basis for assessment of other records (Wells et al., 2001).

A compilation of DNA procedure, shared with new investigative methods and current palaeoclimatic, archaeological and geological studies give important insight into the distribution of genetic diversity around the world.

According to population genetics, no second origin of People was found other than in African continent, which comprises the highest intra-population diversity in phenotypic measurements (Manica et al., 2007).

A Bayesian analysis (Bayesian inference provides a logical, quantitative framework for gathering new data to address remaining questions, then update and refine perceptive to integrate new and old data applied in a multitude of scientific investigations) of the data points to an origin of our species from Out-of-Africa 51,000 BP, other than the African model, the possibility of interbreeding with earlier *Homo erectus* is refuted (Fagundes Nelson et al., 2007).

The Hardy-Weinberg principle is one of the most important concepts in population genetics.

This principle states that both allele and genotype frequencies in a population remain in equilibrium from generation to generation except if definite disturbing influences are established, such as non-random mating, mutations, selection, limited population size, random genetic drift and gene flow. One or more of these "disturbing influences" are always in effect, which makes Hardy-Weinberg equilibrium improbable in nature. Nonetheless, the idea of genetic equilibrium is a essential principle of population genetics that provides the basis for measuring genetic change (Crow, 1999; Edwards, 1977; Emigh, 1980; Ford, 1971; Guo and Thompson, 1992).

The restrictions occur from the information that each individual has thousands of ancestors in a millennium. We observe vast unresolved disparity of the genome fraction preserved in an inheritor from a particular ancestor, with an irregular anticipation bisecting each generation. Only half of male or female genes are passed further by the ancestor to the next generation. The proportion of hereditary genes from the Most Recent Common Ancestor (MRCA) turns out to be a smaller amount at every following generation. As a result, genetic tests can access only a fraction of this inherited material. In reality, an individual's DNA information may have lost completely within 10 to 20 generations, which might have been specific to a particular ancestor. (Hey and Machado, 2003). Total ambiguity surrounds the conclusions drawn on ancestry to foresee the tested individual's genotypes at an unproven locus (a locus – plural loci – supposed permanent location on a chromosome, a biomarker that occupies one or more genes).

Empirical data on population genetics is being published in large number of research papers concerning origins and migrations of people since a decade. However, in almost any of these papers, not much attention is given on difficulties encountered in estimating dates of origins and simulated methods applied to extrapolate the relation between present-day DNA samples and completely missing very large extent of DNA information, most significantly of the periods between 25,000 and 15,000 years ago during LGM.

Population genetics has been a critical issue, raising apprehensions about methods applied in the study. With more and more inventive mathematics, experts seem to spend more time for such theoretical models, without actually testing the representations against empirical data (Wade, 2005).

European population anthology of male genetic markers, demonstrated many levels of configurations (Malaspina et al., 2000; Rosser et al., 2000; Semino et al., 2000). Conversely, many authors have discovered multiple scenarios of geographic distribution of Y markers on European continent. Earliest arrival diversity, is reported to be of Paleolithic period, followed by some migratory patterns seen as re-population of Mesolithic period, spread out of refugia, during later part of the LGM (Achilli et al., 2004; Karafet et al., 1999; Pereira et al., 2005; Rootsi et al., 2004; Semino et al., 2000; Tambets et al., 2004; Toroni et al., 2001; Underhill et al., 2001; Wilson et al., 2001).

This remains as a major conjectural aspect of LGM survival data, based on archaeological evidences. The genetic bottleneck during LGM is more pronounced than extrapolation of real world data without any information from human fossil of that period, stretching almost 10,000 years in Europe.

"...I am not sure we have enough resolution to tease apart events that happened at the beginning of Holocene warming and deviations such as the Younger Dryas. That requires slicing the sausage quite thinly..." (Underhill, 2006).

The next migration, which is effectively the third migration from east, attributed to farming developments of Neolithic periods diffused out of Near East-Asia Minor into Europe (Ammerman and Cavalli-Sforza, 1984; Barbujani et al., 1994; Cavalli-Sforza et al., 1994; Chikhi et al., 2002; Dupanloup et al., 2004; Haak et al., 2005; Pinhasi et al., 2005; Roostalu et al., 2007; Sokal et al., 1991) which is also supposed by some authors, of pre Neolithic movements (Chikhi et al., 2002) and remains a frequently disputed subject.

Reconstruction of population migrations based on Y-chromosomal spread in its varied multiplicity in the world is being investigated since last few years (Jobling and Tyler-Smith, 2003; Underhill et al., 2001). Major advancements in this field were made to come to closer possible affinities of diverse marker distributions with continental perspective.

