

A Gene approach on Sugarcane growth and production: Mini review

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ABSTRACT

The importance of sugarcane as commercial crop has long been known thing. The present review through a light on the genes with different functional properties and mechanism of action. The productivity and growth of sugarcane both dependent on the genes. The high yield of sugar, amino acids, micro and macronutrient absorption in sugarcane crop is systematically reviewed. Further, totally 13 genes have been characterized, SUC Gene Family, SuSy, SAI, PPK, CT Gene Family, CRT/DRE, COR15a, Miscanthus-specific PPK, CDPK, TRICH Gene Family, GL1, GL2, TTG1. Concluded that the functional genes are to taken into explanation along with field conditions, such as area of growth, moisture, water facility and availability of sunlight, micro & macro nutrient accessibility, use of pesticides and other physical and chemical parameters.

Keywords: Sugarcane, Genes, Physicochemical parameters.

INTRODUCTION

Saccharum is a complex genus characterized by high ploidy levels and composed of at least six distinct species – *S. officinarum*, *S. barberi*, *S. sinensi*, *S. spontaneum*, *S. robustum* and *S. edule* (Daniels and Roach, 1987; GRIN, 2004; Naidu and Sreenivasan, 1987). Described as an allopolyploid, modern cultivated sugarcane have approximately 80-140 chromosomes with 8-18 copies of a basic set (i.e. $x = 8$ or $x = 10$ haploid chromosome number) (D'hont et al., 1995; Ha et al., 1999; Ming et al., 2001).

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The wild relative, *S. spontaneum*, comprise about 10% of the cultivated sugarcane as evidenced from in situ hybridization (D'hont et al., 1996) and is credited to impart the needed pest and disease resistance and abiotic stress tolerance due to its wide Eco geographical adaptive distribution (Sreenivasan et al., 1987), there are no active base broadening programs alongside cultivar development programs in most sugarcane breeding stations. This is

compounded by the practice of sugarcane breeders to use the proven cross method of choosing parents. The proven cross method has the bias of recurrently using, in high frequency, parents from good performing crosses. Such concentrated use of a few parental clones each crossing season seems to contradict the base lengthening energies (Heinz and Tew, 1987; Kimbeng et al., 2004). Untested crosses and new parents are relegated to exploratory evaluation and are thus proportionally lesser.

SUC Gene Family

Sucrose (SUC) plays a central role in plant growth and development as it is a major product of photosynthesis and is the major carbohydrate form used as energy source for growth or storage reserves. Sugarcane belongs to a group of plants that are very productive in assimilating its food by efficiently utilizing the C₄ mechanism of CO₂ fixation during photosynthesis (Grof, 2001).

SuSy

Sugarcane is unique because it stores its food not in the form of glucose but in the unstable form sucrose. Sucrose Synthase (SuSy) plays a central role in carbohydrate metabolism in general, and sucrose accumulation in particular in all plant species. It belongs to a family of invertases which are enzymes specialized in hydrolyzing sucrose into glucose and fructose. SuSy catalyzes the reversible cleavage of sucrose and UDP (Uracil diphosphate) to UDP-glucose and fructose (Schafer et al., 2004; Winter and Huber, 2000).

SAI

SAI (Soluble Acid Invertase) activity occurs mostly in the vacuoles of storage parenchyma cells, and a few in the apoplastic cell wall space either as a soluble enzyme or bound to the cell wall fraction (Hawker et al., 1991). SAI activity is regarded to have an inverse relationship with sucrose accumulation in sugarcane, that is, SUC accumulation in the whole stalk and within individual sugarcane internodes was correlated with the down-regulation of soluble acid invertase (Zhu et al., 1997).

PPDK

PPDK (Pyruvate orthophosphate dikinase) is an important rate-limiting enzyme in plant photosynthesis more pronounced in C₄ plants such as sugarcane than in C₃ plants. The C₄ pathway consists of three key steps: the initial fixation of CO₂ in the mesophyll cell cytosol by phosphoenol pyruvate (PEP) carboxylase (PEPC) to form a C₄ acid, decarboxylation of a C₄ acid in the bundle sheath cells to release CO₂, and regeneration of the primary CO₂ acceptor PEP in the mesophyll cell chloroplasts by pyruvate orthophosphate dikinase (Hatch, 1987). Whereas PPDK and its regulatory proteins are found in the chloroplast of C₄ plants, PPDK is only present, and at low concentrations, in the cytoplasm of C₃ plants. Despite C₃ PPDK being highly homologous to its C₄ counterpart, C₃ PPDK is not believed to function in photosynthesis (Minorsky, 2002).

