

New research debunks aryan invasion theory

Kumar Chellappan

Chennai Dec. 10, 2011

In what could be a major setback to dravidian parties in tamil nadu, an inter-continental research in cellular molecular biology has debunked the aryan invasion theory.

"We have conclusively proved that there never existed any aryan or dravidians in the indian sub continent. the aryan-dravidian classification was nothing but a misinformation campaign carried out by people with vested interests," Prof Lalji Singh, Vice-chancellor, Banaras Hindu University, told DNA.

The findings of a three-year research by a team of scientists, including Prof Singh and others from various countries, has been published by American Journal of Human Genetics in its issue dated december 9.

"The study effectively puts to rest the argument that south indians are dravidians and were driven to the peninsula by aryan who invaded north india," said Prof Singh, a molecular biologist and former chief of Centre for Cellular and Molecular Biology, Hyderabad.

According to Dr Gyaneshwer chaubey, Estonian Biocentre, Tartu, Estonia, who was another indian member of the team, the leaders of dravidian political parties may have to find another answer for their raison d'être. "we have proved that people all over india have common genetic traits and origin. all indians have the same dna structure. no foreign genes or dna has entered the indian mainstream in the last 60,000 years," dr chaubey said.

Dr Chaubey had proved in 2009 itself that the aryan invasion theory is bunkum. "that was based on low resolution genetic markers. this time we have used autosomes, which means all major 23 chromosomes, for our studies. the decoding of human genome and other advances in this area help us in unraveling the ancestry in 60,000 years," he explained.

However, Gnani Shankaran, noted dravidian thinker, said the time for writing the last word on dravidian philosophy has not yet come. "We have to find out the credentials of the authors of this research paper and their hidden agenda. In Tamil Nadu, the dravidian and aryan ties are inter-related. the dalits in our land are the descendents of the dravidian brahmins who were pushed to the lowest strata of society by the aryan," shankaran said.

According to Prof Singh, Dr Chaubey, and Dr Kumarasamy Thangaraj, another member of the team, the findings disprove the caste theory prevailing in India. interestingly, the team found that instead of aryan invasion, it was indians who moved from the subcontinent to europe. "That's the reason behind the findings of the same genetic traits in eurasiain regions," said Dr Thangaraj, senior scientist, CCMB.

"Africans came to India through Central Asia during 80,000 to 60,000 BCE and they moved to Europe sometime around 30,000 BCE. The Indian Vedic literature and the epics are all silent about the Aryan-Dravidian conflict," said Dr S Kalyanaraman, a proponent of the Saraswati civilization which developed along the banks of the now defunct river Saraswati.

<http://epaper.dnaindia.com/epapermain.aspx?edorsup=Main&queryed=9&querypage=8&boxid=30677354&parentid=156382&eddate=12/10/2011>

Indian diversity. Last genetic nail driven into the AMT-Aryan-Dravidian divide coffin: (Metspalu, Gyaneshwer Chaubey et al, AJHG, Dec. 2011)

Genetic study finds no evidence for Aryan Migration Theory--On the contrary, South Indians migrated to north and South Asians migrated into Eurasia

What geneticists consider a landmark paper has just been published in a highly reputed scientific journal, American Journal of Human Genetics, authored by an international group of geneticists including Metspalu, Gyaneshwer Chaubey, Chandana Basu Mallick (Evolutionary Biology Group in Tartu, Estonia), Ramasamy Pitchappan (Chettinad Academy of Research and Education, Chennai), Lalji Singh, and Kumarasamy Thangaraj (CCMB, Hyderabad). The study is titled: Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia, The American Journal of Human Genetics (2011), doi:10.1016/j.ajhg.2011.11.010

The study is comprehensive, unlike previous studies of human genome and is unique, because it focuses on large number of populations in South Asia, and India, a region which harbours one of the highest levels of genetic diversity in Eurasia and currently accounts for one sixth of human population in the world.

The study analysed human genetic variation on a sample of 1310 individuals that belong to 112 populations, using new genome-wide data contains more than 600,000 single nucleotide polymorphic sites among 142 samples from 30 ethnic groups of India. The most important scientific findings of the study are:

- . South Asian genetic diversity is 2nd in the world, next only to Africa, mainly due to long periods of indigenous development of lineages and with complex population structure where one can see the different caste and tribal populations.

- . Two genetic components among Indians are observed: one is restricted to India and explains 50% genetic ancestry of Indian populations, while, the second which spread to West Asia and Caucasus region. Technically called "haplotype diversity", it is a measure of the origin of the genetic component. The component which spread beyond India has significantly higher haplotype diversity in India than in any other part of world. This is clear proof that this genetic component originated in India and then

spread to West Asia and Caucasus. The distribution of two genetic components among Indians clearly indicates that the Aryan-Dravidian division is a myth, Indian population landscape is clearly governed by geography.

. A remarkable finding is that the origin of these components in India is much older than 3500 years which clearly refutes Aryan Invasion theory of the type enunciated by Max Mueller ! The study also found that haplotypic diversity of this ancestry component is much greater than in Europe and the Near East (Iraq, Iran, Middle East) thus pointing to an older age of the component and/or long-term higher effective population size (that is, indigenous evolution of people).

. Haplotype diversity associated with dark green ancestry is greatest in the south of the Indian subcontinent, indicating that the alleles underlying it most likely arose there and spread northwards.