Description of two DNA markers, M173 and its descendant M17 strongly suggested, not only of European Origin but also supports the linguistic-farming invasion-migration hypothesis through findings of density percentages of M17 marker in North and South India (Wells, 2002). That was in 2002 or little earlier.

That scenario has changed completely ever since.

In 2003, Oppenheimer completely refutes earlier Aryan theories. M17 is not only more diverse in South Asia than in Central Asia but diversity characterizes its presence in isolated tribal groups in the south, thus undermining any theory of M17 as a marker of a "male Aryan Invasion of India" (Oppenheimer, 2003).

Further investigations show the micro-satellite variation of the antiquity of M17 with regional differentiation in the majority of Indian haplogroups exceeds 10,000 to 15,000 years. The data do not support models that appeal to a distinct recent genetic contribution from central Asia. Associated micro-satellite analyses of the high-frequency R1a1 haplogroup chromosomes signify independent recent account of the Indus Valley and the peninsular Indian region. An Early Holocene development in NW India (including the Indus) added R1a1-M17 chromosomes both to the central Asian and South Asian tribes (Sengupta et al., 2006).

The ancestry of 10 to 15,000 years, precisely the dates of mid-LGM and Younger Dryas, makes M17 the early, major patrilineal contributor, radiating towards west and northwest from Indus region.

Astonishingly, the latest Y-STR analysis proved to be most ancient of R lineage: The Time to the Most Recent Common Ancestor (TMRCA) of the individuals carrying R1a1 Y-chromosome South Asia is estimated around 32,000 years ago (Trivedi et al., 2007).

Comprehensive phylogenetic examinations of diverse population groups and observed maximum frequency (up to 72.22%) of Y-haplogroup R1a1* in Brahmins in South Asia reconfirmed the autochthonous origin of R1a1 lineage in India (Bamezai Rameshwar et al., 2009).

Scrutiny of R1a1* in diverse tribal groups illustrates existence of Y-haplogroup R1a* in associates and comprehensive phylogenetic examinations of the pooled dataset of 530 Indians, 224 Pakistanis and 276 central Asians and Eurasians of R1a1* haplogroup endorsed the autochthonous origin of R1a1 lineage in India and a tribal link to Indian Brahmins (Sharma et al., 2009).

Latest results of large-scale study confirmed that R1A1 associated STR range, the R1a1a*(xM458) chromosomes, is of the maximum multiplicity amid the populations of the Indus Valley, having coalescent times above 14 KYA. The implicit deficiency of M458 chromosomes exterior of Europe corroborate against any significant patrilineal gene flow from East Europe to Asia, as well as to India, since the mid-Holocene (Underhill et al., 2010).

Recent results questioned the re-peopling of Europe by the example of the M173 Y-chromosomal haplotype in Basques and the British.

The Paleolithic ancestry common to European populations does not support Basques as the focus of major population expansions (Alonso et al., 2005).

"The detection of rare R1-M173* and R1a-SRY1532 lineages in Iran at higher frequencies than observed for either Turkey, Pakistan or India suggests the hypothesis that geographic origin of haplogroup R may be nearer Persia" (Regueiro et al., 2006).

The re-population of northern Europe also appears to have characteristics of new arrivals from east around 12,000 or later years ago. Study of hg N with subclade N3, N2 subclusters N2-A and N2-E (Finno-Ugric) is suggested as westward expansion toward Northwestern Europe from an ancestral East Asian source of Paleolithic pedigree (Rootsi et al., 2007).

4. MtDNA haplogroups

Reconstruction of European gene pool by mtDNAs, during late Upper Palaeolithic, around 14,000–11,000 BP, shows that H, V, I, W, T, K are in large percentages and again during Neolithic period around 8000 BP, new arrivals of J, H, T, K were added (Renfrew, 2000). This clearly, undeniably presages the third migration expounded in this study.

Ancient MtDNA lineages are in South Asia, of which, above 90% of observed descendents are in European maternal lineages. The origins of these lineages are of the periods earlier than 50,000 BP in South Asia. Haplogroup U is also most rich mtDNA diversity in India as it is in Europe (Kivisild et al., 2000).

Although the MtDNA Haplogroups H, J, K, and T in India are recent inputs from West Eurasian, the percentage is considered insignificant to Indian gene pool. The period of these arrivals are of 10,000 BP or earlier. A possible retreat from LGM into southern region can be envisaged.

Comparisons between archaeological findings and allele frequencies at protein loci suggest that most genes of current Europeans descend from populations that have been expanding in Europe in the last 10,000 years, in the Neolithic period (Chikhi et al., 1998).

