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WRKY TRANSCRIPTION FACTOR IN PLANTS AND ITS ROLE IN SUGARCANE DEFENSE AGAINST *COLLETOTRICHUM FALCATUM*

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Plants being sessile face various biotic and abiotic stresses in their natural habitat. Adapting to such changes requires high degree of elasticity in their phenotypical characteristics, which is determined by their genomic make-up. Concurrently they face different stresses at a time, which has been overcome by a complex array of physiological and biochemical mechanisms. Response to pathogen invasion occurs by a cascade of signal transduction pathways related to host defence response. In all those pathways, transcriptional control is a major mechanism, whereby a cell regulates its gene expression. Transcriptional reprogramming associated with pathogen infection involves the action of diverse transcription factors, which determines the regulation of a gene. WRKY transcription factor is one among the largest transcription factor families in higher plants and green algae. WRKY transcription factor participates in differential regulation of genes involved in signalling cascades during biotic and abiotic stress responses and more specifically in many disease-related situations. In sugarcane, redrot is a major disease caused by *Colletotrichum falcatum* which causes colossal loss in the yield and recovery of sugar from infected cane and results in greater economic loss.

The significant feature of WRKY is the DNA binding domain, which encodes WRKYGQK amino acid sequence at N-terminus followed by zinc finger motif. Based on this, it is grouped into three groups i.e. I, II and III in which group II is further subdivided into IIa, IIb, IIc, IId and IIe (Eulgem et al., 2000). WRKY transcription factor functions as an important component in the complex signalling pathways during a plant defence response activating defence gene expression against pathogens. In rice, during pathogen interaction OsWRKY 45-1 and OsWRKY45-2 which differs by 10 amino acids were found to act as positive and negative regulators in the *Oryza sativa* subspecies *japonica* and *indica* respectively. OsWRKY 45-1 alters the level of salicylic acid and jasmonic acid while OsWRKY 45-2 alters only jasmonic acid. Several other studies also reveal the role of OsWRKY 82 in the defence response against the pathogen.

In sugarcane, the role of WRKY transcription factors is not well studied. The first attempt identified several EST-contigs encoding homologues of WRKY-like proteins in sugarcane expressed sequence tags (EST) database *in silico*, and its expression analysis showed that these proteins should have an essential role in defence (Marico *et al.*, 2001). In a recent study, a sugarcane ScWRKY gene was isolated and its quantitative expression in real time revealed its active role in the defence response against *Sporisorium scitamineum*, salicylic acid, drought and salinity (Liu *et al.*, 2012). Previous study carried out in our lab to screen different transcription factors expressed in sugarcane during *C. falcatum* interaction showed differential expression patterns of several transcription factors. In that, WRKY showed differential expression pattern in resistant and susceptible varieties in varying time intervals. This proves the possible regulatory role of WRKY transcription factor during *C. falcatum* interaction. Studies are in progress to characterize the regulatory role of WRKY in sugarcane and *C. falcatum* interaction. In addition, the association of WRKY in gene functions involved in defence and signal transduction will also be studied.

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PERSISTENCE OF *USTILAGO SCITAMINEA* SYD THE CAUSE OF SMUT DISEASE, IN RATOON CROPS OF SUGARCANE

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Sugarcane is one of the major commercial crop playing pivotal role in rural and industrial economy of the country. Smut, caused by *Ustilago scitaminea* Syd. is one of the major disease with worldwide distribution. Economic losses due to this disease have been estimated in range from negligible proportion to levels serious enough to threaten the agriculture economy of the area. Besides, heavy quantitative losses, smut also reduce cane quality parameters like Brix, Sucrose and Purity as well. The objective of present study is to assess the persistence of *Ustilago scitaminea* in ratoon crops of two seasons in Tarai (having high moisture content) conditions of Uttarakhand and also to evaluate the resistant germplasm, to be utilized in crop improvement programme of the country.

Forty five genotypes were planted in two row plots of 3 m length with row to row distance of 75 cm during 2008-09. Ratoon crop was maintained for two crop seasons. Artificial inoculations were done by steeping three bud setts for 30 minutes in a spore suspension of over 90% viability and a spore load of one million spores per ml just before planting. Smut infected whips, for the purpose, were collected from the field and air dried by keeping under shade and stored in desiccators having anhydrous calcium chloride in the base of desiccators. Incidence of smut both in plant and ratoon crop

