Sci*Efflux* 2016

12th and 13th August, 2016

8th Annual Symposium

National Institute of Plant Genome Research

Convener: Archana Yadav

Co-Convener: Shraboni Ghosh

Cultural Co-ordinator: Ramgopal

Faculty in charge: Dr. Praveen Verma

Friday, 12th August 2016

09:30 - 9:50 AM	Lightening of the lamp and Vandana Welcome Address: Archana Yadav Inaugural Speech: Dr. Niranjan Chakraborty Vote of thanks: Shraboni Ghosh
1st Session **09:50 - 11:30 AM**	**Chairperson** **Shweta Das**
09:50 – 10:15 AM	Sugar signaling in root responses to drought stress. **Dhriti Singh**
10:15 – 10:40 AM	Functional characterization of AtGBF3 gene under combined drought and pathogen stress in Arabidopsis thaliana. **Sandeep Kumar Dixit**
10:40 – 11:05 AM	Elucidation of molecular basis of tailored adaptation strategies employed by Arabidopsis thaliana against combined drought and bacterial pathogen stress. **Aanchal Choudhary**
11:05 – 11:30 AM	Investigation of Crosstalk between Auxin Signaling and MAP Kinase Cascade during Plant Development. **Stanzin Noryang**
11:30 – 11:45 AM	Tea Break

2nd Session **11:45 – 1:00 PM**	**Chairperson** **Rama Shankar**
11:45 – 12:10 PM	Identification and characterization of genes related to seed development in chickpea (Cicer arietinum L.). **Subodh Verma**
12:10 – 12:35 PM	Functional divergence of glucosinolates transporter gene family in Brassica juncea. **Deepti M. Nambiar**
12:35 – 01:00 PM	Analysis of the role of certain transcription factors and diversity in seed size and weight during rice seed development. **Arunima Mahto**
01:00 – 02:00 PM	Lunch Break

3rd Session **02:00 – 03:40**	**Chairperson** **Vikas Dwivedi**
02:00 – 02:25 PM	Role of jasmonate signaling components in nutrients deficiency response in Rice and Chickpea. **Ajit Pal Singh**
02:25 – 02:50 PM	Identification and Characterization of heat-responsive microRNAs in Solanum lycopersicum L. (Tomato). **Sarita jha**
02:50 – 03:15 PM	Study of oxalic acid responsive metabolic remodeling in crop plants: a functional proteomics approach. **Pramod Kumar Mittal**
03:15 – 03:40 PM	Elucidating the role and regulation of Protein L-Isoaspartyl Methyltransferase (PIMT) in plants. **Shraboni Ghosh**
03:40 – 03:55 PM	Tea Break

4th Session **03:55 – 05.35 PM**	**Chairperson** **Prafull Salvi**
03:55 – 04:20 PM	Genome-wide characterization of functional polymorphism and epigenetic modifications in rice genotypes with contrasting seed size. **Angad Kumar**
04:20 – 04:45 PM	Study of Host-specific Immune Response during Vascular Wilt in Plants. **Pooja R. Aggarwal**
04:45 – 05:10 PM	Protein L-Isoaspartyl Methyltransferase (PIMT): Role and Regulation in Orthodox and Recalcitrant Seeds. **Kamble Nitin Uttam**
05.10 – 05:35 PM	Functional analysis of genes controlling seed size and weight in rice. **Ankit Verma**

Saturday, 13th August 2016

5th Session **09:30 – 11:10 AM**	**Chairperson** **Poonam Mehra**
09:30 – 09:55 AM	Delineating the roles of heat shock protein encoding gene(s) of foxtail millet [Setaria italica (L.) P. Beauv.] during abiotic stress. **Roshan Kumar Singh**
09:55 – 10:20 AM	Mechanistic insights into the mycophagous and antimicrobial properties of Burkholderia gladioli. **Sunil Kumar Yadav**
10:20 – 10:45 AM	Branching wisely: Unravelling the nexus between jasmonic acid and glucose signalling in Arabidopsis. **Manvi Sharma**
10:45 – 11:10 AM	Role of activities and localization of CIPK6 and its interacting proteins in the susceptibility of biotic stress in Arabidopsis. **Niraj Kumar Vishwakarma**
11:10 – 11:25 AM	Tea Break

6th Session **11:25 – 01:05 PM**	**Chairperson** **Alice Kujur**
11:25 – 11:50 PM	Remodeling of the transcriptome, proteome and metabolome of grasspea: the molecular basis of dehydration tolerance. **Divya Rathi**
11:50 – 12:15 PM	Study of differential protein expression in the plasma membrane of chickpea (Cicer arietinum L.) under dehydration stress. **Pragya Barua**
12:15 – 12:40 PM	Regulation and Function of selected Small RNAs in Arabidopsis thaliana Root Development. **Sandeep Yadav**
12:40 – 01:05 PM	Identification, characterization and functional analysis of KIX-TAD interactions in *Arabidopsis thaliana.* **Archana Yadav**
01:05 – 02:00 PM	Lunch Break

7th Session **02:00 – 03:40**	**Chairperson** **Namisha Sharma**
02:00 – 02:25 PM	Computational analysis of the StAR-related lipid transfer (START) domains in plants. **Sanjeet Kumar Mahtha**
02:25 – 02:50 PM	Identification and characterization of candidate gene(s) associated with high-amylose content in foxtail millet Setaria italica L. **Annvi Dhaka**
02:50 – 03:15 PM	Characterization of a novel dehydration-responsive phosphoprotein of chickpea (Cicer arietinum L.). **Lande Nilesh Vikram**
03:15 – 03:40 PM	Twisting Plant Immune Signaling by Fungal Effectors. **Kanchan Prabha**
03:40 – 03:55 PM	Tea Break

8th Session **04:15 – 05.45 PM**	**Chairperson** **Garima Pandey**
03:55 – 04:20 PM	Development of nutrient-responsive differential seed transcriptome and proteome in chickpea. **Arunima Sinha**
04:20 – 04:45 PM	Genetic Dissection of Quantitative Grain Size and Weight Traits in Rice. **Daware Anurag Vasantrao**
04:45 – 05:10 PM	Moving in for the kill: Effector entry and host interaction for nectrotrophy. **Shreenivas Kumar Singh**
05.10 – 05:35 PM	Role of micro RNAs in abiotic stress tolerance in Chickpea. **Nilesh Sharma**

07:00 – 08:20 PM	**RAINBOW - A cultural event by NIPGR students**
08:20 – 08:30 PM	**Concluding remarks and prize distribution**
8:30 PM onwards	**Dinner**

Sugar signaling in root reponses to drought stress

Speaker: Dhriti Singh
Supervisor: Dr. Ashverya Laxmi

Drought is one of leading factors responsible for global food production reduction. A better understanding of mechanisms underlying drought stress and tolerance can help in this direction. Plant response to drought stress is very complicated comprising both ABA-dependent and –independent pathways and their cross-talk with each other. Though there are evidences of both direct and indirect link between sugar signaling and drought stress. Our knowledge about how sugar signaling operates under drought stress is very limited. Roots are the very first place to sense drought stress and drought stress has been reported to affect almost every aspect of root architecture. In addition to this, glucose has also been reported to modulate many root architecture traits, therefore, in this study we tried to understand how sugar signaling and drought stress simultaneously affect root orientation. Although, glucose causes deviation of roots we found that simultaneous application of drought and glucose causes straightening of roots. Auxin, ethylene and cytokinin are the major hormones that regulate root growth and orientation under drought stress along with other factors. In case of auxin signaling, we observed that some auxin signaling and transport mutants failed to show straightening of roots in presense of glucose and drought. Additionaly, glucose and drought can modulate the expression of auxin transport as well as target genes. All these evidences suggest that glucose and drought might directly or indirectly modulate auxin transport and signalingto regulate root orientation. Results also suggest the involvement of cytokinin and ethylene signaling in the interplay of glucose and drought in regulation of root orientation. However, further research is needed to provide more comprehensive picture.

