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Sugarcane belonging to *Saccharum* genus is a monocotyledonous, an economically attractive polyploid C_4_ potential grass with a distinctive feature for accumulating high concentration of sucrose in the internodes of the stem and is cultivated in tropical and subtropical regions of the world. This genus *Saccharum* was first illustrated in the book *Species Plantarum* by Linnaeus in 1753. This C_4_ grass have a photosynthetic pathway linked to specialized Kranz leaf anatomy that particularly helps to adapts hot climates and atmospheres low in the carbon dioxide content. Apart from the traditional use as a source of sugar, sugarcane is fast becoming a source for ethanol and biomass production as an alternative energy source to the nonrenewable resources in many counties as a part to build up their economy from several decades. It efficiently grows in vegetative as well as in reproductive way in the tropical and subtropical regions of more than 90 countries with area under cultivation close to 20 millions of hectares (FAOSTAT 2009; http://apps.fao.org, http://www.illovo.co.za/worldofsugar, Moore et. al. 2013).

Sugarcane is genetically a complex polyploid member of the grass family Poaceae, tribe Andropogoneae and genus *Saccharum*. The genus formally comprises of six hybrids (Price, 1965; Arceneaux, 1967; Berding and Roach 1987) derived from *Saccharum officinarum* L. (2n=80, Noble clones), *Saccharum robustum* Brandes and Jesweit ex Grassl (2n= 60-200), *Saccharum barberi* Jesw. (2n = 111-120, North Indian clones), *Saccharum sinense* Roxb. (2n = 81-124, Chinese clones) and three species viz., *Saccharum spontaneum* L. (2n = 40-128, wild species), and *Saccharum edule* Hassk (2n=60-80 with aneuploid forms). It was demonstrated that the genera *Saccharum, Erianthus, Narenga* and *Sclerostachya* constituted a closely related interbreeding group concerned in the origin of the sugarcane (Mukherjee, 1957).

Above all *Erianthus* was considered the primary member in the *Saccharum* complex (Daniel and Roach 1987). *Saccharum officinarum*, however, is believed to have evolved through hybridization of species such as *Erianthus arundinaceus* (Retz.) Jeswiet, *S. spontaneum*, and *S. robustum*, whereas *S. barberi* and *S. sinense* are the secondary ones believed to be natural hybrids between *S. officinarum* and *S. spontaneum* (Sreenivasan et. al. 1982). The cultivated sugarcane *Saccharum* species are believed to have originated from complex
hybridization events (termed “nobilization”) between *S. officinarum*, *S. barberi*, *S. sinense*, and the wild related species *S. officinarum* (Sreenivasan et. al. 1982), other genera such as *Erianthus* (Michx.), *Miscanthus* (Anderss), *Narenga* (Burkiee), and *Sclerostachya* (Hack A. Camus) are closely related to *Saccharum*. The nobilisation process produced highly polyploid and high chromosome number characterized clones with 80% of the genome derived from *S. officinarum* and the remaining from *S. spontaneum* (Price, 1965). These hybrids contain 2n=100 to 130 chromosomes with an estimated genome size from 760 to 926 Mb, which is twice the size of the rice genome (389 Mb) and similar to *Sorghum’s* (760 Mb) (D’Hont and Glaszman 2001; D’Hont, 2005). The mutual relationship and actual contribution of these different genera, however, remain unclear due to their high and variably ploidy levels (D’Hont et. al. 1996; Hoarau et. al. 2002; D’Hont, 2005; Piperidis et. al. 2004). To comprehend the integrated omics (transcriptomics, metabolomics and proteomics) approaches in sugarcane for the economically important traits such as, sucrose concentration, fibre content, higher yield and tolerance to abiotic and biotic stress conditions, it is important to known about the sugarcane physiology, genome structure, functional integrity and coliniarity with the other more or less similar crops (Lakshmanan et. al. 2005; Devarumath et. al. 2013).

Sugarcane is a typical glycophyte and hence exhibits stunted growth or no growth under salinity, drought and cold conditions with its yield falling to 50 % or less than its true potential. To meet the demands, the development of new sugarcane variety for the improve productivity, tolerance to biotic and abiotic stresses; nutrient management, and improved sugar recovery are some of the challenges that have to be overcome. Worldwide sugarcane researchers are trying to enhance and introduce higher yield and stress tolerant sugarcane varieties. The progression in sugarcane research will integrate better understanding of the genome and gene discovery. Sugarcane improvement, from selection of existing variation in pre-historic time to the current bi/multi-parental crossing and subsequent use of the non-conventional techniques, has been concentrated for the superior sugar content and its yield (Devarumath et. al. 2013). To explore the potential value of sugarcane, combination of conventional and molecular breeding
approaches are been acquired to introduce wild relative species traits to develop *Saccharum* hybrids (Zhu et. al. 2014). In this study, we reviewed the genetic variability of the wild relative species of sugarcane for stress tolerance and employed for *MYB* transcription factor gene characterization. The earlier studies reflected the transcription factors in the wild relative species might be an important aspect towards the tolerance of the crop against several stress conditions (Que et. al. 2012).

