The Bottleneck in Human Evolution

For Prelims: Fast infinitesimal time coalescent process (FitCoal), Genomic Sequencing

For Mains: Genome Sequence and its Significance, Population bottleneck in human evolution and its implications for modern humans.

Source: TH

Why in News?

Recently, a study published in *Science* sheds light on a crucial period in human evolution marked by a **population bottleneck**, providing insights into the challenges our early ancestors faced and the genetic changes that shaped modern humans.

 Researchers from China, Italy, and the U.S. used a novel genomic analysis technique called Fast Infinitesimal Time Coalescent Process (FitCoal) to examine this bottleneck.

FitCoal:

- It is a method of inferring ancient population size and demographic history by using modern-day human genomic sequences and calculates the composite likelihood for the site frequency spectrum (SFS), which is the distribution of allele frequencies in the sequences.
- FitCoal can detect severe bottlenecks and speciation events in human evolutionary history that are otherwise difficult to observe from the fossil record.

Genome Sequencing:

- Genome sequencing is figuring out the order of DNA nucleotides, or bases, in a genome—the order of Adenine, Cytosine, Guanines, and Thymine that make up an organism's DNA.
- The genome sequence will represent a valuable shortcut, helping scientists find genes much more easily and quickly.
 - A genome sequence does contain **some clues about where genes are, even though scientists are just learning to interpret these clues.**

What are the Key Highlights of the Study?

- Population Bottleneck:
 - A population bottleneck is a **sharp reduction in the size of a population due to environmental events or human activities** that kill or prevent the reproduction of a large percentage of the population.

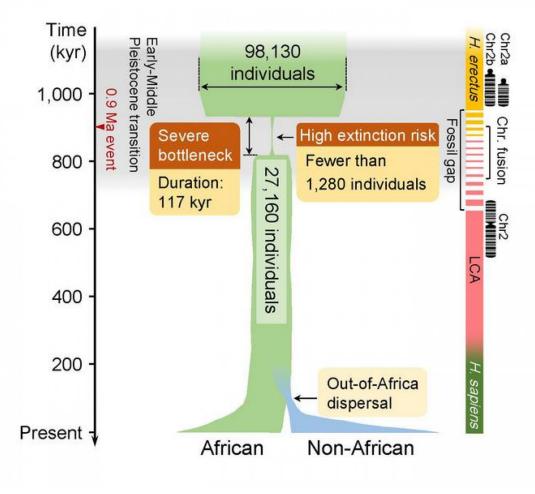
- This **reduces the genetic diversity** and the ability to adapt to changing conditions of the remaining population.
- The study reveals that a **severe population bottleneck** occurred between 800,000 to 900,000 years ago, nearly driving the **human species to the brink of extinction.**
 - During this bottleneck, only approximately 1,280 breeding individuals sustained the entire human population, and this situation persisted for about 117,000 years.

Causes of Bottleneck:

- Environmental Factors:
 - Glaciation events, changes in temperature, and severe droughts were suggested as reasons for the downturn in the size of the human ancestral population.
 - The study suggests that humans persisted in presumably dangerous conditions during the bottleneck period, around **930,000-813,000 years** ago.
 - Loss of other species, **potentially food sources for ancestral humans**, also contributed to the bottleneck.
- Loss of Genetic Diversity:
 - Early human ancestors experienced significant loss of life during the bottleneck period.
 - This resulted in a substantial loss of genetic diversity, with an **estimated 65.85%** of humans' current genetic diversity potentially lost during the early to middle Pleistocene era (from two million to 11,000 years ago).

Speciation Event:

• The bottleneck event in human evolution resulted in the fusion of two ancestral chromosomes, forming chromosome 2 in modern humans, a distinct trait not found in other primates.



UPSC Civil Services Examination, Previous Year Questions (PYQs)

<u>Prelims</u>

Q. With reference to agriculture in India, how can the technique of 'genome sequencing', often seen in the news, be used in the immediate future? (2017)

- 1. Genome sequencing can be used to identify genetic markers for disease resistance and drought tolerance in various crop plants.
- 2. This technique helps in reducing the time required to develop new varieties of crop plants.
- 3. It can be used to decipher the host-pathogen relationships in crops.

Select the correct answer using the code given below:

(a) 1 only

(b) 2 and 3 only

(c) 1 and 3 only

(d) 1, 2 and 3

Ans: (d)

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