It is now regarded that India provides mtDNA ancestry in large part of the multiplicity lineages inherited by

Europeans. Y-chromosomal lineages appear to be much closer in Europe than mtDNA variations (Kivisild et al., 2000).

Indeed, the Late Pleistocene and Early Holocene arrivals in Caucasus and Asia Minor are mostly of Y- chromosome, G-M201, L-M20, R2, L1-M76, H-M52, K-M9, K2, M17 all of Indus Valley and South Asia origin (Table 1).

L-M20 appeared in Kashmir or northwest and northern part. They were the descendants of K-M9, which arrived or was born in India much earlier than 40,000 years ago, and had a lifetime stretched around 10 to 15,000 years in the same cold regions of Kashmir, Hindukush and Pamir knot, the northern side of Kashmir.

Later studies revealed certain discontinuity from observed data for the peopling of southern Europe. Haplogroup J reported as major contributor to Caucasus region and Greek population from the Levant. The subgroups J1 and J2 in the Levant are attributed at the advent of Neolithic farming culture (Di Giacomo et al., 2004).

G-M201 is originated in the Indus Valley between 10,000 and 20,000 years ago. G-M201 is also considered as the farming group (Dr Wells).

Haplogroup G-M201 widely distributed in Eurasia. It is most frequent in the Caucasus, and is also found in Anatolia-Asia Minor, the Middle East, the Balkans, and Italy (Cinnioĝlu et al., 2004).

The subgroup of G, Haplogroup G2 is of large percentage in the populations of Anatolia, the Caucasus, and Europe. G2 and G1, descendents of G have evolved little after the arrival of G-M201, probably around 10,000 years ago. Haplogroup J2 is also generally associated with the spread of agriculture from Anatolia. Haplogroup J with subclades J1 and J2, haplogroups G1, G2, L, and H, R2 spread in varied regions of Anatolia, Caucasus and Europe (Cinnioĝlu et al., 2004). Recent study shows the TMRCA[1] for R2-M124 by Y-STR age estimation to be of 39,647 years old (Trivedi et al., 2007).

The percentage of Y-chromosomes in Iraq is much higher (30%) in Iraq than the mtDNAs (9%). Their arrival in this region is expected from Indus-Persian corridor of Late Pleistocene and Younger Dryas or even Early Holocene periods. The diverse share of distant genetic contribution under pragmatic approach for the mtDNA and the Y chromosome, points toward the gene flow to Asia Minor region largely by males (Al-Zaherya et al., 2003).

The temporal affinity of these markers provides evidence of large influence, not only of a demographic type but also associating with diverse activities on those landscapes. Another carrier, Haplogroup L-M20 (with subclade M11) is of Indian pedigree, with a small percentage of this marker relocated into Anatolia, Mediterranean and Caucasus region. H (M52) line of descent of high frequency in India, appeared between 20,000 and 30,000 years ago on Indian subcontinent, and later was found in Middle East, Anatolia. Further studies revealed a deep coalescence age estimate of H is of Pleistocene origin in South Asian pop-

ulations, approximately 45–50 K years ago (Sahoo et al., 2007).

Descendents of R1b related to haplogroup R1a are common in Eastern Europe, central Asia, and India. Both are descended from R1; the haplogroup R1a is now called M17.

The higher frequency of R1a1-M17 lineages in eastern Turkey is consistent with an entry into Anatolia via the Iranian plateau where the associated variance is appreciably higher (Quintana-Murci et al., 2004).

Some percentage of R1a1 is found among populations of West Asia.

Expanding from Turkey, G and J-12f2 lineages to Egypt (Cinnioĝlu et al., 2004) reached around 10,000 BP including M17. This is expected from earlier introduction of Neolithic ancestry into Turkey migrating to North Africa through the Levantine corridor.

In Egypt, apart from E (39.5%), the Middle Eastern J (32.0%), and the earlier arrivals from East, are G (8.8%), K2 (8.2%), and R (7.5%) (Luis et al., 2004).

In India, the J2 haplogroup is almost absent from tribals, but occurs among some South Asian tribes (11%). The frequency of J2 is higher in South Indian castes (19%) than in North Indian castes (11%) or Pakistan (12%).

Any part of the Proto-Indo-European, Anatolian origin of gene pool in South Asia is discarded. The percentage of J2b2 marker Dravidian speakers is much larger than the supposed Indo-European speakers (Sengupta et al., 2006).

> "G and J haplogroups may have appeared concurrently from M89; the dates of appearance are unclear yet. The more I think about J2b2, I think, J2b2 arose in India. However, I cannot say this of J2 in totality" (Majumdar, 2006).

