

6th World Congress on **Biotechnology**

October 05-07, 2015 New Delhi, India

Proteogenomics based strategy for identification of Fe and Zn transporters: Common bean as a case study

Reetika Mahajan¹, Sufia Farhat¹, R K Salgotra¹, A K Singh¹, Vandna Rai² and Sajad Majeed Zargar¹

¹Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, India

²Indian Agricultural Research Institute, India

Common beans (*Phaseolus vulgaris* L.) are a rich source of iron (Fe), zinc (Zn) and certain other microelements that are generally found to be lower in cereals and other crops. Micronutrients like Fe and Zn play an important role in both plant and animal metabolism. In humans, Fe is essential for preventing anaemia and for the proper functioning of many metabolic processes, whereas Zn is essential for proper growth and for resistance to gastro enteric and other respiratory infections. In Plants, Fe and Zn play important role in maintaining proper metabolic and physiological cellular processes. Deficiency of these nutrients leads to various abnormalities in both plants and animals. In order to enhance their uptake in plants, there is a need to identify genes that are involved in transport of these micronutrients. We here propose proteogenomics based approaches for identification of candidate genes regulating uptake of these micronutrients. We evaluated seeds of 138 diverse common bean genotypes for Fe, Zn and protein contents. We observed significant variation among these genotypes for Fe, Zn and protein contents. The Fe and Zn contents varied from (0.059 mg 100 g⁻¹ to 7.22 mg 100 g⁻¹) and (0.15 mg 100 g⁻¹ to 1.931 mg 100 g⁻¹) respectively. Further, protein content varied from 7.2% to 31.6%. No correlation among Fe, Zn and protein content was observed. Now we are in process of developing a mapping population for identifying genes/QTLs contributing for higher accumulation of Fe and Zn. Moreover, for understanding the genetic regulation of these micronutrients we will focus on gel based proteomic approach.

smzargar@gmail.com

Cloning and molecular characterization of orthologues of bacterial leaf blight resistance gene *Xa27* from wild species of rice

Sangeeta Singh

National Research Centre on Plant Biotechnology, India

Bacterial blight (BB) is caused by *Xanthomonas oryzae* pv. *oryzae* has been one of the most serious diseases in rice. Using PCR based allele mining; the present investigation was done to find out novel alleles of *Xa27* gene from eight wild rice species and 11 cultivated rice lines. This analysis to find out structural variation and its impact on the phenotypes found maximum variation at nucleotide level in the form of transition. Sequence analysis indicated more variation between cultivated and wild species as compared to variation between wild species of rice. The 8 SNPs and 4 InDels found in alleles from Basmati rice varieties may be the reason for its susceptible nature. All nineteen alleles studied in present investigation, have only one exon in its ORF region. Two motifs such as Protein kinase C phosphorylation site and N-myristoylation site have been identified in all the alleles indicating its role in signal transduction process. The *Xa27* alleles have 13 polymorphic sites with nucleotide diversity of 0.01259 and $\theta_w = 0.01114$. Further, the study of Ka/Ks ratio suggests that there is Darwinian pattern of selection which leads to divergent evolution of *Xa27* gene in nature. Important allelic variants found in this study can be used for developing gene specific DNA markers which can be used in resistance breeding. Besides, various resistant alleles cloned from wild species can be exploited in the effective management of bacterial blight disease after transferring these alleles either alone or in combination in the susceptible genotypes.

sangeeta10mar@gmail.com