Regulation of Gene Expression In Plants

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To The Director, Bose Institute

1. Objectives :

Introduction : Basically, we are interested to work out the mechanism of gene expression in roots, leaves, and also in fruits during water stress or salinity stress or fruit ripening in plants. Generally the cis-acting elements present of the upstream of any gene provides basic clue about the expression of that gene. Soon after the sequence of the entire genome of plants like , *Arabidopsis,* rice, and to some extent from tomato, are known, one can explore the presence of the cis-acting elements present on the upstream of any genes. Then experiments to detect the role of the cis-acting elements in the expression of the genes can be done to find out the activity in positive or negative way. Therefore, we are interested to work out the role of the following genes :

i. Mechanism of the RIN gene expression and how the RIN factor is in involved to turn on the ACS4 & ACS2 genes, which triggers the ripening process in climacteric fruits like tomato and banana by analysis of the upstream of the RIN gene.

ii. Identification of the up-regulated genes in Mango fruits during ripening and comparison on their expression in different mango cultivars.

iii. Analysis of the expression of different genes in ABA inducible expression system from the roots and laminar tissue in salt tolerant and salt sensitive rice cultivars in response to dehydration and salinity stress .

2.Institutional Plan Project of Primary Involvement :

Department of Botany now (from 1st April,2010) it is the Division of Plant Biology, Main campus (The other half is the PMCG section in the Centenary Building):

a. RESEARCH : 75 % time,

b. Management of the M.Sc-PhD Course and as Acting Chairman of the Dept of Botany, etc. : 25 % time,

(Research means supervising students, writing papers, preparation and submission of grant proposals, order for the chemicals and equipments from the projects, maintaining record books, etc. **Management** of MSc–PhD programme, preparation of routine for their class and examinations, Board Meeting (along with Prof Sampa Das as Joint Convenor), etc). As Chairman / Acting Head of the Department of Botany I was engaged in running the Office to maintain the Daily Attendance & communication with the Registrar's Office, Order placements, interviews, etc.

3. Work Done During December, 2007–March 2010

A. On Fruit Ripening : From the Tomato genome sequence data the upstream of the RIN gene showed the presence of many cis-acting elements known to be regulated by light, anaerobic condition, and circadian

rhythm, were detected. By EMSA using those cis-acting elements several trans-acting factors were identified. In addition, the transcript level of for RIN, NOR,TAGLII,GBF2 and GBF4 were also found to be enhanced by low level of irradiance than high intensity light. Role of anaerobiosis and circadian rhythm on the binding of trans-acting factors were detected from ripe fruit.

From ripe Banana fruits a MADS-box transcription factor likely to be RIN like factor was isolated and it's expression and activity are being studied. The upstream of the gene for sucrose phosphate synthase (SPS) was amplified and several important regulatory cis-acting elements known to be regulated by light, ethylene, auxin, etc, were detected. Binding of sequence specific trans-acting factors to those sites were detected. The upstream promoter was analyzed through transgenic tobacco system.

Fruit ripening in Mango fruit was studied in detail by comparing the ripening process in four different cultivars like Langra, Chausa, Golapkhaus, and Himsagar. An expression cDNA library was made in from ripe Himsagar fruit and then few of the picked up cDNAs were used as probe for northern blot analysis. Interesting of them are SOD, â1,3-glucanase, and metallothionin genes.

B. On Abiotic Stress in Rice : We have started to compare the expression of several important genes e.g AKT, HKT, SOS3, NhxI (from Zhu's pathway), SAMdC (polyamine biosynthesis) , Rab16a and the transcription factors like OSBZ8, NACI, WRKY, etc., in laminar tissue of salt sensitive and salt tolerant rice cultivars. In addition the upstream of OSBZ8, the transcription factor in ABA inducible system has been amplified, cloned and sequenced from rice. Presence of many cis-acting elements e.g. light responsible elements, binding site for many other important transcription factor. Therefore, their role will be studied in detail to know about the regulation of their expression during water stress or salinity stress.

