

Decrypting genomic data for peep into the history of human populations

Studies have shown that 'Anatomically Modern Humans' (AMH) originated in Africa 200,000 years before present (ybp) and began to migrate out of Africa (OoA) by 60,000 ybp. The OoA migration was like a wave, followed by mass exodus to the furthest corners of the globe. During this migration and colonization of different parts of the world, AMH not only came across a plethora of different environments, but also encountered our 'close cousins' (human like species such as Neanderthals and Denisovans). AMH adapted to these novel environments, experienced various demographic events and also had babies with the Hominins. These and most importantly chance events have shaped their present distribution of genetic variation among different AMH populations.

Dr. Anabha Basu's lab at the department of biotechnology's National Institute of Biomedical Genomics (NIBMG), Kalyani, West Bengal, tries to understand how genetic variation is distributed in space-time and why is it distributed the way it is, i.e., the evolutionary forces that have led to the current distribution of genetic variation. It primarily focuses on the South and South-East Asian regions (S&SEA).

The researchers have shown that genetic variation in mainland India is clustered into 4 major 'ancestral' groups. These ancestral groups are roughly identifiable with the four language families in India – Indo-European (north India), Dravidian (south India), Tibeto-Burman (north-east India) and Austro-Asiatic (fragmented in east and central India; spoken exclusively by the tribals). They have also identified a fifth ancestral lineage that is dominant among the hunter-gatherer tribals of Andaman and Nicobar Islands. India is a 'melting pot' where individual genomes are admixed between these ancestries. These ancestries are obviously not confined within the national borders but are linked to populations of neighbouring countries. They have recently shown that the Austro-Asiatic speakers are the autochthones of S&SEA and they are linked through a deep common ancestry spanning from Central India to peninsular Malaysia.

The genome of an individual is a historical text which contains abundant information about events experienced by the ancestors at different time points in the past. Decrypting that information from large scale genomic data in the era of 'Next-Generation Sequencing(NGS)' provides an unprecedented challenge and opportunity of looking into intricate details of population history. Analyzing Whole Genome Sequences of present day Asians, the researchers have shown that the hunter-gatherer populations experienced population decline contrasting to the agriculturists post invention of agriculture around 10,000 ybp. Using machine learning they are exploring genomic signatures of natural selection that can arise due to their varied evolutionary histories.

Contact Person & Contact Details: Dr.Anabha Basu, Email: ab1@nibmg.ac.in