Functional characterization of *AtGBF3* gene under combined drought and pathogen stress in *Arabidopsis thaliana*

Speaker: Sandeep Kumar Dixit
Supervisor: Dr.Senthil-Kumar Muthappa

The overall response of plants to the combined drought and pathogen stress is governed by the responses which are common to the individual stresses (shared responses) as well as responses specifically evoked under combined stress (unique responses). The genes commonly modulated under combined as well as individual stress constitute the shared response. Elucidation of shared responses will not only shed light on the fundamental defence response of plant to the combined stress, but also help in identification of target genes for the development of multiple stress resistant crops. Among the different genes involved in abiotic and biotic stress signalling pathways, transcription factors are known to contribute substantially in imparting stress tolerance to plants. Based on literature information and preliminary data from our lab, we considered one such candidate gene, *G-box binding factor 3* (*GBF3*). GBF3 belongs to bZIP superfamily transcription factor and has been shown to specifically bind to the G-box elements. Transcriptomic analysis reveals that *AtGBF3* is induced by individual and combined drought and pathogen stress. Expression based studies suggest that *GBF3* is downstream target of ABA and SA-mediated signalling.On the basis of these evidences, we hypothesized that AtGBF3 may be involved in individual and combined drought and pathogen stress tolerance as a part of shared tolerance mechanism. Present study is aimed at deciphering the role of *AtGBF3* gene in individual and combined drought and pathogen (*P. syringae*pv. *tomato* DC3000) stress resistance. The preliminary results of bacterial multiplication assay, disease index, electrolyte leakage and relative water content showed that *Atgbf3* mutants are susceptible under individual and combined drought and pathogen stress. Results from these experiments will be presented.

Elucidation of molecular basis of tailored adaptation strategies employed by *Arabidopsis thaliana* against combined drought and bacterial pathogen stress

Speaker: Aanchal Choudhary
Supervisor: Dr. Senthil-Kumar Muthappa

In the field conditions, plants are oftensimultaneously exposed todrought and bacterial pathogens, whose combined impact can beeither more detrimental or beneficial to plant's survival and performance. However, the mechanisms governing plant's response tocombined stress have not been elucidated yet. When exposed to drought and *Pseudomonas syringae* pv. *tomato* DC3000, *A. thaliana* exhibits responses unique to combined stress and as well as those that are shared between individual stresses. The responses instigated under combined stress are tailored according to the precise environmental conditions encountered by the plant, changing with the varying severity and timing of two stressors. This results in a high degree of complexity making it difficult to predict the outcome of an interaction by studying stresses in isolation. For a comprehensive mechanistic understanding of tailored strategies employed by plants to combat co-occurring stresses, a systematic methodology was developed for an accurate combined stress imposition. Simultaneous exposure to drought and bacterial stress resulted in enhanced bacterial multiplication and a concomitant increase in electrolyte leakage, reflecting the combined stress induced plant susceptibility. Previously, the whole-genome microarray analysis of *A. thaliana* in response to combined drought and *P.syringae* infection revealed a novel transcriptomeseen specifically under combined stress. This transcriptomic data was extensively analysed for identification of genesunique to combined stress.Mutants for the shortlisted genes would be screened under combined stress using the protocol standardized for combined drought and bacterial stress imposition. From this screen, a candidate gene would be selected for functional validation under combined stress for a deeper understanding of the unique mechanisms underlying combined stress tolerance in plants.

Investigation of Crosstalk between Auxin Signaling and MAP Kinase Cascade during Plant Development

Speaker: Stanzin Noryang
Supervisor: Dr.Alok Krishna Sinha

Auxins regulate diverse cellular and developmental responses in plants, including cell division, expansion and differentiation, patterning of embryos, vasculature and other tissues, and distribution of growth between primary and lateral root and shoot meristems. Auxin signaling involve TRANSPORT INHIBTOR RESPONSE/AUXIN-BINDING F-BOX PROTEIN (TIR1/AFB) which is demonstrated to be a auxin receptor , the Aux/IAA transcriptional repressors, and the auxin response factors (ARFs) which directly regulates the transcription of auxin responsive genes.The Aux/IAAs are a family of extremely short-lived nuclear proteins. Aux/IAA genes are induced rapidly by auxin and are found throughout the higher plants.Rice (*Oryza sativa*) have 31 members of Aux/IAA.Auxin might increase the affinity of Aux/IAAs for SCFTIR1 by stimulating their phosphorylation, as supported by increasing body of biochemical and genetic evidence.The MAP kinases comprise of a linear cascade of three consecutively acting protein kinases, namely MAPKs, MAPKKs, MAPKKKs and sometimes MAPKKKKs mediating sequential phosphorylation reactions.Mockaitis and Howell showed auxin stimulated activation of MAPK.Furthermore, specific inhibitors of MAPKs abolish expression from the auxin-responsive BA3 promoter in the root elongation zone (Mockaitis and Howell, 2000).We wanted to decipher the pathway crosslinking MAPK signalling and auxin signaling. Studies will be conducted to evaluate whether Aux/IAA are the genes connecting auxinsignaling and MAPK signaling.Subcellular localizationof both OsIAA1 and OsMPK3 in the nucleus gives a preliminary indication of their interaction. Further,*in-vitro* phosphorylation assay indicated OsIAA1 to be a phosphorylation target of OsMPK3 as well as OsMPK6. However, yeast two hybrid assay did not give a promising result. Further, in-planta interaction of OsMPK3/OsMPK6 and OsIAA1 will be validated using bimolecular fluorescence complementation (BiFc) assay and co-immunoprecipitation assay.

Identification and characterization of genes related to seed development in chickpea (*Cicer arietinum* L.)

Speaker: SubodhVerma
Supervisor: Dr. Sabhyata Bhatia

Chickpea (*Cicer arietinum* L.) is one of the most important food legume crops in the world especially for human consumption as its seeds provide good sources of protein, carbohydrate and minerals. The importance of chickpea seeds in global food as well as nutritional security therefore necessitates genetic and genomics studies especially related to seed development in order to improve seed yield as this is a major target of chickpea breeding. Thus two approaches were used to delineatethe candidate genes involved in chickpea seed development. In the first part, a high-throughput genotyping by sequencing (GBS) method was used to identify QTLs related to seed traits. Analysis of the genomic sequence corresponding to identified QTLs led to the identification of 101 putative candidate genes.In the second part, storage and maturation phase was targeted to explore the dynamics of chickpea seed development. Seed storage proteins (SSPs), the major ingredient affecting the nutritional quality of seeds are synthesized and accumulate during storage phase of seed development by the orchestrated action of several transcription factors (TFs). Regardless of the extensive studies, this obscure regulatory assembly needs further clarification in many crop plants including chickpea. Therefore, genes encoding SSPs and members of the B3 protein family have been identified from chickpea and characterized at molecular level. In order to understand the synthesis and accumulation of SSPs in chickpea seeds, we aimed to characterize CarABI3, gene that co-expresses with SSP genes to regulate these process. The observations we have compiled in this study could further be leveraged to understand various other facets of seed development in chickpea. These may encompass nutritional and yield properties of chickpea seeds for their manipulation and use in various plant breeding programs.