Large multiplicity of haplogroup 3 (R1a1) and 9 (J- 12f2) in India shows the most probable origin of these haplogroups is in India (Kivisild et al., 2003).

The age estimate of the Indo-European language tree is earlier than previously thought, present study correlates R1a1a with the period of subsiding of the LGM and the R1a1a* frequency and diversity is highest among Indo-Aryan and Dravidian speakers. This would exclude any significant patrilineal gene flow from East Europe to Asia (Underhill et al., 2010).

The K2- M70 haplotype was already discovered at low frequencies across Europe (Semino et al., 2000). Large parts of K-M9 lineages (Underhill et al., 2000) make back migration plausible from Asia to Africa, which have been observed only in Asia (Cruciani et al., 2002).

Around 40,000 years ago in southern central Asia or nearby region of Indus Valley, the male marker K (M9) appeared. The subgroup K2 (M70) is observed also throughout Africa, Asia, the Middle East and Southern Europe. K2s origin seems to be intriguing from its wide distribution on three continents. One of the calculations is around 30,000 years ago in Near East (Wells-Genographic project) or Southwest Asia.

K2 is reported in Middle East dating 15 to 10,000 years ago. The expansion time estimated around 13,000 BP (Cinnioĝlu et al., 2004).

It is likely that during LGM, K2 appeared somewhere again in southwestern Asia and then moved further west.

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[1] Arizona.edu. Details on the various assumptions used in computing TMRCA: http://nitro.biosci.arizona.edu/ftdna/models.html.

Table 1
Y-chromosomes.
Tableau 1
Chromosomes Y.

Y-Haplos	Origin date BP	Place of origin	Reappearance Around and later 15,000 BP
G-M201	20,000	Indus Valley	Anatolia, Caucasus and nearby regions
H-M52	30 to 20,000	South Asia	Middle East, Anatolia
R1a1-M17	15,000– or earlier	South Asia	Central Asia- Eastern Europe
K-M9	40,000	Indus Valley-India	Descendents in Europe
K2 -M70	20–30,000	Near East-Southwest Asia?	Africa, Middle East-Asia Minor-Southern Europe
R2-M124	25,000	Northern India	Central Asia Caucasus
L-M20	30,000	Northern India	South west Asia Caucasus-Anatolia -Mediterranean
L1-M76	9,000	India	Central-Western Asia
G1 and G2	10,000?	Descendents of G-M201	Middle Eastern, Anatolia, Caucasus

The only plausible displacement is from central Asia to south during LGM. Back migration of M70 into Africa is considered from near east, which could very well be from central Persia (Cruciani et al., 2002).

Haplogroup L in South India has been reported in earlier investigation to be almost 50% of the population (Wells et al., 2001). Later examinations proved that this haplogroup composition among other Y-chromosome groups makes just one fourth of the total. L1-M76, the subclade of L-M20 was discovered to be not only of Indian origin associating with Dravidian languages but also its spread from South Asia to northwestern region into Persia (Sengupta et al., 2006; Thanseem et al., 2006).

A strong possibility of lineages, Y and mtDNA carriers gathered around Indus region during LGM. People from Persian corridor and central Asia must have moved to western Himalayan region during inhospitable period.

As seen in Back Migration from Asia to Sub-Saharan Africa of E lineage (Cruciani et al., 2002):

"The Y-chromosomal data consistently suggest a largely South Asian origin for Indian caste communities and therefore argue against any major influx, from regions north and west of India, of people associated either with the development of agriculture or the spread of the Indo-Aryan language family." (Sahoo et al., 2006).

The possibility of pre-LGM subclades matching some markers in some other region cannot be neglected. In this case pre-LGM lineage can always be in Persian-Near Eastern corridor of LGM periods, those non-recombining types remained in isolation. This does not mean that few of those found in northern Caucasus belong to surviving marker of LGM in South East Europe; rather those could very well have migrated in Late Pleistocene periods from Near East.

Europe has been more scrupulously examined than any other continent; yet there is no general agreement on the origins of the European gene pool.

The Y chromosome analysis revealed a considerably larger genetic input from Neolithic farmers.

The demic diffusion model introduced by Ammerman and Cavalli-Sforza (1984) captures the major features of this dramatic episode in European prehistory (Chikhi et al., 2002).

5. Data simulation

The ingenuity of computational phylogenetics, the computing models created by the people involved in Mathematical Genetics and bioinformatics is indeed quite remarkable.

The use of mathematical models in population genetics to describe the gene frequency distributions, frequency dynamics by deterministic methods and fluctuations in finite population size in developing populations is given considerable importance since last few decades. Crow and Kimura (1970); Karlin (1968); Moran (1962); Nagylaki (1992); Yu et al. (1990) and many others still continue to develop new models.

