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"Indian science in genomics has been able to place itself on the global map"

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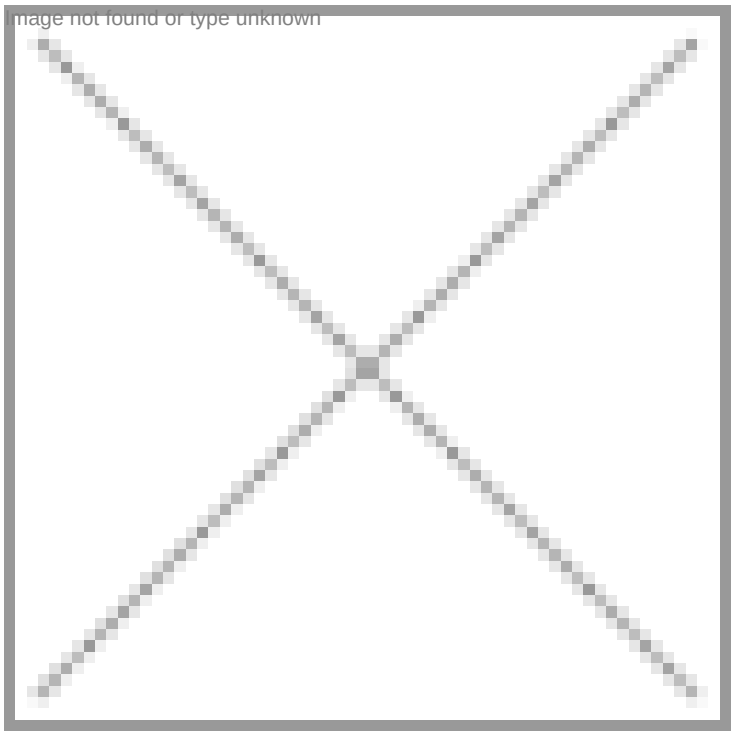
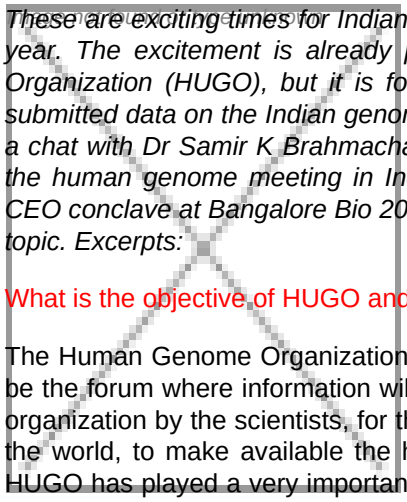


"Indian science in genomics has been able to place itself on the global map"

-Dr Samir K Brahmachari, Director General, CSIR, Delhi



These are exciting times for Indian science. India is all set to play host to the 13th human genome meeting in September this year. The excitement is already palpable since it not only happens to be the 20th anniversary of the Human Genome Organization (HUGO), but it is for the first time that the Human Genome Meeting is being held in India. India has also submitted data on the Indian genome variation that has been published in the Journal of Genetics, (Vol.87, No.1, April 08) . In a chat with Dr Samir K Brahmachari, Director General, CSIR, BioSpectrum finds out more about HUGO and the buzz about the human genome meeting in India. Incidentally, Dr Samir Brahmachari will be delivering the special address during the CEO conclave at Bangalore Bio 2008 on this topic. Excerpts:

What is the objective of HUGO and when was it formed?

The Human Genome Organization was formed at the very beginning of the human genome project with an idea that this will be the forum where information will be shared across the world without any restriction of geographical boundaries. This is an organization by the scientists, for the scientists all across the world, in order to disseminate the human genome information to the world, to make available the human genome sequence in the public domain so that everyone has equal access to it. HUGO has played a very important role in not only making the human genome sequence open source and publicly available,

but also making the knowledge available and also addressing the ethical, social and legal issues that would concern the society. As per its policy, five percent of its fund utilized for research is used to address ethical, legal and social implications of the human genome sequencing that were understood as early as the 1990s.

The human genome project was initiated in the late 1980s under the funding of the Department of Atomic Energy (DAE). HUGO was formed as an organization in Switzerland wherein HUGO US and Moscow were associated members. In 1990, I was the one of the early members elected to HUGO along with Prof. Notani of BARC from India with 100 odd scientists. The original objective of HUGO was to coordinate the mapping of the genome. So the human genome mapping workshop was initiated. And it was only in the late 1990s when the mapping was completed, that the Human Genome Meeting was actually started . So in this series, we shall be hosting the 13th Human Genome Meeting in India in Hyderabad from September 27-30, 2008.

Please elaborate on the Human Genome Meeting (HGM) being held for the first time in India.

In the beginning HGM was held for a year in Europe and then in the US. It was only in 2002 that the HGM came to China for the first time. This was because China participated from the developing world in the human genome sequencing project from 1999-2001. Japan has been a major player along with the US and Europe and hence recognizing this, the meeting came back to Asia again, in 2005 in Japan. This is the third time the meeting is coming to Asia and this time it is India. We have chosen Hyderabad for the meeting, since it has one of the best convention centers in the country where a meeting of such a global stature can be held.

How do you see the significance of the meeting coming to India?

This signifies the contribution that India has made in genomics by developing the Indian genome variation landscape. This is something unique because this is the first time that 55 populations across a country have been mapped for various gene risk alleles. This signifies that Indian science in genomics has been able to place itself on the global map. Accepting to hold the meeting in India and directing me to chair is the recognition of this.

What are the key features of the meeting?

We are expecting a participation of 500 students in the meeting. We are organizing special satellite meetings, a "Know your Genome" meeting for students to make them aware of the human genome, and a clinical genomic workshop for clinicians amongst others. The meeting also aims to address the ethical and legal issues associated with the human genome. We are also thinking of a session on the business of genomics and new biology for young entrepreneurs. There will be an exhibition of new instruments and technologies as well as many presentations on technological aspects as well. It will be a platform to showcase the Indian industry to the world. Besides, people will get to see and listen to the who's who of genomics, such as Craig Venter.

What are your expectations from the meeting?

When I was young and molecular biology had just come, we hardly had any resources, capabilities or access to information. Today this new biology is bringing to the fore the champions working at the frontiers. I want to expose Indian scientists to them and make them realize that things are not difficult for us and that India is no longer behind. This would enable them to think bigger.

The Indian genome variation study uses disease markers instead of neutral markers. Kindly elaborate.

Certain areas of the genome are neutral under natural selection, so if one wants to know who is related to whom and how are different populations related, neutral markers would provide the requisite information. But we realized that our objective was to find how various disease gene risk alleles are distributed in the population, which is why we used disease markers.

What are the advantages of using disease markers in the study?

This helps us get background control information so that we know what is the general variability across the population, if a disease is high risk or low risk and thus helps us address the stratification problem. Second, it also helps us understand how the drug responds across different populations, to see how some drugs which may not be working in the Japanese population may not be working in the North-East region but might work in the southern region of India. Thereby India can have a low cost drug in the market using pharmacogenomic principles. What it demonstrates is that irrespective of using markers, which are disease linked markers, we are able to cluster the Indian population into four major clusters. It has further been revalidated. It is interesting to note that both the neutral marker and the disease markers could reasonably segregate the population. The study also found that despite linguistic variability, there is enormous genetic heterogeneity across the Indian

population.

Shalini Gupta