Functional divergence of glucosinolates transporter gene family in *Brassica juncea.*

Speaker: Deepti M. Nambiar
Supervisor: Dr. N. C. Bisht

Glucosinolates are secondary metabolites containing a thioglucose core and a sidechain derived from amino acid. These compounds on hydrolysis by myrosinases yield isothiocyanates which play an important role in plant defense. Besides, Isothiocyanatesalso cause the characteristic taste and odor of commercially important Brassicaceae crops. Some isothiocyanates are goitrogenic to livestock while some like Sulforaphane are known to be anticarcinogenic. Glucosinolates are synthesized in the leaves and transported to the seeds through long-distance phloem transport. In *Arabidopsis* GTR1 and GTR2 are characterized as high affinity glucosinolate transporters, belonging to the proton-dependent oligopeptide transporters family. Targeting these transporters holds the potential for selectively altering the glucosinolate translocation to seeds without compromising on plant defense.

*Brassica juncea*is an important oilseed crop derived from natural hybridization of *B.rapa* (AA genome) and *B.nigra* (BB genome). Both progenitors have three orthologues each of *GTR1* and *GTR2* all of which have been isolated and sequenced. Redundancy of genes is an indication of functional diversity in the proteins encoded. qRT-PCR has been performed to study spatial and/ temporal regulation of the *GTR* homologues. Promoter-GUSassay is also in progress. Transporter overexpression studies in *Arabidopsis gtr1gtr2* double mutants are being conducted to study the extent of glucosinolate restoration in *gtr1gtr2* by each transporter. This experiment is expected to yield data on differential transport efficiencies as well as substrate affinities of the transporters. In addition,a plant cell linebased transport assay has been standardized which is being used to investigate the functional divergence of the GTR transporters. Correlation between the functional and expression data would be a prerequisite for biotechnological alteration of the glucosinolate transport machinery.

Analysis of the role of certain transcription factors and diversity in seed size and weight during rice seed development

Speaker: Arunima Mahto
Supervisor: Dr. Pinky Agarwal

Rice serves as an ideal model crop for studying seed development and seed size related traits because it is the staple food for approximately 70% of Indian population, it has a small diploid genome for which good quality sequence information is available and the information extracted can be extrapolated to other monocot crops for crop improvement. Transcriptome studies have been widely employed to study seed development and seed size traits in rice. These studies capture the information about the genes and pathways that affect developmental processes leading to the phenotype under investigation. Small RNA profiling also gives an idea about the regulation of seed development through transcript level regulation. However, there is still scope in the area of identification of key genes and regulatory mechanisms that govern seed size traits in rice. In the last decade, studies on embryo, endosperm and various seed developmental stages have highlighted that transcription factors and small RNAs might be few of the determinants of seed development and seed size. Based on the above knowledge, comparative transcriptome and small RNAome study of five seed developmental stages of two rice varieties, with contrasting seed size traits, has been undertaken. The aim of the study is to decipher the key molecular factors, such as genes, regulatory pathways and biological processes that control seed size in rice. Also, to explore the role of transcription factors in seed development, functional characterization of two *ZOS* transcription factors that are highly expressed in seed stages is underway. For this, plants with altered expression of the genes are being raised. We aim to molecularly characterize these two genes for their roles in seed development and identify genes responsible for seed size/weight traits by comparative transcriptomics.

Role of Jasmonate Signaling Components in Nutrients Deficiency Response in Rice and Chickpea

Speaker: Ajit Pal Singh
Supervisor: Dr.Jitender Giri

Mineral nutrients play critical role in the physiology and development of plants. Therefore, optimum supply of each nutrient is essential for the proper growth of plant. Nutrient deficiencies are major obstructions for the crop yield. In order to supplement the deficient nutrient, farmers apply chemical fertilizers which have been proven to disturb the natural conditions of the soil and its microenvironment leading to the soil degradation and nutritional imbalance. Moreover, reserves of these fertilisers are limited.Therefore, novel approaches are required to improve the nutrient-use-efficiency of the plant and to cope with grain losses due to soil nutrient deficiencies.

Nutritional deficiencies modulate rootsystemarchitecture to enhance the acquisition of essential nutrients from the soil. Jasmonic Acid (JA), a phytohormone, is well-known for inhibiting root elongation and plays a key role in root meristem alteration under phosphate deficiency. Transcriptome analysis revealed that many JA responsive genes are differentiallyregulated under nitrogen and potassium deficiency. These studies have confirmed a prominent role of JA signaling in the regulation of multi nutrient homeostasis, making it rational to study the role of jasmonate signaling components under different nutrient deficiencies. Therefore, in the present study we are investigating the role of JA signaling components in the regulation of various nutrient deficiency responses in rice and chickpea. Since, rice is the main source of energy for 2/3rd of the world's population while chickpea is the world's third most important legume crop; these two systems were taken to have a comparative study onresponse mechanisms opted by a monocot and a dicot. Our analysis has shown a certain level of specificity of various JA associated genes towards different nutrient deficiencies in both rice and chickpea.

Identification and Characterization of heat-responsive microRNAs in *Solanum lycopersicum* L. (Tomato)

Speaker: Sarita Jha
Supervisor: Dr.Saloni Mathur

Heat stress has negative impact on the growth and development of plants. In crops like tomato, vegetative as well as reproductive stages are affected, resulting in reduced crop yield. To combat such adverse environmental conditions, plants need to respond fast to adapt and survive. MicroRNAs (miRNAs) have emerged as key molecular regulators of several important processes in growth and development as well as in response to various environmental stresses. However, an exhaustive study on heat responsive miRNAs is completely lacking in tomato. The aim of the study is to identify and characterize heat-responsive miRNAs and their targets in the vegetative and inflorescence stages of tomato. This will be achieved by first screening for a heat-tolerant and heat-sensitive tomato cultivar in response to heat stress during various stages of vegetative and flower development in nine cultivars of tomato, followed by comparative analysis of their miRNomes. For achieving this feat, survival assays following heat stress at seedling and one month old stage were performed. Further physiological parameters like relative water content, electrolytic leakage and proline content in heat-stressed plants in comparison to control plants for all selected cultivars were studied. Correspondingly, a comparative analysis of these cultivars at reproductive stage at field scale and at pilot scale in growth chamber was evaluated for flowering, fruit set and yield. The cumulative analysis of parameters enabled to select the most heat tolerant and heat sensitive tomato genotypes. Further, Pollen survival assays under heat stress has been studied in these two contrasting varieties as means for pollen development and viability to decipher the flower development stages most sensitive to heat stress. RNA from one-month-old leaves of contrasting cultivars has been isolated and sent for small RNA library preparation and sequencing. Also, tissue from inflorescence stages is being collected which will also be utilised similarly. The study will aid in understanding the complex miRNA-mediated networks in providing thermo-tolerance in tomato.

