J Clin Cell Immunol 2015, 6:3
http://dx.doi.org/10.4172/2155-9899.S1.022

OMICS International
conferenceseries.com

Application of plant innate immunity for the functional genomics in rice through virus induced gene silencing (VIGS) and revelation of RTBV encoded silencing suppressors

Ravi Kant and **Indranil Dasgupta**
University of Delhi South Campus, India

Rice is the staple food of about half the world's population and it is the second largest produced cereal in the world. Therefore, implementation of novel tool and techniques for the enhanced yield, crop improvement and defence against various biotic and abiotic stresses are foremost objectives. Although rice genome has been sequenced however, functions of many essential genes still need to be elucidated. Virus induced gene silencing (VIGS) is one of the promising loss of function technology, which exploits the host induced RNA silencing pathway to dissect out the characteristic function of plant genes. We present here, that *Rice Tungro Bacilliform Virus* (RTBV) derived VIGS system to silence *Phytoene desaturase* (pds) gene and chlH subunit of *Mg chelatage* gene in rice through agroinoculation. The RTBV VIGS-pds inoculated plants resulted photobleaching phenotype in the emerging leaves and 50-80% reduced accumulation of pdstranscript level in 60% of inoculated plants. The effect of insert orientation on the VIGS mediated gene silencing efficiency in rice has also been explained using Mg-chlH as another reporter gene. Virus encoded RNA silencing suppressor proteins are recruited as a counter-defense against host innate immunity i.e. RNA silencing. In this study, RTBV encoded PRT (protease) and ORF IV have been identified as local as well as systemic silencing suppressors through agroinfiltration assay in *N. Benthamiana*16C plants. Thus, plant innate immunity can be utilized as a critical avenue for the study of plant-pathogen interaction and their functional genomics.

ravikanthpu@gmail.com

The role of innate immunity in the pathogenesis of Pityriasis Rosea

Rania Abdel Hay
Cairo University, Egypt

Pityriasis Rosea is a common papulosquamous skin disease in which infective agent may be implicated, most probably due to viral infection. Innate immunity is made possible by a network of germ-line encoded pattern-recognition receptors (as Toll-Like Receptors, which detect pathogen-associated molecular patterns on invading microbes and trigger immunological responses. The aim of the work is to evaluate the role of innate immune response in Pityriasis Rosea through the detection of Toll-Like Receptors expression in the skin of affected patients. This may in turn provide a new approach to defining the disease status and may help to open up a new era in the therapeutic modalities of Pityriasis Rosea.

Method: This was a case-control study that included 24 patients with pityriasis rosea and 24 normal human controls. The study was carried out to detect the expressions of TLR3, 7, 8 and 9 in the skin of these subjects by Real-time PCR.

Results: The mean TLR3, 7, 8 and 9 expression level was significantly higher in patients in comparison to controls ($P<0.001$). There were significant negative linear correlations between TLR8 with both ESR1 and ESR2 in the patients group ($r=-0.461$, $p=0.024$ & $r=-0.426$, $p=0.038$, respectively).

Conclusion: the significant elevation of TLR3, 7, 8 and 9 in cutaneous lesions of PR detected in our study, beside the detection of HHV-6 and HHV-7 DNA in PBMCs and in IgM and IgG (antibodies to HHV-6 and HHV-7), adds another proof for the viral etiology of this disease.

raniamounir@kasralainy.edu.eg