

Analysis of Codon Preferences in WRKY Genes of *Arabidopsis thaliana*

Snigdha Srivastava, Sheetal Chayal and GoharTaj

*Department of Molecular Biology and Genetic Engineering, College of Basic Sciences and Humanities
G.B Pant University of Agriculture and Technology, Pantnagar, Uttarakhand-263145*

Abstract—With the advancement in gene cloning and sequencing techniques a number of plant gene sequences have been added in databases. An important plant gene family of transcription factors which play an important role in the regulation of responses generated in plants against biotic and abiotic stress is 'WRKY'. The study of preferred codons helps in the identification of differences in the level of gene expression present within the genes of the same species. Considering the importance of codon preference studies the analysis of total seventy WRKY transcription factor genes of *Arabidopsis thaliana* was done. The GC codon status was 44 percent in *Arabidopsis*. The GC content at the first, second and third codon position was found out to be maximum 18 percent. The Relative synonymous codon usage analysis (RSCU) of codons revealed that codon (AGA) coding for arginine was given higher preference as compared to other codon in all the WRKY genes observed. Based on the hierarchical clustering it was investigated that WRKY genes having the same functions came together in the same cluster. Among the eighteen amino acids observed, it was seen that a particular codon was given higher preference for each amino acid. On the basis of literature natural selection was the main dominating factor guiding the evolution of different WRKY genes in *Arabidopsis thaliana*.