Study of oxalic acid responsive metabolic remodeling in crop plants: a functional proteomics approach

Speaker: Pramod Kumar Mittal
Supervisor: Dr. Subhra Chakraborty

Oxalic acid (OA), a simple low-M_r two-carbon dicarboxylic acid and a natural plant metabolite is ubiquitous among fungi and plants as an inert end product of carbon metabolism. Epidemiologically, it is known to be associated with a variety of nutritional disorders such as nephrolithiasis, nephrocalcinosis, besides cardiovascular disease in human and fungal diseases in plant; while its derivative β-N-oxalyl-α,β-diaminopropionic acid (β-ODAP) causes neurolathyrism in human. Thus OA is considered as a potential anti-nutrient, virulence determinant and elicitor molecule.Following the accumulation of anti-nutrient and recognition of patho-stress, the activation of complex signaling networks leads to a massive translational and metabolic reprogramming. Fruits, vegetables and legumes are the primary source of vitamin C and β-carotene and other essential minerals, proteins and the major contributors are tomatoes, spinach, soybean, grasspea and groundnut. Nonetheless, the nutritional quality of these crops is largely compromised due to the presence of high OA while their productivity is threatened by the necrotrophic phyto-pathogen *Sclerotinia*sp wherein OA is the virulence determinant. Recently, our laboratory and others have shown that downregulation of OA following overexpression of a fungal oxalate decarboxylase (*FvOXDC*) improve nutritional quality with enhanced immunity in crop plants. Furthering the work our laboratory has very recently developed low oxalate and fungal tolerant over-expression lines in spinach by engineering *FvOXDC*.To understand the molecular and biochemical consequences of OA downregulation in spinach, a proteomic study has been conducted that identified 639leaf proteins withdiverse function and cellular physiology in wild type spinach.Furthermore,to investigate the OA-responsive proteomic pathways and metabolic consequence in seed tissue groundnut has been transformed with *FvOXDC*.Investigation of cellular remodeling upon downregulation of OA may form an important basis for breeding nutritionally improved and environmentally adapted cultivars.

Elucidating the role and regulation of Protein L-Isoaspartyl Methyltransferase (PIMT) in plants

Speaker: Shraboni Ghosh
Supervisor: Dr. Manoj Majee

Abiotic stresses usually lead to deterioration of structure and function of proteins. Maintenance of such proteins during stress condition is vital for survival under stress. PROTEIN L-ISOASPARTYL METHYLTRANSFERASE (PIMT, EC.1.1.77) is a protein repairing enzyme that is known to repair damaged and aged proteins. Here we examine the function of PIMT in *Arabidopsis thaliana* plants under various abiotic stresses. Involvement of PIMT in stress tolerance was investigated by analysis of PIMT overexpression and RNAi lines in seedlings as well as in mature plants. During stress conditions elevated PIMT activity was seen which limitsthe accumulation of abnormal L-isoAsp residues. The RNAi lines exhibited greater sensitivity to the stress conditions whereas constitutive overexpression of both cytoplasmic (AtPIMT1) and nuclear (AtPIMT2) PIMT confers tolerance to various stresses. The damage caused by induced stresses was assayed in terms of malondialdehyde content, chlorophyll estimation and H_2O_2 accumulation. *In situ* localization of superoxide radical and hydroxyl radical revealed accumulation of ROS species during stress. Higher activity of antioxidative enzymes like catalase and ascorbate peroxidases in overexpression lines lead to lesser ROS accumulation as compared to RNAi lines. The overall higher PIMT activity and lower isoaspartyl accumulation leads to improved survival of the transgenic plants. The results indicate that PIMT not only functions in seed vigor and longevity but also provides stress tolerance to plants by repairing isoAsp mediated damaged proteins particularly anti-oxidative enzymes and proteins which in turn limit reactive oxygen species formation.

Genome-wide characterization of functional polymorphism and epigenetic modifications in rice genotypes with contrasting seed size.

Speaker: Angad kumar
Supervisor: Dr. Jitendra K. Thakur

Over half of the world's population consume rice as a staple food which is also considered as an important feedstock for livestock. The rice grain is mainly endosperm tissue. Endosperm stores energy primarily in the form of starch, storage proteins, and lipids. In a living cell the genetic material is stably maintained and inherited via Mendelian rules whereas the epigenetic marks (DNA methylation and histone modification) can be reversibly deposited. Epigenetic modifications drastically impact genome expression via chromatin remodelling, genetic imprinting and hence significantly affect the phenotype. Development process is governed by finely tuned transcriptional regulation of appropriate genes. In rice, several genes contributing to seed or grain size have been identified and characterized, but their regulatory mechanism (genomic and epigenomic) for proper rice endosperm development is still largely unknown so far. In the proposed study, we are analyzing the genome wide DNA polymorphism in four contrasting seed size rice genotypes and also the epigenomic dynamics during their seed development stages. So, an endeavour to understand the differential expression of various genes via an integrated approach of genomics and epigenomics and further screening of some unique QTLs and haplotypes under epigenetic influence for improved quality of rice seed traits may prove to be answer to future rice scarcity.

Study of Host-specific Immune Response during Vascular Wilt in Plants

Speaker: Pooja R. Aggarwal

Supervisor: Dr. Subhra Chakraborty

Disease incidence is the most crucial factor that negatively influences plant growth and limits productivity worldwide. Although vascular wilt caused by *Fusarium oxysporum* is often pervasive in plants, pathotype-genotype dependent compatible vs. incompatible interaction determines susceptibility and/or immunity. Plants have various innate mechanisms that confer the capability to perceive the signal and translate the perception into specific response to particular pathogen. One of the big gaps in our understanding of plant immunity is in the regulatory and signaling pathways that operate immediately after pathogen recognition. These molecular events involve gene expression reprogramming, differential transcript and protein accumulation, signal transduction dependent activation or repression of target factors, and various post-translational events. To understand the immune response during vascular wilt, we performed RNA-seq analysis of *Fusarium oxysporum* inoculated and mock treated chickpea roots. A total of 407 million paired-end reads were generated from pathostress-responsive root libraries which were assembled into ~64,500 transcripts. Together a total of ~3550 host genes were differentially expressed during root infection, including several canonical and non-cannonical transcription factors. Considering the complexity of the wilt disease, significantly more genes and proteins are likely to be involved in defense. To further identify the protein regulatory network involved in disease response, we developed the nuclear proteome and phosphoproteome and identified 250 proteins. In addition, we have identified a novel chickpea gene, *CabHLH1* exhibiting sequence specific DNA binding activity that acts as transcriptional repressor. We also found that the mutant of *CabHLH1* homolog in *Arabidopsis thaliana* is sensitive to *Fusarium* infection and shows wilting under pathogen-stress condition. Furthermore, overexpression of *CabHLH*1 in arabidopsis wild-type enhances host tolerance to *Fusarium* infection. Based on these results, we propose that *CabHLH1* might be involved in transcriptional regulation of immunity related genes in response to patho-stress.

Protein L-Isoaspartyl Methyltransferase (PIMT): Role and Regulation in Orthodox and Recalcitrant Seeds.