The gene for the ddNTP sensitive DNA Pol lambda (previously we called it as Pol beta) has been amplified from rice and after cloning the upstream portion was sequenced. Several cis-acting elements like light responsive elements, heat shock elements, and dehydration responsive elements were identified. Salinity stress induced chromosomal abnormalities and enhancement of the activity of DNA polymerase lambda was observed in the rice seedlings.

4. Immediate Goals (within 100 words) :

a. The expression of RIN,ACS2 & 4 and sucrose phosphate synthase genes during fruit ripening will be continued to know their regulation.

b. The expression of the ABA inducible different genes and their miRNA in roots of both salt sensitive and salt tolerant rice cultivars in relation to abiotic stress will be checked.

d. In addition we are working on overexpression of few important genes in rice plants e.g SAMdecarboxylase, Rab16a, OSBZ8.

5. Publications during this period (publishes, accepted or submitted) :

1. Roy, Sujit., RoyChaudhury, Swarup, Mukherjee,S and **Sengupta . D. N. (2007)** Tobacco proliferating cell nuclear antigen binds directly and stimulates both activity and processivity of ddNTP- sensitive mungbean DNA polymerase. **Archives of Biochemistry and Biophysics. Volume 468, 22-31.**

2. Roy Choudhury., A.,Gupta, B.,and **Sengupta . D. N. (2008)** Trans acting factor designated OSBZ8 interacts with both typical abscisic acid responsive element as well as abscisic acid responsive element like sequences in the vegetative tissue of India rice cultivars, **Plant Cell Reports. Vol 27,779-794.**

3. Roy Chowdhury, Swarup, Roy,S., Saha,P.P., Singh,S.K., and **Sengupta, Dibyendu, N., (2008)** Charaterization of differential ripening pattern in association with ethylene biosynthesis in the fruits of five naturally occurring banana cultivars and detection of a GCC-box-specific, **Plant Cell Reports, 27:1235-1249**.

4. RoyChoudhury Aryadeep, Basu Supartim., **Sengupta . D. N. (2008)** Comparative physiological and responses of a common aromatic indica rice cultivar to high salinity with non-aromatic indica rice cultivars. **Plant Cell Reports, 27, 1395 – 1410.**

5. Roy, Sujit, Roy Choudhury, Swarup, and **Sengupta, Dibyendu N.** (**2008)** Analysis of processivity of mungbean dideoxynucleotide-sensitive DNA polymerase and detection of the activity and expression of the enzyme in the meristematic and meiotic tissues and following DNA damaging agent, **Archives of Biochemistry and Biophysics, 475:55-65**.

6. Roy Choudhury. Swarup, Roy. Sujit, and **Sengupta. Dibyendu N. (2008)** Characterization of transcription profiles of MA-ACS1 and MA-ACO1 genes in response to ethylene, auxin, wounding, cold and different photoperiods during ripening in Banana fruit. **Journal of Plant Physiology, 165, 1865 – 1878.**

7. Roy Choudhury. Swarup, Roy. Sujit, Ranjan Das and S**engupta, Dibyendu N. (2008)** Differential transcriptional regulation of banana sucrose phosphate synthase gene in response to ethylene, auxin, wounding, low temperature and different photoperiods during fruit ripening and functional analysis of banana *SPS* gene promoter". Planta, 229, 207 - 223.

8. Roychoudhury A., Basu,S., and **Sengupta, Dibyendu.N**. **(2009)** Effects of exogenous abscisic acid om some physiological responses in a popular aromatic indica rice with those from two traditional non-aromatic rice cultivars **Acta.Physiol.Plant,** 31,915-926.

