

## Need to organize periodic conferences for developing strategies in education, science and technology

A key element in the economic development and progress of a nation lies in the extent and quality of education, science and technology (S&T) of its people. In the present world, with globalization of the competition, the education, S&T environment has become volatile. Plans for teaching S&T and research need to be evolved continuously in order to optimize and obtain best results. The best producing years of an individual are usually during their youth. It is a time when one is bubbling with unending energy and innovative ideas. And as is noted, usually the best research is done before a scientist hits 30.

The average age of India's population is 25 years, which means that a large proportion is very young and in their college-going years. Certain percentage of any population is gifted and smart. Therefore, India is producing a rich crop of super brains too. No wonder that multinationals are exploiting this resource to their advantage by outsourcing to India many of the knowledge-based jobs. But how is the nation attempting to develop the vitality of this pool of outstanding human resource and initiate involvement

in the gigantic effort of its own development?

A S&T programme must have a utility value for the common man. If it does not contribute to problem-solving for wide-ranging social issues, it is not justified to be pursued on public money. And the social issue should include the impact of the programme on the development of the student community as well. The government needs to review its policies in respect to maximizing the above aspect of its current S&T programmes.

The nation has invested in creating a vital scientific and technological resource by developing a series of national laboratories. These laboratories are no doubt doing a stupendous job with their own set of personnel. There is a certain extent of involvement of outside human resources within the country by way of sponsored projects. Some cooperation is developed with the international community by sharing of programmes and databases. However, the involvement of youth has remained rather sidelined thus far. Thus the ever-renewing resource of brain power available to the nation has remained unexposed to the enormous and multilevel possibili-

ties that can be generated by bringing in the IISc, IITs, National Academies and other institutions as full partners in the endeavours of the national laboratories and other entities. This will expose our students to the real-world problems and equip them to take on challenges of the state-of-the-art S&T and usher in a revolution in the society. How can this be achieved? The details of the options could be discussed, reviewed and new ways recommended in broad-based periodic workshops on strategies for national development. It is hoped that students, and all concerned scientists, educationists, etc. will come forward to discuss this idea – as otherwise, to paraphrase Plato, 'One of the penalties for refusing to participate in politics is that you end up by being governed by your inferiors', or 'One of the penalties for refusing to participate in policy making is that you end up by being overwhelmed with inferior systems'.

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## Criteria for the choice of plant species for genome sequencing to advance plant biology and agriculture

Information from genome sequences is essential to understand the organization of genomes, chromosomes, genes, regulatory and repetitive elements present in plant genomes and also to understand the evolutionary significance of variations observed in genome compositions. Understandably, the plant genome sequencing effort has been growing in recent years, since the plant genome organization is not fully understood. The genome sequences of *Arabidopsis thaliana* and rice have been completed and a draft sequence of the poplar genome (<http://genome.jgi-psf.org/Poptr1/Poptr1.home.html>) has also been completed. Many more species are undergoing genome sequencing, albeit in

most cases euchromatic regions of their genomes are being sequenced (National Centre for Biotechnology Information Entrez Genome Projects website: <http://www.ncbi.nlm.nih.gov/genomes/leuks.cgi>).

It is noted that majority of the species that have been chosen for partial and complete genome sequencing belong to the category of food and horticultural crops and forest trees, of economic importance. There is a concern whether the choice of species based upon economic importance will cover enough of phylogenetic variation present in plant species, to reveal all the important features of genome structure. Hence we discuss strategies for any further choices of species for

genome sequencing, to avoid haphazard selection and to facilitate diligent selection of species, whereby new information about plant genome structure is likely to be generated.

Plant comparative genomics spurs functional analysis of the identified plant genes and thereby supports integrative plant biology. Identification of genomic/gene sequence homologies allows both vertical and horizontal integration of species and helps in the understanding of genomic content changes associated with species evolution. Complete or partial euchromatic genome sequencing of a large number of plant species is also bound to speed up functional genomics and thereby increase

the impact of plant integrative biology. In this regard the important question is what should be the relative criteria to select plant species for complete and/or partial genome sequencing?