Speaker: Kamble Nitin Uttam
Supervisor: Dr. Manoj Majee

PROTEIN L-ISOASPARTYL (D-ASPARTYL) O-METHYLTRANSFERASE (PIMT EC 2.1.1.77) specifically recognizes and repairs the isomerized and racemized products of aspartate and asparagine in Ado-Met dependent manner which are otherwise degraded via proteolytic pathways. Among plants, PIMT genes have been cloned only from *Arabidopsis*, wheat, chickpea and rice. In contrast to desiccation tolerant orthodox seeds, recalcitrant seeds are desiccation sensitive and are unable to survive for prolonged period of time (longevity). Altogether, recent studies revealed that PIMT plays an important role in seed vigor and longevity in orthodox seeds (*Arabidopsis*, chickpea and rice). However, it remains a question whether PIMT enzyme is necessary in recalcitrant seeds or not. In this study, a comparative analysis of PIMT has been conducted using two rice species *Porteresia coarctata* and *Oryza sativa/Oryza rufipogon* which are characterized by contrasting responses to seed desiccation tolerance and longevity. In contrast to the high PIMT activity in rice orthodox seeds, a significantly reduced PIMT activity has been observed in recalcitrant seeds of *Porteresia coarctata*. Subsequently PIMT encoding genes were cloned from both the species and sequences were compared. Sequence analysis revealed that *PIMT1* from *Oryza sativa /Oryza rufipogon* (*PIMT1*) and *Porteresia coarctata* (*PcPIMT1*) are fairly similar while *PIMT2*-2 from *Porteresia coarctata* is rather different from *Oryza sativa/Oryza rufipogon PIMT2* (OsPIMT2). Biochemical analysis revealed similar yet distinct enzymatic properties between PcPIMTs and OsPIMTs. PIMT activity, isoAsp accumulation and western blot analysis in dry seed, organs and during seed development revealed the differential regulation of PIMT in orthodox and recalcitrant seeds. For functional analysis of PIMTs, over expression, RNAi, promoter gus lines for *PcPIMTs* and *OsPIMTs*, were generated. Analysis of orthodox *OsPIMTs* over expression lines revealed that PIMT plays an important role restricting deleterious isoasp accumulation; repairs antioxidative enzymes and proteins which restrict ROS accumulation, lipid peroxidation to improve seed vigor and longevity in orthodox seeds.

Functional analysis of genes controlling seed size and weight in rice

Speaker: Ankit Verma
Supervisors: Dr. Pinky Agarwal and Prof. A. K. Tyagi

Rice (*Oryza sativa*) grain size/weight is an important agronomic trait for yield production. In rice, grain yield is a complex trait and is determined by three typical quantitative component traits: number of panicles per plant, number of filled grains per panicle and grain weight. Grain weight is positively associated with grain size that is defined in terms of its length, width and thickness. All these yield component traits are controlled by naturally occurring quantitative trait loci (QTLs). Several (QTLs)/genes regulating grain size have been identified and functionally characterized to find out molecular components and genetic regulatory mechanisms controlling grain size trait in rice. Still the molecular basis of grain development is largely unknown. The study of genes underlying seed development and their genetic regulatory networks is necessary to understand the mechanism of grain development which will provide clues about yield and quality improvement. In plants, transcription factors (TFs) play important roles in regulation of all biological processes such as development and stress responses. So, in order to understand the regulatory network of TFs in seed development, we aim to study three genes, *GRAIN WIDTH2 (GW2)*, *BASIC LEUCINE ZIPPER (bZIP)*, and *ZOS* in detail which shows seed-specific/preferential expression. In order to understand the molecular functions of these genes in seed development, we aim to raise rice transgenic plants with altered expression of these genes. For this purpose, RNAi & antisense plants have been raised for *GW2* and the construction of RNAi plants for *bZIP* and OE plants for *ZOS* is underway. The presentation will include the progress and observation made with respect to functional characterization of these genes and their roles in controlling seed size/weight.

Delineating the roles of heat shock protein encoding gene(s) of foxtail millet [*Setaria italica* (L.) P. Beauv.] during abiotic stress

Speaker: Roshan Kumar Singh
Supervisor: Dr. Manoj Prasad

Plants in the environment are exposed to several abiotic and biotic stresses which pose serious threat to their survival and productivity; however, plants are naturally evolved with sophisticated molecular machinery to sense and circumvent the stresses. Heat shock proteins (HSPs) perform significant roles in conferring abiotic stress tolerance to crop plants. In view of this, HSPs and their encoding genes were extensively characterized in several plant species; however, understanding their structure, organization, evolution and expression profiling in a naturally stress tolerant crop is necessary to delineate their precise roles in stress-responsive molecular machinery. In this context, the present study has been performed in C_4panicoid model, foxtail millet, which resulted in identification of 20, 9, 27, 20 and 37 genes belonging to *SiHSP100*, *SiHSP90*, *SiHSP70*, *SiHSP60* and *SisHSP*families, respectively. Comprehensive *in silico* characterization of these genes followed by their expression profiling in response to dehydration, heat, salinity and cold stresses in foxtail millet cultivars contrastingly differing in stress tolerance revealed significant upregulation of several genes in tolerant cultivar.Several fold up-regulation of *SisHSP*-27 in response to heat, salt and dehydration stress in tolerant cultivar stress hinted the role of this gene in conferring stress tolerance.Therefore, the gene was over-expressed in yeast, and interestingly, yeast cells transformed with *SisHSP*-27 demonstrated tolerance to several abiotic stresses.Presently, over-expression of this gene in foxtail millet and rice systems are in progress, and if successful, the study will delineate the role of this novel gene in conferring durable stress tolerance.Altogether, the study provides novel clues on the role of HSPs in conferring stress tolerance.

Mechanistic insights into the mycophagous and antimicrobial properties of *Burkholderia gladioli*

Speaker: Sunil Kumar Yadav
Supervisor: Dr. Gopaljee Jha

Plant diseases possess a serious threat towards the emerging food demand for the ever growing human population. Therefore, effective biological control strategies need to be formulated to prevent plant diseases and minimize the yield loss caused by them. Recently a plant associated bacteria *Burkholderia gladioli* strain NGJ1 was isolated in our lab, which demonstrated antifungal and mycophagous (fungus eating) properties against *Rhizoctonia solani*, an important fungal pathogen of rice. We explored this interaction in detailed during this study and observed that the bacterium also demonstrates mycophagous property on model fungi *S. cerevisiae* as well as *Candida albicans*. The bacterium also exhibited strong antibacterial activity against *E. coli, Bacillus subtilis, Ralstonia solanacearum, Xanthomonas oryzae* and *Pantoea ananatis* etc. In order to understand the molecular mechanism behind mycophagy and antibacterial properties, we established genetic transformation protocol. During the seminar, I would elaborate our effort in this direction and discuss data revealing important insights into the molecular intricacies of mycophagous and anti-bacterial activities of *B. gladioli* strain NGJ1. Further, I will present my current and future research initiatives in this direction.