We considered the sugarcane and its wild/closely related species to *Saccharum* genus namely; *Saccharum officinarum* (Vellai), *Saccharum barberi* (Pathri), *Saccharum spontaneum*, *Saccharum robustum*, *Erianthus arundinaceus*, *Erianthus ciliaris*, *Erianthus elegans*, *Erianthus arundinaceus* (Mythan C) and Narenga were considered for the isolation of *MYB* transcription factor (TF) genes, tobacco plant transformation of these *MYB* genes, their protein expression studies in *Escherichia coli* (*E. coli*) and *in silico* analysis of the protein sequences were carried out at Molecular Biology and Genetic Engineering laboratory, VSI, Pune.

*Saccharum officinarum* has cytotpe 2n = 70 to 140 and is a large perennial tropical grass similar to bamboo cane in appearance and is known to reach of 3-6 meters upright. The sugarcane is widely cultivated and supply roughly 70 % of the worlds sugar production. The cane has experienced many adverse conditions with respect to the susceptibility towards diseases and factors like temperature, salinity and drought (D’hont et. al. 1996, D’hont 2005).

The *Saccharum barberi* (Pathri) has the cytotype 2n=81-124 and is the cane of North India. It has the contrasting characteristic to *Saccharum officinarum* in respect to floral characteristics, thinner stalks, lower sucrose content, high fiber, greater tolerance to the adverse conditions (D’hont et. al. 2002).

The *Saccharum spontaneum*, a wild relative of sugarcane, has played a major role in the development of many improved sugarcane varieties. *S. spontaneum* has x=8 chromosomes (Daniels and Roach 1987) but imparts great variation in chromosome numbers with five main cytotypes: 2n=62, 80, 96, 112 or 128 (Sreenivasan et. al.
1982). *S. spontaneum* is highly polymorphic, vigorous, fibrous thin stalk with low sucrose content. Nevertheless, its potentiality in contributing valuable gene trait complexes for high fibre, biomass and possessing genes for adapting several diseases (Panje and Babu 1960) and adverse conditions with excellent ratooning ability appears to be very attractive (Naidu and Sreenivasan 1987; D’Hont et al. 2002). This wild species has been a potential resource for genetic improvement for sugarcane, with a strong interest amongst sugarcane breeders in incorporating desirable traits, particularly vigor and adaptation to adverse environments.

*Erianthus*, closely related to genus *Saccharum*, has a high potential of biomass production, multiple ratoonability, drought tolerance and resistance to diseases and pests (Nair et al. 2006). Introggression of *Erianthus* genome into sugarcane was a challenge to sugarcane breeders because of wide genetic distance between the genera and frequent occurrence of low fertility in the hybrids (Piperidis et al. 2004). *Erianthus* being a potential resource for genetic improvement for sugarcane is having strong interest amongst sugarcane breeders in incorporating desirable traits, particularly vigor and adaptation to adverse environments (D’Hont et al. 1994). Despite the interest and promise of this genus to introgress characters in sugarcane varieties for crop improvement, over many years, no conclusive success has been documented for performance of yields or other traits (D’Hont et al. 1995; Piperidis et al. 2010). Studies show that *E. arundinaceum* was previously focused largely on the morphological aspect (Yang 1997), chromosome aberrations (Liu et al. 2004), and physiological resistance (Zhang et al. 2004; Guo et al. 2005). Consequently, characterization and utilization of this germplasm for identifying and isolating the stress tolerant genes would be a better approach for producing stress tolerant sugarcane varieties (Que et al. 2012).

As sugarcane is time again attacked by different bacterial, fungal and viral diseases and environmental stress conditions the cost of productivity of the crop has been in question.

Thus the experimentation to hybridize the genus *Saccharum* with closely related species illustrated the gene flow in the hybrids emerged to be very stumpy. To
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enhance the insight of the response to the changing environments the present study aims for understanding the role of MYB transcription factors in the control of plant-specific processes and tolerance to drastic environmental stress was encouraged. We concentrated on the MYB transcription factor family for its unique multifunctional behavior for biotic and abiotic stress tolerance, developmental processes, secondary metabolite production etc (Dubos et. al. 2010).

The present study gives a brief account of initiating the work on MYB transcription factors, their isolation using MYB specific primers, expression studies in tobacco plant and E. coli and in silico sequence characterization. The insight of these sugarcane MYB transcription factors were enhanced by comprehending their functionality in a tobacco plant model system. The response of the transcription factors against the abiotic stress mainly drought was perceived in this study. Furthermore, the protein expression studies of these sugarcane MYBs was performed under drought stress to understand the response and effective production of proteins under the stress. The docking studies of the MYBs were performed to enhance approach between protein-DNA interface interactions. The in silico studies of these MYBs were executed for detailed characterization and annotations.

The importance of this study chiefly projected the isolation of MYB transcription factors of sugarcane and decipher their putative importance in improving the cultivars and introduce new vision for sugarcane transformation era.

The subsequent study was carried out considering the mentioned aims and objectives:

1) To isolate the MYB transcription factor genes from sugarcane and its wild relative species and its sequence analysis.

2) To conduct comparative transformation studies of the isolated EaMYB2R, SsMYB2R and SoMYB2R transcription factor genes in the model plant, Nicotiana tabaccum.
3) To perform protein expression studies of the isolated \textit{EaMYB2R}, \textit{SsMYB2R} and \textit{SoMYB2R} under stress and docking studies of DNA-protein interface interaction with \textit{MYBCORE} motif.

4) To execute the \textit{in silico} studies and annotate the predicted 3D models of \textit{EaMYB2R}, \textit{SsMYB2R}, \textit{SbMYB2R} and \textit{SoMYB2R}. 