Analabha Basu has been consistently and profoundly contributing to genomics of human populations in India and health-genomics. His contributions are harmonized with what the Science Council of the World Health Organization (WHO) has emphasized in its Report titled "Accelerating Access to Genomics for Global Health;" that genomics research and technologies "are critical for improving the health and livelihood of people in all parts of the world, regardless of economic status". I was an expert chosen by the Science Council to present views on the topic; I presented some results from Analabha's research that were greatly appreciated. Thus, Analabha's work has received global attention and appreciation.

There are two major components of Analabha's research; to understand human genome diversity and human genome evolution with special reference to South and South-East Asia, and to connect the knowledge so derived to decipher genomic underpinnings of multifactorial common diseases. In the conduct of these studies, Analabha has been consistently innovative and has developed statistical and machine-learning methods for data analysis, when off-the-shelf methods were unavailable or when available methods were inefficient to draw robust inferences. In particular, Analabha has developed innovative statistical methods of gene-mapping using data derived from admixed populations. He has taken leadership to undertake large-scale studies of gene-mapping for metabolic diseases, an enormous health burden in India.

Analabha's most significant contribution has been to unravel the mosaic of complex population admixture and the deep intricacies of migration in south and south-east Asia, and utilize this knowledge for fine-mapping of genetic architectures of diseases common in India. He has identified four ancestral components that have contributed to Indian population groups, which was a significant advance from the then prevailing notion of two ancestors. He estimated proportions of these ancestral components in individual ethnic populations and, using some robust techniques that he himself invented, dissected genetics of traits of biomedical significance. His work has underscored the importance of including hitherto under-represented populations in studies of genetic variation. It laid the foundation to construct the framework to undertake studies on genomics-driven health solutions. The Department of Biotechnology, Government of India, in recognition of the importance of his contributions, has provided leadership status to him to plan and conduct a national study of population genetic variation in relation to human health. This study is nearing completion. As a member of the Monitoring Committee of this study, I am certain of its large impact on biomedicine.

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