Branching wisely: Unravelling the nexus between jasmonic acid and glucose signalling in Arabidopsis

Speaker: Manvi Sharma
Supervisor: Dr. Ashverya Laxmi

Plant root system is highly flexible and acclimatizes to its surrounding environment by changingits architecture. The overall plant architecture defines their foraging capacity for resources. While primary root is more gravitropic, lateral roots (LR) are often maintained at specific angles to gravity, a quantity called gravitropic set-point angle (GSA). The prime role of LR is to allow plants to optimise the capture of resources and provide anchorage in soil. Although, most of the studies are confined to main root gravitropism, recent reports on LR GSA have provided insights into the mechanisms governing GSA. The role of auxin in steering GSA formation has been well established. In this work, we introduce jasmonic acid (JA) as a new player in controlling LR branch angle with respect to primary root. We show that JA inclines the LR to a more vertical orientation. JA signalling through receptor $SCF^{COI1}$and its downstream signalling element MYC2 is required for this response. We further analyzed the independent and combined effect of glucose on branch angle change. Glucose alone does not alter the LR angle as WT seedlings behaved similarly to different glucose concentrations. In the absence/low conc. of glucose, MeJA caused more vertical orientation of LR, while in higher concentration of glucose; MeJA could not execute the similar effect, suggesting an antagonistic interaction between exogenous glucose and JA in controlling LR angle.However, glucose, in a hexokinase dependant and G-protein independent manner interacted with JA to control change inLR angle. Finally we show that JA-Glc requires auxin transport and signalling to regulate LR angle and acts downstream to JA signal transduction.

Role of activities and localization of CIPK6 and its interacting proteins in the susceptibility of biotic stress in Arabidopsis

Speaker: Niraj Kumar Vishwakarma
Supervisor: Dr. Debasis Chattopadhyay

Ca^{2+} is the most common second messenger in plants and animals. When cell experiences any external stimuli, spatial and temporal changes in [Ca^{2+}] occur. CIPK (CBL interacting protein kinase) family is one of the important protein kinase families in calcium signalling network. These proteins interact with calcium sensor relay CBLs (calcineurin B-like proteins) for their kinase activity. These kinases form a novel plants specific family of Serine/Threonine kinase and are most similar to SNF1 (sucrose non-fermenting) kinases. CIPKs were mostly shown involved in abiotic stress responses. Previously, our laboratory and others have shown CIPK6 from chickpea and Arabidopsis is involved in salt stress tolerance. Recently, tomato CIPK6 was shown required for pathogen-mediated hypersensitive response. In our laboratory, it was observed that Arabidopsis CIPK6 acts as a negative regulator of plant immunity against phytopathogen *Pseudomonas syringae* DC3000. In order to study the role of kinase activity of CIPK6 in susceptibility to *Pseudomonas syringae*, atcipk6-/- lines complemented with different AtCIPK6 constructs have been made.

Remodeling of the transcriptome, proteome and metabolome of grasspea: the molecular basis of dehydration tolerance

Speaker: Divya Rathi
Supervisor: Dr. Niranjan Chakraborty

It is least likely that the varied molecular basis of stress tolerance in members of legume family, Fabaceae, constituted by 946 genera, can be accurately unraveled in a few species. Despite their hardiness, the major constraints to global legume production have been the multivariate environmental stresses. Grasspea (*Lathyrus sativus* L.) is one of the best examples of an orphan legume, which has thus far received little research attention. Grasspea cultivars are capable of withstanding a myriad of abiotic and biotic stresses, making it one of the best systems to study stress tolerance. We therefore investigated molecular basis of stress tolerance in grasspea subjecting 3-week-old seedlings to dehydration for duration of 144 h. There were no visible changes in the seedlings till 48 h of dehydration and the leaflets curled after 60 h and displayed chlorosis. Physicochemical analyses were conducted by parameters such as relative water content, membrane stability, and impact on accumulation of proline and photosynthetic pigments. The temporal effects of dehydration were evaluated at the transcriptomic, proteomic and metabolomic levels using *de novo* RNA-seq, 2-D gel electrophoresis and GC-MS, respectively. The 2-DE analysis revealed 163 proteins that were differentially regulated in a qualitative as well as quantitative manner. Conversely, approximately hundred-fold transcripts were found to be dehydration-responsive when compared to the proteins. Furthermore, dehydration-responsive metabolome profile displayed significant alteration in 30 metabolites associated with global metabolic pathways. The combined analysis of the multi-omics landscape of grasspea would not only provide useful insights into underlying mechanism of stress tolerance, but also enlist the novel biomarkers that could be used for targeted genetic manipulation for crop improvement.

Study of differential protein expression in the plasma membrane of chickpea (*Cicerarietinum* L.) under dehydration stress

Speaker: Pragya Barua
Supervisor: Dr.Niranjan Chakraborty

Plasma membrane (PM) encompasses total cellular contents regulating all cellular exchanges in a spatio-temporal fashion. Most of the essential tasks of PMs, including molecular transport, cell-cell interaction and signal transduction, are carried out by their proteinaceous components, which make the PM protein repertoire to be diverse and dynamic. Therefore, we carried out systematic analysis of PM proteome of a grain legume, chickpea.Proteins were extracted from PM-enriched fraction of four-week-old seedlings using aqueous two-phase partitioning. To address a population of PM proteins that is as comprehensive as possible, both gel-based and gel-free approaches were employed, which led to the identification of a set of 2754 non-redundant proteins. These included both integral proteins having bilayer spanning domains as well as peripheral proteins associated with PMs through post-translational modifications or protein-protein interactions. Further, the proteins were subjected to various *in-silico* analyses and functionally classified based on their gene ontology. A complete set of PM proteins, previously reported from several monocot and dicot species, was generatedand compared with the generated PM protein dataset of chickpea. Furthermore, we characterized a dehydration-responsive DREPP-domain containing phosphoprotein, designated CaDREPP1.Subcellular localization analysis in tobacco and onion peel, and stably transformed Arabidopsis protoplast confirmed CaDREPP1to be localized to the plasma membrane. Next, we generated YFP-fused deletion variants of CaDREPP1 and revalidated its membrane association. CaDREPP1 was shown to have lipid binding properties. The comparison of wild type, T-DNA mutant and overexpression in Arabidopsis suggest its possible role stress adaptation.

Regulation and Function of selected Small RNAs in *Arabidopsis thaliana* Root Development

Speaker: Sandeep Yadav
Supervisor: Dr. Ananda K. Sarkar

Being a model plant, *Arabidopsis thaliana* provides us an excellent root system to better understand the factors (genes, non-coding RNAs and proteins) quintessential for its growth and development. Small RNAs are classified into two broad groups based on their precursor sequence: hairpin RNA (hpRNA) and short interfering RNA (siRNA). miRNAs are well studied subset of hpRNAs defined by the highly precise excision of one or more functional products, which are called mature miRNA. It is likely that at any given time of development most biological processes are modulated by one or more miRNAs, which are also subject to regulation.

Expression pattern of a gene is a cumulative effect of regulatory sequences present in the promoter region and the chromatin state maintained by chromatin modifiers due to the presence of differential epigenetic marks. In plants, homologs of chromatin modifiers have been found and most of them are evolutionary conserved in functions. Previous work in our lab had shown that *SWIRM domain PAO protein* (*SWP1*), a component of plant specific co-repressor complex, is a negative regulator of root growth and branching. We have identified differentially expressed miRNAs between *swp1*-1 and *Col-0*. We are doing the functional characterization of selected miRNAs (MIR167, MIR172 and MIR832) and their targets by utilising both gain of function and loss of function approaches. Expression of miR167a-d is spatiotemporally regulated in embryonic and postembryonic root and shoot tissues. Down regulation or ectopic expression of these miRNAs or their targets showed their role in meristem function and root architecture. MIR167 negatively regulates both shoot and root development by altering the auxin homeostasis.Further experiments are required to better understand their role in root development.