The genome structural variations are reflected in sizes of individual chromosomes and the number of chromosomes in diploid genomes and additionally by levels of auto- or allo-ploidy in polyploid genomes. Complete genome sequences provide information about molecular processes responsible for diversity in genome structures. It will be necessary to obtain complete genome sequences of several to many diploid and auto- and allo-polyploid plant species varying in genome sizes, to comprehend the dynamics of plant genome structure evolution. Genomic analysis of polyploids is necessary to understand the impact of regional, as well as whole-chromosomal duplications. Among angiosperms, both monocotyledonous and dicotyledonous species need sampling. Species of gymnosperms, pteridophytes, bryophytes and eukaryotic algae must also be included. Their analyses will reveal the genome dynamics associated with gross changes in reproductive mechanisms and plant morphology. The cost estimates dictate that complete genome sequencing be limited to a rather small number of species. Sequencing of crop plant genomes of varying sizes is already in progress. The auto- and allo-polyploids may be chosen from among the relatives of plant

species of heterologous genome sizes already sequenced or undergoing complete sequencing. It may also be possible to isolate inordinately long or short chromosomes from certain species on the basis of size-discriminative particle separation techniques. Sequencing of such chromosomes, in addition to complete sequencing of as many plant genomes as possible, will also be helpful in understanding the determinant features of chromosome size in plants. The sequencing of individual chromosomes will be cost-effective.

Sequencing of phylogenetically diverse plant species is desired to ultimately reveal variation in the structure, function and regulation of genes. Such information can largely be derived by the sequencing of euchromatic chromosomal regions of the genomes of chosen plant species. The plant species for genome sequencing should not only be selected on the basis of different phylogenetic lineages, but also some important additional criteria. These may include smallness of genome size, simple distribution of eu- and heterochromatic regions, sexual fertility and short seed-to-seed cycle, in each phylogenetic group. Among those that possess the above properties, the species that can vegetatively propagate may be preferred. To speed up and lower the cost of sequencing of coding regions, the selected species should be amenable to molecular marker linkage mapping and molecular-cum-cytogenetic karyotype analyses of eu- and hetero-

chromatin regions. Partial sequencing will be meaningful and effective only if the boundaries of the euchromatic regions of chromosomes are molecularly marked in advance. The economically important species may be preferred in each phylogenetic group, provided they meet the various criteria listed above. Pyro-sequencing should help further reduce the cost of expanded comparative plant genomics enterprise.

Progress in plant genome biology is a pre-requisite for the breeding of new types of crop varieties that will meet the challenges of climate change, water scarcity, pollution, pathogen diversity and increased demands for food and feed, bio-fuels and industrial raw materials. Genome sequencing of phylogenetically diverse plant species selected by intelligent use of suitable features, some of them identified here, will help in the detection, marking, isolation and manipulation of agronomically and industrially important genes and their alleles to evolve crop varieties for future agriculture.

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## Chikungunya outbreaks in Andhra Pradesh, South India

Chikungunya fever is caused by the chikungunya virus (CHIKV), which is spread to humans by mosquito bites. Chikungunya literally means bentover in the local Mekonde language. CHIKV is an *Alpha-virus* belonging to the family *Togaviridae*<sup>1</sup>. It was isolated<sup>2</sup> for the first time from a Tanzanian outbreak in 1952. CHIKV is geographically distributed in Africa, India and Southeast Asia. In Africa, the virus is maintained through a sylvatic transmission cycle between wild primates and mosquitoes, such as *Aedes* species<sup>3</sup>. In Asia, CHIKV is transmitted to humans mainly by *Aedes aegypti* and to lesser ex-

tent by *Aedes albopictus* through an urban transmission cycle.

The most recent epidemic re-emergence was documented in 1999–2000 in Kinshasa, where an estimated 50,000 persons were infected<sup>4</sup>. The first Asian outbreak was recorded in 1958 in Bangkok, Thailand. Outbreaks were also reported in Cambodia, Vietnam, Laos, Myanmar, Malaysia, the Philippines and Indonesia<sup>5</sup>. CHIKV caused epidemics in India during 1824, 1871, 1901 and 1923. The most recent epidemic re-emergence was documented in 2001–03 in Java, and 2004 in an island of the Southwestern Indian

Ocean. More recently an outbreak was reported in Madagascar<sup>6</sup>.

CHIKV was first isolated<sup>7</sup> in Calcutta in 1963, and the last outbreak<sup>8</sup> occurred in India in 1971. Presently there is an outbreak of chikungunya in several states of India. At present Andhra Pradesh and some neighbouring states like Karnataka, Tamil Nadu and Chhattisgarh are reeling under the epidemic of chikungunya. Millions of people have been affected mainly with morbidity and sporadically with mortality.

Currently, we have two full genomic sequences of CHIKVs, the first isolated