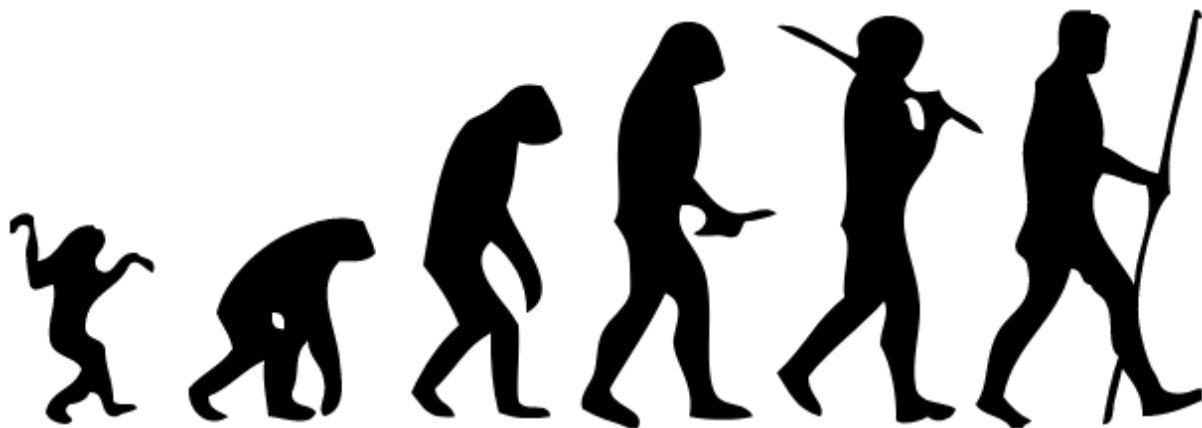


DBT-NIBMG study to unravel the adaptive history of S.Asian populations

New Delhi, Sep 01: Anatomically Modern Humans (AMH) inhabit a diverse range of environmental conditions across all the continents except Antarctica. After their origin in Africa approximately 200,000 years ago, they started dispersing out of Africa around 60,000 years ago to different parts of the world. They rapidly colonized different habitats across the world despite encountering a host of novel environments such as the extreme cold climate in the Americas and Eurasia during the last glacial maximum, changes in exposure to sunlight and new pathogens, among many others. Moreover, cultural inventions such as the advent of agriculture and improved hunting techniques altered their dietary habits.



Therefore, like most other living organisms, the Anatomically Modern Humans have also adapted to these novel environments through means of Darwinian natural selection. Biological adaptation by natural selection is primarily a genetic process and manifests in changes to patterns of genetic variation. Consequently, the effect of natural selection on human populations, similar to other evolutionary events such as migration, divergence and admixture between populations and changes in population size, is expected to leave its imprint on individual genomes. Whole genome sequence data therefore provides an access to study the rich history of human adaptations.

The primary focus of a team of researchers at the Department of Biotechnology's National Institute of Biomedical Genomics (DBT-NIBMG), Kalyani, West Bengal, has been to infer the adaptive history of South Asian (SAS) human populations by studying their whole genome sequences. South Asia harbours a heterogeneous group of human populations with varied ancestry that inhabit diverse geographic regions. The genetic diversity of these populations is therefore expected to reflect not only the different ancestral admixture and demographic events but also local adaptations to these varying environments.

The team led by Dr. Diptarup Nandi, a National Postdoctoral Fellow (SERB), has detected several genomic regions that have been under selection, while investigating the genomes of different South Asian ethno-linguistic groups belonging to the 5 main language families that are found on the Indian mainland (Indo-Aryan, Dravidian, Austroasiatic, Tibeto-Burman) and the Andaman and Nicobar islands (Andamanese).

These genomic imprints of natural selection in the SAS populations indicate shared adaptive histories with other global populations as well as selective events specific to South Asia. Differences in the genomic signatures of selection between the different SAS populations also imply their distinct adaptive histories.

Using machine learning based tools, they are attempting to further identify the genes involved in these adaptive processes and to ascertain the traits that have potentially played a key role in the evolutionary histories of these populations.

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