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Interviews of 2007 Shanti Swarup Bhatnagar Prizes winners

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Eleven scientists have been selected for 2007 Shanti Swarup Bhatnagar Prize for science and technology.

The Shanti Swarup Bhatnagar (SSB) Prizes are awarded annually by the Council of Scientific & Industrial Research (CSIR) for notable and outstanding research, applied or fundamental, in biological, chemical, earth, atmosphere, ocean and planetary, engineering, mathematical, medical and physical sciences. The purpose of the prize is to recognize outstanding Indian work in science and technology.

Any citizen of India engaged in research in any field of science and technology up to the age of 45 years is eligible for the Prize. The Prize is awarded on the basis of contributions made through work done primarily in India during the five years preceding the year of the Prize. The SSB Prize comprising a citation, a plaque and a cash award of Rs 200,000.

BioSpectrum caught up with three prize winners in the following categories:

Medical Sciences: Dr Pundi Narasimhan Rangarajan, Indian Institute of Science, Bangalore

Biological Sciences: Dr Upinder Singh Bhalla , National Centre for Biological Sciences, Bangalore and

Dr Narayanaswamy Srinivasan , Indian Institute of Science, Bangalore

Excerpts of the interviews in the ensuing pages:

Eukaryotic gene expression researcher

Dr Pundi Narasimhan Rangarajan, IISc, Bangalore

What has been the focus area of your research?

The main focus of my research has been eukaryotic gene expression and infectious diseases.

I was the first to initiate research on DNA vaccines in India as well as virogenomics and my research has spanned the development of DNA vaccines against Japanese encephalitis virus (JEV) and rabies virus as well as study of host gene expression during virus infection. My research on virus-inducible gene expression changes in mouse brain has led to identification of several novel genes. These include:

A novel Virus Inducible Non Coding RNA (VINC) which was recently shown to be associated with SC35 nuclear speckles (Hutchinson et al., BMC Genomics 2007, 8: 39);

GARG39/IFIT2, a novel microtubule-associated protein enriched in the mitotic spindle of actively dividing normal and cancer cells.

The JEV-repressible murine Ca2+/calmodulin kinase II inhibitor (CaMKIIN) which was localized for the first time in the post synaptic density (PSD) of mouse brain.

I developed a novel strategy of enhancing the potency of rabies DNA vaccine which was granted patents in Europe, South Africa, India, Canada and China. The preclinical toxicity studies of this novel combination rabies DNA vaccine has been completed and the vaccine is likely to be introduced in the market as DINARAB by Indian Immunologicals Ltd (IIL), Hyderabad after obtaining regulatory approvals.

What are your current research areas?

I am currently heading a new research program on the study of biology of non-conventional yeasts at IISc, funded by the Department of Biotechnology. Realizing the importance of microbial expression systems in biotechnology and the lack of knowledge on basic mechanisms of gene regulation, I had initiated a new research program on the biology of Pichia pastoris, a methylotrophic yeast widely used for recombinant protein expression. Such studies have led to several interesting findings including the isolation of yeast homologue of vertebrate lens-specific zeta crystallin (ZTA1) and its identification as a single stranded DNA binding protein. Using the Pichia recombinant protein expression system, we developed recombinant yeast strains expressing high levels of Hepatitis B surface antigen. These strains were transferred to two companies in Hyderabad, one of which (Biological E) produced the recombinant hepatitis B vaccine and launched it as BEVAC on December 22, 2004 while the other company (Indian Immunologicals Ltd) launched it as ELOVAC-B on September 26, 2006.

What have been your contributions to collaborative research?

My ongoing collaboration with
Prof. G Padmanabhan at IISc on malaria has led to the identification of a novel heme biosynthetic pathway in the malarial parasite as well as discovery of antimalarial activity of curcumin, a component of widely used Indian spice turmeric. Based on this research, human clinical trials of artemisinin-curcumin combination therapy for malaria have been initiated recently.

Computational biology expert

Prof. N Srinivasan, Molecular Biophysics Unit, IISc, Bangalore

What has been the focus area of your research?

I would like to mention that the award this time is also a special recognition for computational biology which is emerging as an important branch of modern biology. My area of research interest is evolution of structure, function and interactions of proteins. We develop and use computational biology approaches to address fundamental questions in this area. World-wide genome sequencing projects of human, model organisms and pathogens results in the availability of amino acid sequences of all the proteins encoded in the organisms. However, information on functions and biological roles of many of these proteins is yet unknown. Unless we have a reasonable understanding of the functions of these proteins, we cannot hope to use the genome information in an effective way. For example, understanding of functions of proteins encoded in the genome of a pathogen contributes profoundly in the understanding of associated disease process and hence in the design of inhibitors which may emerge as drugs.

We employ computational tools, developed by us as well as by others, in recognizing functions and other properties of proteins encoded in genomes of hundreds of organisms. We recognized functions of many proteins in various organisms; particularly those involved in cellular signal transduction. Often we provided three-dimensional viewpoint of proteins using computational approaches that enabled appreciation of molecular basis of protein function. Our analysis of interaction between proteins provided new insights influencing our understanding of choice of protein-protein partnerships.

Computational neuroscientist

Prof. Upinder Bhalla, NCBS, Bangalore

What is the area of research that you are specifically focused upon?

The major focus of my research has been computational neuroscience of memory and olfaction. My scientific contributions, as I see it, are in the analysis of information flow and memory storage at the synapse, which is a structure that communicates between nerve cells and secondly studying information processing in the sense of smell. In two major papers early in my career we showed how such information processing could occur, first through simulations (Bhalla and Iyengar Science 1999), then through combined experiments and models (Bhalla, Ram and Iyengar, Science 2002).

At the macro level we use parallel electrical recordings to study detection and signal encoding (receptors, olfactory bulb) right through to the storage of olfactory memories (piriform cortex, hippocampus). We train animals on odor memory tasks to put these recordings into a functional context. At the micro level, we use microscopy and detailed computer simulations to explore the networks of signaling chemicals that operate in olfactory neurons. A key finding of our work is that inside cells, beyond the slow 'calculations" of DNA, the signaling system itself has sufficient complexity to operate as an independent, rapid computing system that can process and store olfactory information. We have also experimentally identified molecular circuits capable of another fundamental type of neural computation, time measurement. Having also demonstrated several time-related behaviors of the olfactory system as a whole, we are now well-positioned to compare the functional contributions of what are possibly the two most complex systems known-the circuitry of the brain, and its microcosmic equivalent, the circuitry of the cell.

What are your other achievements?

Our group has developed a database of signaling network models, doqcs.ncbs.res.in, which was one of the first such resources. We have also been developing simulation software for biochemical and neuronal modeling for many years. This was earlier part of the GENESIS project and is now a new initiative called MOOSE (http://moose.ncbs.res.in)