Identification, characterization and functional analysis of KIX-TAD interactions in *Arabidopsis thaliana*

Speaker: Archana Yadav
Supervisor: Dr.Gitanjali Yadav

Regulation of transcription is an integral part of gene expression in all living organisms.The kinase-inducible domain interacting (KIX) domain is a highly conserved independently folding three-helix bundle present in coactivators that serves as a docking site for transcription factors, whereupon promoter activation and target specificity are achieved during gene regulation. This event leads to the transcription assembly and gene expression. KIX domains have been characterized in transcriptional coactivators such as p300/CREB-binding protein (CBP) and mediator of RNA polymerase II transcription subunit 15 (MED15), and even recQ protein-like 5 (RECQL5) helicases in various organisms. Their targets are often intrinsically disordered regions within the transactivation domains of transcription factors that attain stable secondary structure only upon complexation with KIX. These regions further consists of small nine amino acid long motifs called nine amino acid transactivation domain (9aaTAD) which are considered sufficient to induce transactivation.Despite playing an important role in transcription, overall knowledge of KIX domain as well as KIX-TAD interaction is significantly limited and more so in plants as no plant KIX structure is characterized yet. The specific aim of this study is to predict and validate TADs in plant transcription factors, identify and analyse KIX domains in plants and characterize KIX-TAD interactions. A computational program has been developed to predict 9aaTADs in *Arabidopsis.*A web resourse called KIXBASE has also been developedto serve asa global repository as well as a prediction tool for KIX domains in any organism. Hidden markov models have been coupled with tertiary fold recognition in order to predict KIX domains in approximately 600 organisms spanning metazoans, fungi and plants. The evolutionary analysis of selected KIX domains has been carried out.

Computational analysis of the StAR-related lipid transfer (START) domains in plants

Speaker: Sanjeet Kumar Mahtha
Supervisor: Dr. GitanjaliYadav

The steroidogenic acute regulatory protein (StAR) related lipid transfer (START) domain is an evolutionary conserved domain of approximately 200 amino acids implicated in lipid/sterol binding and transport. This domain belongs to a wide set of α/β helix-grip-fold structures forming the SRPBCC (START/RHO_alpha_C/PITP/Bet_v1/CoxG/CalC) superfamily in the NCBI Conserved Domain Database. START protein domains are conserved, making them candidates for involvement in both animal and plant lipid/sterol signal transduction.They play a crucial role in transfer of lipid/sterol, lipid signaling and modulation of transcription activity in plants. START domains are more abundant in plants than in animals.There is extensive variation in the gene family size of START domain between species, ranging from 1 to 6 in lower plants like chlorophytes, to amplification of upto ~70 START domains in some angiosperm genomes.Domain structural analysis shows that in lower plants the majority of START domains are either minimal START (having no additional domain) or having single additional domain (DUF1336). But in higher plants such as angiosperms, the START domains are associated with several additional domains with various combinations.In plants,START domains are primarily found within homeodomain (HD) transcription factor families. Gene structural analysis shows extensive variation of exon-intron architecture in STARTdomain containing protein in plant kingdom. The phylogenetic tree was constructed based on representative sequences to study the extent of similarity and divergence between START domains.

Identification and characterization of candidate gene(s) associated with high-amylose content in foxtail millet *Setaria italica* L.

Speaker: Annvi Dhaka
Supervisor: Dr. Manoj Prasad

Starchy foods are potential candidates for reducing glycaemic and insulinemic responses. High amylose content (AC) in cereal grain is a source of resistant starch (RS) which passes the small intestine and gets fermented in the large intestine to produce short chain fatty acids, which ultimately results in gradual and progressive release of glucose in blood. RS has been reported to decrease the postprandial blood glucose and insulin levels, lowers cholesterol and improves gastrointestinal health. Adequate levels of RS in diet assists in overcoming obesity-related conditions including cardio-vascular disease and Type-2-diabetes, and also consumption of RS reduces the risk of colorectal cancer. Noteworthy, foxtail millet (*Setaria italica*) is rich in RS and high fiber (β-glucans) in its whole and partly-milled grains, and a positive relationship between RS and AC has been established in several studies. In view of this, an attempt has been made to identify and characterize the genes involved in amylose biosynthesis. Key gene families involved in starch biosynthesis pathway namely adenosine 5' diphosphate-glucose pyrophosphorylase, starch synthase, starch branching enzyme, starch debranching enzyme, starch phosphorylase and starch disproportionating enzyme have been identified and characterized using computational approaches. Further, biochemical profiling of starch and amylose content in released foxtail millet varieties was performed, which showed variation in the contents. Presently, phenotyping of cultivated as well as wild *Setaria* sp. for amylose and starch content is being carried out. This information will be used to identify the genetic determinants of starch biosynthesis in foxtail millet genome using genotyping-by-sequencing approach.

Characterization of a novel dehydration-responsive phosphoprotein of chickpea (*Cicer arietinum* L.)

Speaker: Lande Nilesh Vikram
Supervisor: Dr. Niranjan Chakraborty

Post-translational modification of proteins, particularly phosphorylation, plays a key role in regulation of various stress-responsive pathways. The importance of protein phosphorylation, as a ubiquitous regulatory mechanism, is well established. We aimed to characterize a PDZ domain containing phosphoprotein of chickpea (*Cicer arietinum* L.), designated CaPDZ1. In our previous proteomics study, the protein was found to be differentially regulated under dehydration stress. Screening of the amino acid sequenceof CaPDZ showed the presence of both PDZ and TPR domains. Furthermore, sequence alignment of CaPDZ domain containing proteins in selected monocot and dicotspecies indicated that in addition to the presence of chloroplast transit peptide, there is a high representation of consensus residues among the sequences. Phylogenetic analysis with the orthologues showed CaPDZ to be the closest to its homologues present in *Medicagotrancatula* and *Glycine max*.Subcellular localization study by western blot analysis revealed its high abundance in the chloroplast fraction, which is similar to its homologues in Arabidopsis and maize. To further validate, intact chloroplasts were isolated from 3-week-old chickpea seedlings and a reference proteome map was developed. The proteomic analysis led to the identification of a total of 2451 proteins that include CaPDZ. The bioinformatics prediction of protein localization suggested 1700 proteins to be localized to the chloroplast.Gene ontology-based annotation and classification showed that majority of the proteinsmight be involved in biosynthetic pathways.

