**Understanding the Role of WRKY Transcription Factors in Early Blight Disease of Potato Caused by*Alternaria solani***

Abstract:

WRKY transcription factor is a large gene family that plays an important role in biotic stress responses in plants. This study focused on the genome- and transcriptome-wide identification of the WRKY transcription factors in potatoes and the expression patterns of the shortlisted StWRKY genes identified in the potato genome. Eighty WRKY genes were identified in the potato genome (v6.1) and were mapped across 11 out of 12 chromosomes. Based on sequence similarity, the StWRKY genes were classified into three groups (Group I, II, and III), with Group II further divided into five subgroups (IIA, IIB, IIC, IID, and IIE). Gene duplication events were observed, revealing 23 pairs of duplicated StWRKY genes. Additionally, synteny analysis revealed the collinear StWRKY genes between*S. tuberosum* and*A. thaliana* and between*S. tuberosum* and *S. lycopersicum* along with duplication events. Gene structure and motif analyses of StWRKY sequences were performed. Prediction of promoter cis-regulatory elements showed the presence of defense and stress-responsive, drought-responsive, and hormonal-responsive elements, with examples of salicylic acid-responsive and gibberellin-responsive elements. *In silico* protein-protein interaction, analyses were performed to better understand the co-expression network of the StWRKY proteins. Selected StWRKY genes showed differential expression patterns in two cultivars with varying susceptibility to *Alternaria solani*, the causing agent of early blight,during infection. The sequence and the expressional analyses of the selected StWRKY genes lay the foundation for further studies to reveal the involvement of WRKY genes in potato early blight and other stresses.