Population genetics research is carried out by developing many abstract mathematical statistical reproductions to study gene frequency dynamics, genotypes, phenotypes, evolutionary process through natural selection, genetic drift, mutations and gene flow, which strives to achieve certain results from those models, about the likely blueprint of genetic variation in present populations. Further, these results are tested against empirical data.

It is well known that age estimates are assumed on numerous invalid hypotheses involving large number of mutations in historical human constitution. However, that uncertain information is taken as basis for assessment of other records.

Isolated population genes are related by phylogenetic reconstructions, which are hypotheses of the historical relationships of those samples with the various episodes of migrations that influenced an area and to guess the impact of gene flow, by discerning Y chromosome mixed characteristic from the source regions. Often it carries some degree of ambiguity because the existing gene groups reflect the outcome of many intricate events in human history, which involves incorporation of repeat sequences, the entire series of matters concerning population dynamics, sample biases, and sample sizes, sampling inaccuracies, statistics of markers used, selection of markers, numerical representations chosen for investigation, polymorphism (diverse alleles) subjected to limited positive choice resulting in congregating progression. Despite these multiple intricacies, the experts are trying to do their best.

Dating is then based on calculations of mutation rate, which can be controversial and always have very wide "error margins". Or they are based on suggested correlations with climatic events (like the LGM), which make assumptions about which environments would or would not have been habitable (Based on Experts comments, 2006).

Some calculate standard errors without clarification on real uncertainties involved, which are widely distributed in statistical methods in estimating coalescence time scales having standard deviations carrying large temporal factors. Indeed, the uncertainties and large intricacies involving in age estimation of population gene history will remain with many unanswered questions for a long time.

Almost all experts give the age estimations on the basis of coalescent theory, including here in the table. These dates are in Before Present (BP).

Coalescent theory, a retrospective representation of population genetics, uses a sample of individuals from a population to outline all alleles of a gene common to all members of the population to a single ancestral copy, known as the most recent common ancestor MRCA (Arenas and Posada, 2007, in press).

The inheritance associations involving alleles are in general characterized as a gene genealogy which attempts the statistical properties of the coalescent under different conjectures, which outlines the basis of coalescent theory. The coalescent makes replications of genetic drift (change in the relative frequency in which a gene variant or allele, occurs in a population due to random sampling and chance (Futuyma, 1998) backward in time to examine the genealogy of ancestors (Arenas and Posada, 2007; Nordborg, 2001; Stephens, 2001).

The number of markers studied to get information for comparatively accurate correlation, through admixture magnitude of individuals, linkage disequilibrium which is genetic linkage, the rate of recombination, mutation rate, random drift or non-random mating, population structure and groups or groups again mixing other groups, is largely inadequate, and approximation usually will have, in statistics called, extensive "confidence intervals" (Pfaff et al., 2004).

Since a century, the debates on whether mathematics represents "Reality" have been widely known. For many scientists, including theoretical physicists, the mathematical models are just aesthetic characters represented in equations not having observed confirmation.

Mathematically, we may describe some aspects or attributes of a physical phenomenon but we cannot create a physical reality through arithmetic. In some cases, we may use available "Matter" to produce a mathematically conceived "Product", which in real sense, is a "Factory Product", not found in Nature.

Creating a non-existent entity in numbers for our own convenience is simply an exercise of "Make Believe".

The mathematician Henri Poincaré argued that the laws of science did not relate to the real world at all, but signify random conventions intended to support a supplementary suitable and "functional" depiction of the analogous phenomenon.

Albert Einstein once stated that "as far as the laws of mathematics refer to reality, they are not certain; and as far as they are certain, they do not refer to reality."

The use of mathematical models in population genetics to describe the gene frequency distributions, frequency dynamics by deterministic methods and fluctuations in finite population size in developing populations is given considerable importance since last few decades. Crow and Kimura (1970); Karlin (1968); Moran (1962); Nagylaki (1992); Yu et al. (1990) and many others still continue to develop new models (Meligkotsidou et al., 2005).

Almost a decade now, progression of population migrations based on Y-chromosomal spread in its varied multiplicity in the world is being investigated (Jobling and Tyler-Smith, 2003; Underhill et al., 2001). Major advancements in this field were made to come to closer possible affinities of diverse marker distributions with continental perspective.

Ever larger data of genetic markers with their micro-satellite variations of samples taken from present population is fed in computer programs to get results of population genetic history covering a time scale of thousands of years of deep ancestry, which are numerical products of assumptions.