. The study refutes Aryan migrations into India suggested by the German orientalist Max Muller that ca. 3,500 years ago a dramatic migration of Indo-European speakers from Central Asia shaping contemporary South Asian populations, introduction of the Indo-European language family and the caste system in India. A few past studies on mtDNA and Y-chromosome variation have interpreted their results in favor of the hypothesis, whereas others have found no genetic evidence to support it. The present study notes that any migration from Central Asia to South Asia should have introduced readily apparent signals of East Asian ancestry into India. The study finds that this ancestry component is absent from the region. The study, therefore, concludes that if such at all such a dispersal ever took place, it should have occurred 12,500 years ago. On the contrary, there is evidence for East Asian ancestry component reaching Central Asia at a later period.

. India has one of the world's fastest growing incidence of type 2 diabetes as well as a sizeable number of cases of the metabolic syndrome, both of which have been linked to recent rapid urbanization. The study points to a possible genetic reasons and recommends further researches on four genes - DOKS, MSTN, CLOCK, PPARA - implicated in lipid metabolism and etiology of type 2 diabetes.

Kalyanaraman

Dec. 9, 2011

Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia

Mait Metspalu^{1, 2, 13, ,}, Irene Gallego Romero^{3, 13, 14}, Bayazit Yunusbayev^{1, 4, 13}, Gyaneshwer Chaubey¹, Chandana Basu Mallick^{1, 2}, Georgi Hudjashov^{1, 2}, Mari Nelis^{5, 6}, Reedik Mägi^{7, 8}, Ene Metspalu², Mairo Remm⁷, Ramasamy Pitchappan⁹, Lalji Singh^{10, 11}, Kumarasamy Thangaraj¹⁰, Richard Villems^{1, 2, 12} and Toomas Kivisild^{1, 2, 3}

¹ Evolutionary Biology Group, Estonian Biocentre, 51010 Tartu, Estonia

² Department of Evolutionary Biology, Institute of Molecular and Cell Biology, University of Tartu, 51010 Tartu, Estonia

- 3 Department of Biological Anthropology, University of Cambridge, Cambridge CB2 1QH, UK
- 4 Institute of Biochemistry and Genetics, Ufa Research Center, Russian Academy of Sciences, and the Department of Genetics and Fundamental Medicine, Bashkir State University, 450054 Ufa, Russia
- 5 Department of Biotechnology, Institute of Molecular and Cell Biology, University of Tartu and Estonian Biocentre, 51010 Tartu, Estonia
- 6 Department of Genetic Medicine and Development, University of Geneva Medical School, 1211 Geneva, Switzerland
- 7 Department of Bioinformatics, Institute of Molecular and Cell Biology, University of Tartu, 51010 Tartu, Estonia
- 8 Genetic and Genomic Epidemiology Unit, Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford OX3 7BN, UK
- 9 Chettinad Academy of Research and Education, Chettinad Health City, Chennai 603 103, India
- 10 Centre for Cellular and Molecular Biology, Hyderabad 500 007, India
- 11 Banaras Hindu University, Varanasi 221 005, India
- 12 Estonian Academy of Sciences, Tallinn, Estonia

Corresponding author

13 These authors contributed equally to this work

14 Present address: Department of Human Genetics, University of Chicago, 920 E 58th Street, CLSC 317, Chicago, IL 60637, USA

Abstract

South Asia harbors one of the highest levels genetic diversity in Eurasia, which could be interpreted as a result of its long-term large effective population size and of admixture during its complex demographic history. In contrast to Pakistani populations, populations of Indian origin have been underrepresented in previous genomic scans of positive selection and population structure. Here we report data for more than 600,000 SNP markers genotyped in 142 samples from 30 ethnic groups in India. Combining our results with other available genome-wide data, we show that Indian populations are characterized by two major ancestry components, one of which is spread at comparable frequency and haplotype diversity in populations of South and West Asia and the Caucasus. The second component is more restricted to South Asia and accounts for more than 50% of the ancestry in Indian populations. Haplotype diversity associated with these South Asian ancestry components is significantly higher than that of the components dominating the West Eurasian ancestry palette. Modeling of the observed haplotype diversities suggests that both Indian ancestry components are older than the purported Indo-Aryan invasion 3,500 YBP. Consistent with the results of pairwise genetic distances among world regions, Indians share more ancestry signals with West than with East Eurasians. However, compared to Pakistani populations, a higher proportion of their genes show regionally specific signals of high haplotype homozygosity. Among such candidates of positive selection in India are *MSTN* and *DOK5*, both of which have potential implications in lipid metabolism and the etiology of type 2

diabetes.

[http://www.cell.com/AJHG/abstract/S0002-9297\(11\)00488-5](http://www.cell.com/AJHG/abstract/S0002-9297(11)00488-5)

Free pdf download full text: <http://download.cell.com/AJHG/pdf/PIIS0002929711004885.pdf>

Full text with large figures: [http://www.cell.com/AJHG/fulltext/S0002-9297\(11\)00488-5?large_figure=true](http://www.cell.com/AJHG/fulltext/S0002-9297(11)00488-5?large_figure=true)

Indian Diversity, genetic study (Metspalu, Gyaneshwer Chaubey et al, AJHG Dec. 9, 2011)

Kalyanaraman