

Unravelling climate change

Hurricane Hannah hit Haiti and Ike struck the Texas Gulf coast, as the Atlantic Ocean continues to churn more storms, leaving people dead and displaced. Back home, it was the overflowing Kosi river that had displaced 25 lakh people in Bihar and 12 lakh in Assam. 'Climate change' is gradually morphing into a gruesome reality. India along with its North West Frontier neighbours and sub-Saharan Africa is at a disadvantage regarding natural calamities due to its social, economic and demographic fabric. Fluctuating climatic conditions are likely to cause heavy rainfall and droughts¹, affecting the productivity of farmers in Asia and Africa. Approximately, two-thirds of India's population depend directly on the climate-sensitive zone for their survival². An alteration in climate is likely to have heavy consequences on all the natural ecosystems, thereby affecting the socio-economic systems³.

The oft-quoted blame on anthropogenic changes for inducing global warming has been authenticated in a study⁴ at NASA's Goddard Institute for Space Science in New York. The scientists correlated temperature-related changes in all the continents with responses in physical and biological systems. Changes in natural systems as well as those in regional climate were attributed to anthropogenic warming. The 'joint attribution' method was used to link climate models with statistical models to simulate changes in natural systems and compare them with the observed changes in natural systems. Observed changes in the Arctic and Canada were consistent with the response

due to anthropogenic climate change. However, the retreat of two glaciers in Switzerland and Norway could not be explained by natural variability.

Data ranging from 1970 to 2004 were analysed to study multiple physical and biological systems at a global and continental scale. Maximum temperature-related changes were seen in Europe, North America and North Central Asia, with least responses observed from Latin America, Africa and Australia. The lesser magnitude of warming as seen in the latter regions was thought to be caused by large-scale climate variations than due to anthropogenic factors. Of the 829 documented physical changes, 95% was coherent with warming events such as glacier melt and earlier spring river peak. Phenological plant changes such as leaf unfolding, early blooming and change in migration patterns of animals accounted for 90% of the staggering 28,800 documentations in the biological systems.

Among other drivers of environmental change, land-use change is said to indirectly affect the physical and biological systems through climate. The Fourth Assessment Report of the IPCC Working Group found that since the mid-twentieth century, the increase in global temperature is likely due to increase in anthropogenic greenhouse gas concentrations and concluded that significant warming over the past fifty years occurred in each continent, except Antarctica⁵.

However, the synthesis of a huge amount of data to quantify the climate impact has aggravated fears among

experts, terming it a rather difficult task⁶. The 'spatial congruence' statistic that assumes local climate changes are confined to that region may not be able to enumerate biological impacts arising from remote climate changes. They emphasize that to determine the magnitude of anthropogenic contribution, it is necessary to undertake direct attribution of the causes of change in the affected systems rather than using a two-step joint attribution system that ascribes climate change to external influence and alterations in physical and biological system. Hence, an end-to-end modelling system that gives a holistic view on climate change is required.

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RT-PCR technique for rapid detection of CHIK virus

Chikungunya is a viral disease caused by the Chikungunya (CHIK) virus, which is an alphavirus belonging to the family Togaviridae. CHIK virus is transmitted to humans by various *Aedes* mosquito species. It causes an acute disease which can be fatal. It was first reported in India in 1963 and caused an epidemic¹ here in 2005.

The CHIK virus infection has many similarities with that of dengue virus. Hence its identification was a problem,

resulting in delayed control measures. Earlier, virus isolation and serological testing were the two methods to detect the virus. But both the methods are time-consuming, expensive and sophisticated¹.

Joseph *et al.*¹ (Molecular Biology Laboratory, SCMS Institute of Bioscience and Biotechnology Research and Development, Cochin) have developed a new, simple, more sensitive and fast method for detection and characterization of

CHIK virus in human serum samples collected from febrile patients during a recent outbreak of viral infections in Kerala. The method is called RT-PCR.

The RT-PCR technique requires no high-precision instrument except a PCR machine. No viral culture for RNA extraction is required; rather RNA is isolated directly from 200 µl of the patient's serum. Joseph *et al.*¹ performed RT-PCR amplification of the viral RNA using two