COTTON Innovate

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Scientific Talk

Prof. Chuan Xi Zhang, Institute of life Sciences, Zhijiang University, Hangzhou, China, delivered a talk entitled “Co-operative triple-genome of the rice-pest brown plant hopper and its endosymbionts” on Feb.7,2015 at CICR, Nagpur under the aegis of Innovation Cell. Dr. M. M. Rai, Co-ordinator, Centre for Sericulture and Biological Pest management Research, RTMNU, Nagpur and Dr. K.P. Arun Kumar, Staff Scientist and Group Leader, Laboratory of Molecular Genetics, Centre for DNA fingerprinting and Diagnostics, Hyderabad accompanied him. Dr. K. R. Kranthi, Director, CICR, welcomed the delegates. All the Scientists, technical staff, RAs and SRFs attended the lecture. An interactive session was held at the end of the lecture.

Rice Brown Plant Hopper (*Nilaparvatha lugens*), causes huge loss in rice production of Asia. In his lecture, Dr. Zhang explained about the wing dimorphism of BPH, the short winged and the long winged forms. The long winged forms are quite destructive as they migrate to longer distances. Their migration pattern is of two types – overwintering and non-overwintering mechanism. He also briefed the mechanism of wing polyphenism. If only wing switch1 is involved wing genes are normally expressed and if both wing switch1 and 2 are involved, wing genes are inhibited. In addition to the hopper burn caused directly by the brown plant hoppers they transmit viral diseases to rice such as Rice Stripe Viral disease, Ragged Stunt viral disease, Rice Black Streaked dwarf disease etc. He attributed the quick adaptation of BPH to gradual enrichment of minor resistant genes, epigenetics, symbionts and resurgence. BPH have developed resistance to insecticides.

The genome size of BPH is 1141 Mb with 27,571 genes; 7 times as larger than fruit fly and 3 times as larger than silk worm. The larger genome size is due to 48.6 % repeats. The host specific related genes like genes coding for Odorant Binding Protein (OBP) and Chemosensory Protein (CSP) are vital in identifying the host. Molting of BPH is done by 1+5+1+3 enzymatic pattern where 1 Chitin Synthetase, 5endochitinases, 1 exochitinase and 3 chitin deacetylases are involved.

He also elaborated on the function of endosymbionts in BPH. Two major endosymbionts were identified: *Arsenophonus nilaparvatae,* bacterial symbiont with a genome size of 2.96Mb (2762 genes) and Yeast like Symbiont (YLS) with a genome size of 26.81 Mb (7155 genes). The symbiotic relationship was explained by him on the basis of requirement of metabolites to complement each other’s development. Steroids are required for BPH molting and fungal growth. Rice sap is scarce in steroids. Either BPH or YLS could not synthesize steroids by itself. However the complementary genes for synthesis of steroids which are present in BPH and YLS meet the requirement of steroids. Bacterial symbiont provides the essential vitamins to BPH and YLS as they are don’t have a complete set of genes for vitamin biosynthesis. He mentioned that RNAi of the gene saccharopine dehydrogenase (SDH), an intermediate enzyme in lysine biosynthetic pathway of YLS retarded the growth of BPH. *NIBicC* gene of BPH was identified as most sensitive gene to RNAi with 0.05 pg per insect ds RNA causing defective oogenesis.

Meetings Attended

Dr. K.R.Kranthi, Director, CICR, participated in the 12th Agricultural Science Congress with the theme “Sustainable Livelihood Security for Small Holder Farmers” at NDRI, Karnal from 3rd to 6th February, 2015.

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