Introduction and Perspective

Increase in agricultural productivity has to out-pace the rate of growth in population. This has to happen despite all the adverse abiotic and biotic stress factors under the climate change regime. India, with more than one billion population to be provided with adequate food and nutrition cannot relax. Besides, sustainability of the agricultural production systems, profitability and greater competitiveness in the world market make the task of meeting the targeted growth in agriculture a formidable challenge.

Genetic enhancement has been successful in meeting the demands of the ever-increasing population largely because of discovery and use of novel genes. The dwarfing genes in wheat and rice, and rust resistance genes in wheat are some of the burning examples, which stand testimony to the power of genetic technology that ushered in green revolution and subsequently helped sustaining the productivity gains. The conventional methods however are limited by sexual compatibility barriers. With the advent of new biotechnology tools and techniques, it has been possible to access genes from diverse biological systems and deploy in target species. This has rendered the whole living world a single gene pool. Use of crystal protein genes from the soil bacterium *Bacillus thuringiensis* in genetic engineering of crops like cotton clearly depicts how genes from evolutionarily distant organisms can bring new revolution in agricultural production. Besides Bt genes, several other genes have also been prospected, validated and are being deployed to gain commercial advantage. These efforts encourage prospecting of novel genes and new alleles of the known genes from diverse biological sources cutting across taxa and phyla and functionally validate them for future deployment to enhance and sustain agricultural productivity.

Perspective

India is fortunate to have a rich bio-diversity. Characterisation and utilisation of this diversity is essential to meet the challenges of biotic and abiotic stresses under changing climate. The present project proposal is a step in this direction. A long-term perspective of this project is to i) Prospect novel genes, promoters and alleles for economically important traits using indigenous bioresources, ii) Functionally validate the new genes in model systems and different genetic backgrounds, iii) Transfer of the validated genes and alleles to recipient species cutting across biological barriers and iv) Develop highly competent groups of scientists of international standard drawn from various disciplines and institutions for undertaking research in genomics and its application for improvement of agricultural species. This would require elaborate efforts not only for identification of new genes and alleles both for biotic and abiotic stress tolerance, but also for their functional validation and deployment. Liberal funding for a longer period would be essential for its success.

In short-term, the project seeks support through NAIP for three years to specifically address four main objectives: i) Generation of genomic resource base to facilitate gene prospecting and allele mining, ii) Prospecting for new genes and alleles for abiotic stress tolerance (moisture stress, salinity and sodicity, soil acidity, adverse temperature and submergence/anoxia), iii) Functional validation of the identified genes in model plant systems and iv) Use of the identified genes/allele in genetic enhancement of target species.

The project will try the following innovations and strategies to achieve the above objectives: i) Use of high throughput genome-wide approach in genotyping using sequence based markers is an innovative way to discover new genes and alleles in the project, ii) Exploitation of natural adaptive mechanism for abiotic stress tolerance in diverse biological systems including microbes, plants, animals and fishes, iii) Utilization of expertise cutting across diverse biological sciences to combat the effects of global climate change, iv) Design and use of new algorithms in the area of statistical and computational genomics that would accelerate application of genomic technologies for utilization of genetic resources and enhancement of agricultural species. There will be involvement of expertise available in 36 different institutions of the country including ICAR institutes, state agricultural universities, central universities and IIT. The organisms from which genes will be sourced for abiotic stress tolerance are microbes particularly the extremophiles, rice, maize, *Sorghum*, *Lathyrus*, *Ziziphus*, *Cucumis*, *Vigna*, camel, goat, trout, catfish, and shrimp.

Probability of success, expected output and possible impact

This project aims at preparing for meeting the challenges of abiotic stresses under the changing climate. The target traits are genetically very complex and thus problems posed are highly intractable. However, recent developments in the area of genomics encourage initiation of concerted efforts that might lead to finding solutions in long-run. The species chosen for prospecting genes and mining alleles are genetically and biologically diverse with varying resource base. Fortunately, a plenty of genetic and genomic resources are available in some of these species such as rice and maize. Besides, a great deal of information is already generated internationally on the genetic variation in respect of the chosen traits in these crops. Therefore, there is a greater chance of success in meeting the objectives in these two species. Similarly, the probability of success is also high in case of microbes. Relative simplicity of genomes and far greater genetic diversity of the microbial systems would allow gene discovery and allele mining at a faster pace than in case of plants and animals. In case of other species such as camel, goat, fishes, *Lathyrus*, *Vigna* etc., with very little or even a lack of basic physiological and genetic information on abiotic stress tolerance, the rate of progress would be slow. Addressing the proposed objectives in these species would require a longer period. However, keeping in view the robust genetic mechanism for abiotic stress tolerance these species represent, it is worthwhile to initiate efforts to generate basic resources including genetic and physiological information in these species.

The expected outputs of the project would include i) A knowledge database on bioprospecting and allele mining in the target microbe, plant, animal and fish species for future use, ii) Well characterized germplasm resources and core sets of germplasm in different species, iii) New genomic resources, genes, alleles, technology and genetic stocks in target species for abiotic stress tolerance, iv) New information on the SNP/haplotype structure in different species, v) Information on spatial distribution of genetic diversity and structure of populations in relation to useful allelic variations, vi) A pool of trained human resources and state-of-art infrastructure to handle large scale genotyping of germplasm and vii) Capacity building in statistical and computational genomics.

The present project will act as pilot for the second phase in which the resources generated and the experience gained are efficiently used. Possible overall impact of the project would include the following: i) Enhancement and stabilization of food production under changing global climate in long-term, ii) Greater precision in genetic improvement programmes thereby increasing the capability of Indian agricultural research system to meet the challenges to productivity and its sustainability, iii) Better understanding, value addition and protection of indigenous biological wealth, and iv) A core group of scientists to provide cutting edge leadership in research in the field of gene and allele prospecting.