Twisting Plant Immune Signaling by Fungal Effectors

Speaker: Kanchan Prabha
Supervisor: Dr. Praveen Verma

The ongoing race between plants and phytopathogens determines the susceptible and resistant phenotype of the host plant. Over the time, plant defense machinery has undergone evolutionary changes to fortify its defense mechanisms. The PTI (PAMP Triggered Immunity) response is the first level of defense posed by plant after pathogen attack.To suppress PTI fungal pathogens releases effector molecules inside the host which either induces ETI (Effector triggered Immunity) or ETS (Effector Triggered Susceptibility). The most devastating fungal phytopathogens are the necrotrophic pathogens that results in great yield losses every year. Our laboratory focuses on Ascochyta blight of chickpea which is caused by a necrotrophic fungi *Acochyta rabiei*, infecting all the aerial parts of the plant and causing necrotic lesions. On the basis of *de novo* genome assembly generated in our lab, several genes have been discovered which encodes for toxins, primary and secondary metabolites, transporters and secretory proteins. The comprehensive secretome analysis was performed which resulted in 758 potential secretory proteins.One of the secretory protein identified which may have function in pathogenesis of *Ascochyta rabiei* is a salicylate hydroxylase, which is well studied in *Pseudomonas putida* and known by the name *NahG*. The salicylate hydroxylase is an enzyme which belongs to NADB Rossmann superfamily. Its known function is to convert the salicylate into catechol in the presence of FAD as a cofactor via decarboxylative hydroxylation and it is known that catechol induces the production of ROS in plants. Bioinformatics analysis revealed that it has a PEXEL (Plasmodium Export Element) motif. Hence, it is expected that PEC8 (PEXEL Effector Candidate) can behave as an effector molecule and may have role in pathogenesis. Our study involves the functional characterization of such genes which are either directly involved in pathogenesis or indirectly helping the pathogen during infection.

Development of nutrient-responsive differential seed transcriptome and proteome in chickpea

Speaker: Arunima Sinha
Supervisor: Dr. Subhra Chakraborty

Storage organs display diverse nutritional quality and complex multistep development highly related to nutrient metabolism and transport as an intense sink activity in plants. Seeds, a major source of nutrients for human and animal livestock show significant diversity in reserve synthesis and accumulation that also affect growth, development, and productivity. The major events associated with nutritional status in seed are a complex process, and are majorly divided into four main steps: pre-storage, synthesis, accumulation and utilization of nutrients. To better understand the molecular mechanisms and signaling pathways controlling seed nutritional status, relationship between mRNA and protein patterns from early stages of seed filling to desiccation was established. To gain insight on nutrient-responsive genes, Illumina HiSeq 2000 paired-end sequencing technology was used that revealed a total of 192.3 million reads assembled into 191,487 total numbers of contigs. Out of the total 60,584 transcripts, 6582 were found to be differentially expressed at one or more developmental stages which were further categorized based on function.Furthermore, the nutrient-responsive seed proteome and phosphoproteome showed high level of reproducibility and led to the identification of 96 differentially expressed proteins after MS/MS analysis accounting for 71% unique proteins.Transcript and protein profiles showed considerable similarityacross the stages of seed development with some divergent patterns indicating post-transcriptional events. These findings may provide new direction for metabolic engineering in plant.

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Genetic Dissection of Quantitative Grain Size and Weight Traits in Rice

Speaker: Daware Anurag Vasantrao

Supervisors: Dr. Swarup K. Parida & Prof. Akhilesh K. Tyagi

Rice is an important staple food crop and targeted extensively for genetic improvement to ensure global food and nutritional security amidst current climate change scenario. Genetic mapping and map-based cloning of genes/QTLs for diverse yield component traits coupled with marker-assisted selection have been proved instrumental in enhancing rice grain yield. Grain size/weight is among the most vital yield-contributing complex quantitative traits in rice. Especially, the long-grained aromatic rice is of high consumer preference and fetches premium price in Basmati trade and commerce. Significant efforts have been made to identify/map genes and QTLs regulating grain size/weight which essentially identified >400 major QTLs. The potential genes underlying a diverse array of these QTLs have also been isolated and functionally characterized through positional cloning and functional genomics approaches. However, most of these identified grain size/weight genes, except few like *GS3* have failed to explain grain size/weight variation existing especially within Indian *indica* rice accessions. This major drawback can primarily be ascribed to considerable difference in genomic constitution of Indian rice accessions from the Chinese *indica* and *japonica* accessions, using which most of these grain size/weight genes and QTLs have been documented so far. In this context, possible involvement of either entirely different set of novel genes or different alleles of already known/cloned genes in regulating grain size/weight trait variation in Indian *indica* rice accessions cannot be ruled out. Henceforth, identification and marker-assisted introgression of superior natural allelic variants of known as well as novel genes/QTLs governing grain size/weight using Indian *indica* and aromatic rice accessions will be crucial for increasing rice grain yield and productivity in India. Keeping this in view, preliminary efforts have been made to map major genes underlying grain size/weight robust QTLs by deploying a novel integrated genomic approach for marker-assisted genetic enhancement of rice.

Moving in for the kill: Effector entry and host interaction for nectrotrophy

Speaker: Shreenivas Kumar Singh
Supervisor: Dr. Praveen Verma

Being sessile in nature, plants have to cope with both biotic and abiotic factors in their niche. The biotic factors include several phytopathogens. One of the necrotrophic fungal phytopathogens *Ascochyta rabiei* is highly devastating to chickpea (*Cicer arietinum*). The notion of the necrotroph has evolved from toxic chemical secreting to effector secreting pathogens. Effectors are secreted specialized molecules intended to establish pathogenicity in host. Earlier, genome sequencing and secretome analysis of *A. rabiei* has revealed plenty of PEXEL motifs containing secretory effectors molecule. One such effector obligatory for *A. rabiei* virulence is PEC25 (PEXEL-like Effector Candidate 25). The Plasmodium Export Element (PEXEL) is the characteristic of malarial parasite *Plasmodium spp.* Its 1st, 3rd and 5th residue is conserved in *Plasmodium spp,* phytopathogens and animal pathogens. Translocation of effectors from fungus to host is assisted by conserved PEXEL sequence. Therefore, to look into the role of PEC25 PEXEL-like motif (RTLND), its conserved residues i.e., R, L and D were mutated. Mutational analysis revealed surprising difference in effectors localization compared to wild type. The functional role of this motif is being further established by various methods. Translocated effectors interact with some central player of plant immune signalling and initiate a sequence of events that leads to an immunologically compromised situation in host called EffectorsTriggered Susceptibility (ETS). Earlier, yeast two-hybrid and Bimolecular Fluorescence Complementation (BiFC) screening has identified a chickpea transcription factor AT-hook an interacting partner of PEC25. *In planta* Co-IP strategy, where PEC25 has been used as bait will certainly shed light on some other important prays of PEC25. Subsequently binary interaction between bait and prays and between prays will be confirmed by Y2H screening. Overall, the functional implication of PEC25 and its possible host targets will be discussed.

Role of micro RNAs in abiotic stress tolerance in Chickpea

Speaker: Nilesh Sharma
Supervisor: Dr. Debasis Chattopadhyay

MicroRNAs (miRNAs) are 20~24 nucleotides long endogenous small RNA molecules involved in the regulation of gene expressions in multiple developmental and signaling processes. miRNAs are non-coding RNA entity which negatively regulate their respective targets at post transcriptional level. Recent studies demonstrate that the expression of miRNAs is altered in several stress responses including both abiotic and biotic stresses. Root development is imperative for plant development and stress tolerance, and the miRNAs involved in root development are crucial for both development and stress tolerance of plant.
Chickpea is a leguminous plant with strong tap-root and many lateral roots which help in water and nutrition uptake from deeper soil profile.Being a semi-arid zone crop, chickpea gets affected by many environmental stresses.A comparative microRNA expression profile of two chickpea varieties having contrasting root phenotype and stress tolerance would provide insight of the role of miRNAs in root development and stress tolerance. This study has been initiated and the preliminary results obtained will be discussed.