However, all researchers know that there is no "Live Skeleton", which would yield human DNA information analogous to "Real World". Hence program does not sufficiently deal with the complexity of all aspects of historical developments. The case of Natufians and Catalhouk in Middle East and Turkey is evident.

"It must be noted that these age estimates are dependent on many, possibly invalid, assumptions about mutational processes and population structure. Nonetheless, they constitute a basis for comparison to other data" (Wells et al., 2001).

Other such cases, to a large extent further puzzling and extremely speculative in estimating genetic history, are a propos, complete missing factual World data of Middle Eastern, European and central Asian prehistory, extending the whole period of LGM of almost 10,000 years between 25,000 BP and 15,000 BP.

All attempts to establish Paleolithic origins, especially of mitochondrial European ancestry, through computer models are apprehensive, simply because:

> "European ancestry is not a living fossil of the Paleolithic maternal deme; rather, demographic events during the Neolithic and post-Neolithic periods appear to have had substantial impact on the European genetic record" (Coffman and Levy, 2005).

Despite all above-mentioned difficulties, we still continue with the same hypothesis of European population origins in the periods of Early and Middle Pleistocene, with a new terminology used, "Out of Asia" (Dennella et al., 2009).

The present DNA data of the existent world of the periods between Late Pleistocene and Early Holocene, and incongruent archaeological data concerning survivors of last glacial periods, give irrefutable evidence, not only of third migration of people from east to west, but also making

Indus Valley region and Persian passage, literally a genetic and cultural junction. No doubt, here was the beginning of modern human civilization.

In other words, with simple straightforward analysis of present DNAs, both mtDNA and Y-Chromosomal, looked into for ancestry, from the extant of European gene pool, we will certainly come back in time through regions of Asia Minor, central Asia, Persia-Indus corridor to South Asia. The maximum age limit reached will definitely be between 15,000 and 5,000 BP.

Correlation drawn from prehistory with the DNA markers of "present" samples is literally an extreme case of quantum leap in "time", making incoherent ancient genetic mapping. Descendents of mtDNA Haplogroup U estimated with Paleolithic pedigree in Europe is also an example.

> "If we take the MRCA age as the age of a colonization process we would end up with a radically different and absolutely meaningless datation of the human expansions. Therefore, there are dates in our DNA, but if we are interested in historical processes of population movement, those dates are simply wrong" (Barbujani, 2008).

Apart from incertitude and incongruent aspect of population genetics age estimations by coalescent theory, geneticists have some responsibility of social scientific kind.

Based on African genetic variation, all population geneticists predict that Africa is the source of all modern humans.

Have we considered the actual source of this genetic variation, which could be by large activities of forced mating?

We know that many groups of females, even in large-scale women communities were victims of physical abuse, mostly the tribal and nomadic women of Africa. These females have been subjects of forced breeding by men from all directions of Africa in the past hundreds or thousands of years.

These are the cases of a type of human random breeding or in other words, these are the cases where the children born from such acts will have genetic variations, which is the percentage of gene loci in individuals that are heterozygous.

The source of these variations is by the recombination of chromosomes that occurs during sexual reproduction.

We know that non-random mating, called outbreeding, has an augmented possibility that individuals with a particular genotype will mate with individuals of another particular genotype. Outbreeding can lead to an increase in genetic variation.

Millions of women in Africa are victims of forced mating by men of other regional origins since hundreds of years (Africa war zones, 2008).

In short, are we sure of "Out-of-Africa" hypothesis based on genetic variation?

The United Nations reported that 27,000 sexual assaults were reported in 2006 in South Kivu Province alone, and that may be just a fraction of the total number across the country.

In eastern Congo, is estimated that 8,000 females suffering from sexual violence need treatment in this year alone. Malteser International, a European aid organization said that in one town, Shabunda, 70% of the women reported being sexually brutalized.

The epidemic of rapes seems to have started in the mid-1990s. That coincides with the waves of Hutu militiamen who escaped into Congo's forests after exterminating 800,000 Tutsis and moderate Hutus during Rwanda's genocide 13 years ago.

According to UNICEF, in Sudan, Chad and the Democratic Republic of Congo, it is estimated that more than 200,000 females living in the Democratic Republic of the Congo today have been raped in recent conflicts. Rwandan Genocide report suggests 500,000 women were raped during the 1994 (Fourth Annual Report of the International Criminal Tribunal for Rwanda).[2]

The Bantu languages constitute a traditional sub-branch of the Niger-Congo languages. There are about 250 Bantu languages by the criterion of mutual intelligibility. Bantu languages are spoken largely in the regions of central Africa, East Africa, and southern Africa.

The DNA samples were taken from many regions the Africa mentioned above.