9. Roy Choudhury, Swarup, Roy,Sujit, and **Sengupta, D.N. (2009)** A comparative study of cultivar differences in sucrose phosphate synthase gene expression and sucrose formation during banana fruit ripening, **Postharvest Biology and Technology, 54,** 15-24

10. Roy Chaudhury, Swarup, Roy,Sujit, and **Sengupta, Dibyendu,N. (2009)** Characterization of cultivar differences in â-1,3 glucanase gene expression, glucanase activity and fruit pulp softening rates during fruit ripening in three naturally occurring banana cultivars, **Plant Cell Reports,**

11. Roy Chaudhury, Swarup, Roy,Sujit, and **Sengupta, Dibyendu,N. (2010)** Understanding the molecular mechanism of transcriptional regulation of banana Sucrose Phosphate Synthase (SPS) gene during fruit ripening , Plant Signaling & Behavior,5:5,1-5

6. Extramural Projects at hand :

	Title	Sponsoring Agent	Date	Amount of Support
1.	The Molecular Analysis of the Expression of the Gene for Sucrose Phosphate Synthase (SPS) in Banana Fruit Ripening in Different cultivars	CSIR,ND	2008 -2011	Rs 9.64 Lakhs for 1st year, Rs. 4.58 lskhs for the 2nd year
2.	Mapping the binding of Transcription Factors on the Upstream and Promoter Activity Analysis of ACS2 and ACS4 genes in fruits of wild type and mutants plants by cloning of those trans-acting factors.	DBT,ND	2009-2011	Rs. 21.24 Lakhs for the 1st year, Rs. 9.58 lakhs & Rs 10.20 lakhs for 2nd & 3rd year
3.	Novel Genes and their Regulatory elements for salt tolerance from the wild halophytic rice *Porterisia coarcata* L Introgression into cultivated Rice".	DBT, ND	2008-2011	With Prof. Lahiri Majumder, Centenary Campus, Bose Institute

Projects submitted :

1. PI:- Prof. A. N. Lahiri Majumder- Part I, II, Co-PI:- Prof. D. N. Sengupta- Part III and Dr. Subho Chaudhury, Part IV.,

   Title: Generation of salt tolerant & nutritionally Improved Crop plants A Translation Approach , Submitted to DBT, Govt of India.

7. Number of students (including post-doctoral associates):

TWO Post-doctoral Associates and **SIX** students are working for PhD. (One RA is in my CSIR project, One RA on her own fellowship from IISc, Bangalore, One SRF from the Institute, Two JRF from my DBT project, One Teacher fellow on lien from his college, one Technical Asisstant from the Institute.)

8. Any other information (50 words maximum) :

In addition to the research and administrative jobs I am also engaged in teaching in MSc–PhD students in Plant Molecular Biology & Biotechnology in our institute and M.Tech students on Plant Biotechnology at the WBUT, Salt Lake.

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So gene expression is regulated. How exactly are genes regulated? Let's find out.Â Origin of Life and its Related Experiments H. Regulation Of Gene Expression. Protein synthesis begins at transcription, ends at translation and involves multiple steps. Therefore, regulation of gene expression can happen at any of these steps. In eukaryotes, gene regulation occurs at any of the following steps: Transcriptional level i.e. during the formation of the primary transcript. Processing level i.e. at the stage of splicing. During transport of mRNA from the nucleus to the cytoplasm. Translational level. A great example of coordinated gene regulation is the development and differentiati mentals and intricacies of the. regulation of gene expression in. plants, and the impact that this. regulation has on plant developÂ Aox expression patterns display variability and typically Aox genes fall into two discrete subfamilies, Aox1 and Aox2, the former being present in all plants and the latter restricted in eudicot species. Typically, although not exclusively, the Aox1-type genes are induced by many different kinds of stress, whereas Aox2-type genes are expressed in a constitutive or developmentally regulated way. Specific Aox alleles are among the first and most intensively stress-induced genes in several experimental systems involving oxidative stress. The regulation of gene expression conserves energy and space. It would require a significant amount of energy for an organism to express every gene at all times, so it is more energy efficient to turn on the genes only when they are required. In addition, only expressing a subset of genes in each cell saves space because DNA must be unwound from its tightly coiled structure to transcribe and translate the DNA.Â Gene expression in prokaryotes is mostly regulated at the transcriptional level (some epigenetic and post-translational regulation is also present), whereas in eukaryotic cells, gene expression is regulated at the epigenetic, transcriptional, post-transcriptional, translational, and post-translational levels. Review Questions.