



REGIONAL CENTRE FOR BIOTECHNOLOGY
Seminar series

**Genomics to epigenomics: an integrated approach to
understand stress adaptation in plants**

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**Thursday, August 16, 2012
11:00 am
Seminar Room**



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Abstract

Abiotic stresses such as water-deficit and high salinity are the most serious problems that limit growth and productivity of crop plants. Several molecular and genetic studies have revealed that a plethora of genes implicated in various pathways are involved in stress responses. Recent evidences indicate that epigenetic mechanisms also play a crucial role in adaptation to environmental stresses. Recent technological advances and availability of genomic resources have set the stage for epigenomic studies in crop plants. Chickpea is an important food legume crop because of its nutritious seeds and ability to fix atmospheric nitrogen. However, the availability of limited genomic resources has been an important constraint in chickpea improvement. We *de novo* sequenced and characterized the transcriptome of cultivated and wild chickpea using next-generation sequencing technologies to obtain a snapshot of gene space. Numerous transcripts expressed in tissue-specific manner were identified. Several genetic variations between cultivated and wild chickpea related to important agronomic traits have also been identified. These studies provide rich genomic resources and will accelerate functional genomic studies and breeding programmes in chickpea. Recently, we sequenced the transcriptome of chickpea seedling subjected to various abiotic stresses, to study gene regulation in response to stress. Several stress-responsive genes involved in various biological processes and molecular functions were identified. The integration of gene expression profiling with epigenetic marks, including DNA methylation patterns and histone modifications, and small RNA regulation will provide comprehensive understanding of the regulatory mechanisms underlying stress adaptation in chickpea and other crop plants.