Most recently, not only the absence of genetic information but also the earlier Out-of-Africa migration into South Asia is questioned. Petraglia (2010), stated that numerous populations came Out-of-Africa in the period between 120,000 and 70,000 years ago," (Alcock, 2010, Science reporter, BBC News).

The absence of ancient DNA to make additional tests made this area of investigation much less reliable. The human populations were present in India prior to 74,000 years ago, or about 15,000 years earlier than expected based on some genetic clocks (Petraglia, 2010).

If we still insist that the Out-of-Africa hypothesis is true, then the only possible deeper ancestry correlation with Out-of-Africa extrapolation is with South Asian, Southeast Asian and few in far eastern populations. The large time scale of LGM calamity did not create any drastic impact on demographic structure in these regions.

Methodological research into the nuclear DNA requires painstaking cautious approach as it turns out to be more complex. According to such technical research, there won't be any adducible DNA affinity between people from long distances with a past covering many of generations (Panse, 2005).

However, another deep insight refutes the exclusive Out-of-Africa correlation of humans:

> "...data from the nuclear genome not only fail to support this model; they do not support any simple model of human demographic history. Numerical simulations of this process replicate many of the seemingly contradictory features of the genetic data, and suggest that as much as 80% of nuclear

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[2] Fourth Annual Report of the International Criminal Tribunal for Rwanda to the General Assembly September 1999.

loci have assimilated genetic material from non-African archaic human" (Eswaran et al., 2005).

This suggests possibility of interbreeding between recent Out-of-Africa *Homo sapiens* and earlier archaic genus *Homo erectus*.

Current studies of Persian corridor concerning paternal lineages conducted on haplogroups B, C, E, F, G, H, J, K, L, N, O, Q, and R. One would have expected some details of events around LGM period and analysis of possible back migrations or regrouping of few lineages from central Asia and Near East into Indus-Persian passage of that period. Instead a general statement is made saying, "the Iranians carry signature lineages with origins in Asia, Africa, and Europe" (Regueiro et al., 2006).

A commendable compilation of investigations of multi-regional sites in Iran gives reports of Late, Middle and Upper Paleolithic cultures in those regions (Otte et al., 2006).

Latest investigations in the regions of Zagros at Yafteh Cave, Lorestan in Iran by Otte et al. (2007) reported origin of Aurignacian culture, which dates back to about 35.5 KBP.

This advocates east to west diffusion of this tradition dating Middle Paleolithic period.

Large-scale continental Y chromosome and mitochondrial DNA datasets were investigated for understanding dispersal of humans in Eurasia.

These studies establish pertinent demic diffusion of inherited genetic traces from east to west by migrating individuals, during Palaeolithic times, around 60 ky (Chaix et al., 2008).

Rezvani and Vahdati Nasab (2010) have accounted their studies from the archaeological sites in Mirak, Semnan Province, Iran are of major Middle Palaeolithic events.

The data of original mtDNA and Y-chromosome antiquity, from the regions of Near Eastern-Persian corridor needs further testing. This should lead to some or substantial detection of back migration from Near Eastern and central Asia into Persian-Indus corridor during LGM.

Back migration in the regions inhabited by ancestral groups will produce mutations through amalgamation of people, which will complicate for precise sequence analysis. Later as in case of late LGM and after, the re-migration will be of both the ancestral markers and new admixture. These would have passed 100s of generations during whole of LGM period and again, there is no certainty of how many directions, the new migrations have taken on one or more continents. This would have extreme complexities in sampling, analyzing data sequence of all subclades with large number of micro-satellite variations, linkage disequilibrium, including original marker of a particular haplogroup, which may migrate after LGM. How precise one can detect that marker of origin, migrating after Late Glacial with other groups, though it may be of non-recombining type, is a big question.

During the Last Ice Age, depopulation of Europe is more apparent than survival at archeological sites. In an extremely perilous inhospitable and frozen environment, for 10,000 years, reasonable guess is relocation or nobody survived. The assumption that the survivors passed whole of LGM period appears to be farfetched. A reasonable guess about the peak of glaciations time scale is before warm and

cold episodes, the Younger Dryas, which is of about 5000 years. This means, the assumed survivors have passed at least 200 generations. Even if we consider half of these generations number, perhaps very young and old members of each generation group being confined to that small area, the refugia must be filled with 1000s of human fossils. There are no such archaeological evidences, nor could geneticist extract any human DNA from those refuges. Paintings in those caves, we know, are not living human DNA prints.

Extensive studies around Indus region gave substantial archaeological data, which also was congruent with forensic anthropological investigations on inhabitants of northwestern India. Results showed arrivals of few markers into the subcontinent from the northwest during the Late Pleistocene period between 15,000 and 10,000 BP (Kennedy, 2000).

