

Cordially Invites you to the
INSTITUTE COLLOQUIUM
(Biological Sciences Division)

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**The tiger-lily talks: Codes for the making of a rice
flowering stem**

Date : Monday, 16th February 2015
Venue : Faculty Hall, Main Building
Time : 4-00 p.m.

Prof Anurag Kumar, Director
will preside

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Abstract:

'O Tiger-lily, I wish you could talk!' 'We can talk,' said the Tiger-lily: 'when there's anybody worth talking to'. Through the Looking Glass, Lewis Carroll

Unravelling the logic behind the development of multicellular organisms from a fertilized single cell has fascinated philosophers for millenia. In more recent times biologists use the tools of genetics and developmental biology to decipher the complex interactions between genes and environment in the making of the striking structure and patterns of we see in the mature organism. Studies in convenient laboratory organisms, illustrate how a few key 'master' regulators can have large- cascading- and cumulative- effects on how growth and the emergence of form takes place.

In higher plants, flowering comes about by a remarkable transformation from a basal state where cells destined to be leaves or branches are transformed to a floral fate. Our knowledge on how this transformation is controlled comes largely from experimental studies with *Arabidopsis thaliana*, a model laboratory plant. These studies have given a remarkable insight on key regulators of flower development. Yet, given the diversity in flowering time and floral architectures that occur in nature, an outstanding question is about how these evolutionarily conserved regulators relate to the emergence of new patterns and variations in flowering stems and flowers.

We study development of the rice flowering stem (inflorescence) and rice flowers with the overall goal to understand the relationship between factors and signals that control fate of plant stem cells (meristems) and those that determine the identity of organs formed from meristems. I will summarize our studies that identified novel functions in rice flowering, stem-branching and meristem development for a gene call *RICE FLORICULA LEAFY (RFL)*, an evolutionarily conserved transcription factor whose functions in *Arabidopsis thaliana* are largely confined to floral meristems. We have also investigated, using functional genomic tools, the roles for other genes called MADS domain transcription factors, in floret meristem formation, organ development and meristem termination. Studies such as ours and those in leading laboratories worldwide on the genome-wide effects of rice transcription regulators would in the future allow one to build dynamic gene-regulatory networks. Comparisons with data emerging from other plant models including *Arabidopsis* will be insightful to understand how function in a specific species shapes the network properties.

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Tea : 5-00 p.m.

ALL ARE WELCOME