

# Evolutionary Expansion of WRKY Gene Family in Banana and Its Expression Profile during the Infection of Root Lesion Nematode, *Pratylenchus coffeae*

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## Abstract

The WRKY family of transcription factors orchestrate the reprogrammed expression of the complex network of defense genes at various biotic and abiotic stresses. Within the last 96 million years, three rounds of *Musa* polyploidization events had occurred from selective pressure causing duplication of *Musa*WRKYs with new activities. Here, we identified a total of 153 WRKY transcription factors available from the DH Pahang genome. Based on their phylogenetic relationship, the *Musa*WRKYs available with complete gene sequence were classified into the seven common WRKY sub-groups. Synteny analyses data revealed paralogous relationships, with 17 *Musa*WRKY gene pairs originating from the duplication events that had occurred within the *Musa* lineage. We also found 15 other *Musa*WRKY gene pairs originating from much older duplication events that had occurred along Arecales and Poales lineage of commelinids. Based on the synonymous and nonsynonymous substitution rates, the fate of duplicated *Musa*WRKY genes was predicted to have undergone sub-functionalization in which the duplicated gene copies retain a subset of the ancestral gene function. Also, to understand the regulatory roles of *Musa*WRKY during a biotic stress, Illumina sequencing was performed on resistant and susceptible cultivars during the infection of root lesion nematode, *Pratylenchus coffeae*. The differential WRKY gene expression analysis in nematode resistant and susceptible cultivars during challenged and unchallenged conditions had distinguished: 1) *Musa*WRKYs participating in general banana defense mechanism against *P.coffeae* common to both susceptible and resistant cultivars, 2) *Musa*WRKYs that may aid in the pathogen survival as suppressors of plant triggered immunity, 3) *Musa*WRKYs that may aid in the host defense as activators of plant triggered immunity and 4) cultivar specific *Musa*WRKY regulation. Mainly, *Musa*WRKY52, -69 and -92 are found to be *P.coffeae* specific and can act as activators or repressors in a defense pathway. Overall, this preliminary study in *Musa* provides the basis for understanding the evolution and regulatory mechanism of *Musa*WRKY during nematode stress.