In other regions a possible scenario is, humans relocated for survival from extreme aridity of central Asia and Asia Minor-Persia. Most certainly, people gathered round hospitable environment in the vicinity of Indus region, Himalayan steps and Kashmir valleys.

6. Linguistic fallacy and the truth

Linguistic hypothesis of Anatolian or any other southeastern European origin, a Glottochronology, has been always controversial with too many blemishes.

Without euphemism, William Jones, a British orientalist, in 1786 invented an idea that Sanskrit, Greek and Latin may have a common root. This hypothesis created a conjecture of racial and linguistic invasion of Indus Valley.

The foundations of "Racial Evil" were fabricated by few western Europeans and spread like wild fire all over Europe, which lead to holocaust of last world war.

Instead of conjured "common source", the question should have been:

"How did some Sanskrit words and sounds appear in western languages?"

The results supporting earlier hypothesis were by the spread of proto–Elamo-Dravidian accompanied by farming (McAlpin, 1974, 1981), small number of Dravidian-the Brahui speakers in Pakistan (Renfrew, 1996) which then conceived to be by possible word borrowing process (Blazek and Boisson, 1992). Later research regarding farming discovered that plant domestication in South Asia is by indigenous peoples (Fuller, 2003).

Current results showed the Indian origin associating Dravidian languages and its spread from South Asia to northwestern region into Persia and no major incursions of Indo-European speakers altering radically the Indian Y lineages (Sahoo et al., 2006; Sengupta et al., 2006; Thanseem et al., 2006).

The "autochthonous" Indian mtDNA and Y chromosome lineages are broadly stretched across languages in the Indian subcontinent, which makes linguistic affinities of diverse Indian populations (Chaubey et al., 2007).

Archaeo-anthropological investigations reported on Indus Valley research:

"For more than four millennia, agricultural and pastoral communities in what are now Pakistan and western India traded with one another and shared ritual practices and customs... Although there is ample evidence for walled towns and cities, there is no indication so far that military force was used by one settlement to conquer another." (Kenoyer, 1998)

All scientific disciplines, archaeology, forensic anthropology and genetics have deprecated the linguistic hypothesis, through which the racial identity was concocted, which then was associated with the mythical invasion of Indus valley.

Archaeological investigations confirmed the farming and plant domestication in South Asia is by indigenous peoples (Fuller, 2003). Effectively, the linguistic developments after LGM could elucidate in the Indus-Persian corridor.

After LGM, undeniably, the central Asian and Persian plateau was interactive terrain between nomadic tribes from both sides east and west and around Hindukush, north and south. Genetic admixture through interbreeding by migratory groups had taken place between those different geographical regions. Development and spread of other languages, Elamite, Hittite etc. is of natural process within interactive groups in those areas. Sanskrit verbal influence continued during all those interactions.

"Certainly people migrate with genetics and language and culture, but cultures also evolve and change and languages can be abandoned or mixed long the way." (Fuller's comments).

Pre-LGM and after, other continents and regions, Africa, America, Far East and South East Asia, must have had several indigenously developed languages, mostly only spoken. Sanskrit and Vedas were "*Shrutis*", Spoken, Vedas never said that they were "*Likhit*" Written. Many perhaps are extinct today, Sanskrit and Vedas still continue in the daily culture of Hindus and many other regional languages continue today, with Sanskrit influence. It is unattainable to establish precise date for origin of Sanskrit and Vedas, because, these were spoken. To establish a date or origin of any 'Spoken Language' in ancient times is unfeasible. Any claim by those who are at far distant, to know origins of spoken languages on any continent is simply a political rhetoric and wasted self gratification, which will be controversial and rejected at all cost.

The inadvertent argument expressed, devoid of exhaustive thought, holds some ground:

"If we were to use the same arithmetic and logic (sensu haplogroup 9 is Neolithic) to give an interpretation of this table (Table 17.3), then the straightforward suggestion would be that both Neolithic (agriculture) and Indo-European languages arose in India and from there, spread to Europe" (Kivisild et al., 2003).

Detailed, especially large-scale investigations are required of Near East-Persia-Indus corridor, including some parts of South Asia and central Asia to discover how many subclades and micro-satellite variations would correspond to the periods of LGM, Late Pleistocene and Early Holocene, with their origins and places, which will bring significant clarity in present genetic composition of Europeans.

With the new perspective based on DNA research and clear evidences of migrations out of Northwest of South Asia, during late LGM and after, with Paleoclimatological vegetation implications, we have to establish all linguistic and cultural ideas in details with more research in all disciplines.

Acknowledgments

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