Mohammed Nuruzzaman et al., Agrotechnol 2016, 5:3(Suppl)
http://dx.doi.org/10.4172/2168-9881.C1.021



# Rice AP2/EREBP transcription factor family members are differentially expressed in response to six different viruses

**Mohammed Nuruzzaman[1, 2, 3], Akhter Most Sharoni[1], Kouji Satoh[1], Mohammad Rezaul Karim[2], Jennifer Ann Harikrishna[2], Shoshi Kikuchi1** and **Md Muklesur Rahman[3]**
[1]National Institute of Agro-biological Sciences, Japan
[2]University of Malaya, Malaysia
[3]University Malaysia Terengganu, Malaysia

Expression profiles of the 147 AP2/EREBP gene family members were studied in rice infected with Rice grassy stunt virus (RGSV), Rice transitory yellowing virus (RTYV), Rice gall dwarf virus (RGDV), Rice black-streaked dwarf virus (RBSDV), Rice ragged stunt virus (RRSV), and Rice dwarf virus (RDV). Microarray analysis showed that 80% of the OsAP2/EREBP genes were differentially regulated during virus infection compared with the control. Rice infected with either RGSV or RBSDV showed the highest number of upregulated OsAP2/EREBP genes, while RTYV infected plants had the lowest. These results correlate with the severity of the syndromes induced by the different viruses. Most (60%) of the genes in the RAV subfamily and B5 subgroup were more highly expressed during RDV-O and RDV-S virus infections, while most (53%) of the genes in the A3 subgroup were down-regulated during RGSV infection, suggesting roles in response to virus infection. The number of genes activated during RDV infections was greatest during infection with the S-strain, followed by the D84-strain and the O-strain, with three OsAP2/EREBP genes up-regulated during infection by all three strains. A common set of 12 genes showed higher expression during infection by at least three viruses, of which, Os05g47650 showed up-regulation during infection with five of the six viruses. Putative cis-elements related to strongly up-regulated genes included, which may assist in assigning these important genes to their functional pathways. We also found several duplicate genes that are classified as neo-functional and sub-functional according to their expression patterns among six virus infections.

## Biography

Mohammed Nuruzzaman is the Senior Lecturer of School of Food Science and Technology, University Malaysia Terengganu. He is one of the top most Molecular Biologist, and he is basically working on gene functional analysis on abiotic and biotic stress.

mnzamanrice@umt.edu.my

**Notes:**