CT Gene Family

Among the cold tolerance genes used in this study were C-repeats/Dehydration Responsive Element (CRT/DRE), COR15a, Mischantus-PPDK and Calcium-dependent protein kinases (CDPK). Sugarcane is essentially a tropical crop.

CRT/DRE

CRT (C-repeats), DRE (Dehydration Responsive Element) are cis-element found in the promoter regions of many cold and dehydration genes. A family of transcription factors known as CBFs or DREB1 binds to this element and activates transcription of the downstream cold and dehydration responsive genes (Liu et al., 1998; Stockinger et al., 1997). Interestingly, the CBF/DREB1 genes are themselves induced by low temperatures. This induction is transient and precedes that of the downstream genes with the CRT/DRE cis-element (Thomashow, 1999).

COR15a

Cold acclimation in plants is associated with the expression of COR (cold-regulated) genes. Artus et al. (1996), working with COR15a, provided the first direct evidence for a cold induced gene having a role in freezing tolerance. COR15a encodes a 15-kDa polypeptide that is targeted to the chloroplasts. Upon import into the organelle, COR15a is processed to a 9.4-kDa polypeptide designated COR15 am. Artus et al., (1996) demonstrated that constitutive expression of COR15a in non acclimated transgenic *Arabidopsis thaliana* plants increases the freezing tolerance of

both chloroplasts frozen *in-situ* and isolated leaf protoplasts frozen *in-vitro* by 1 to 2°C over the temperature range of -4 to -8 °C.

Mischanthus-specific PPDK

Owning the well-organized C₄ photosynthetic pathway yet tolerant of cool temperature climates, *Mischanthus* (*Mischanthus x giganteus*) is potentially an ideal energy crop and has found use as a bioenergy product in most of Europe (Bioenergy Information Network, 1999). The rhizomatous perennial grass *Mischanthus x giganteus* is from the same taxonomic group as sugarcane, sorghum (*Sorghum bicolor*), and maize (*Zea mays*) and uses the same C₄ photosynthetic pathway (Naidu and Long, 2004). It was hypothesized that the low-temperature tolerance in *Mischanthus x giganteus*, in addition to high effectiveness in photosynthetic rate, resemble to its maintenance of high levels of total soluble protein, particularly PPDK and 12 Rubisco (Naidu et al., 2003). The gene sequence used here is a *Mischanthus x giganteus*-specific PPDK reported by Naidu et al., (2003).

CDPK

CDPK (calcium-dependent protein kinases) sequence used here are from a report using *Saccharum officinarum* EST database (Casu *et al.*, 2004). CDPK, a large superfamily of kinases are thought to function in signal transduction pathways that utilize changes in cellular Ca⁺⁺ concentration to couple cellular responses to extracellular stimuli (Harmon *et al.*, 2001). CDPK phosphorylate and regulate the activity of PEP carboxylase, an enzyme important in C₄ metabolism and is also involved in photosynthesis as well as stress like cold tolerance (Winter and Huber, 2000).

TRICH Gene Family

Phenotypic variability for pubescence (trichomes) among sugarcane clones range from no pubescence to very pubescent. Sugarcane breeders do not pay much attention to phenotypic variability for hairiness during selection, although pubescence has been implicated in insect resistance in other crops such as cotton and tomato (Kennedy, 2003; Lahtinen *et al.*, 2004; Wright *et al.*, 1999).

GL1

The glabrous1 mutant (gl1), which lacks trichomes on most surfaces, was used in early gene mapping studies (Marks, 1997). The GL1 gene encodes a protein with two myb transcription factor repeats and a carboxy-terminal domain of approximately 120 amino acids. 13 Myb are a large family of transcription factors encoding proteins that are crucial to the control of proliferation and differentiation in a number of cell types.

GL2

In-situ hybridization analysis indicates that GL2 mRNA is expressed strongly in developing trichomes. Immunolocalization of the GL2 protein and the analysis of plants containing a GL2 promoter GUS reporter gene construct (GL2GUS) indicate a more complex pattern of expression. By genetic analysis, GL2 function downstream of GL1, but GL1 does not control the non trichome expression pattern of GL2. Although the GL1 protein does not regulate the early expression pattern of GL2, it or another myb protein could influence the expression of GL2 in developing trichomes by binding to the myb binding site (Marks, 1997).

TTG1

It has been found that plants doubly heterozygous for both weak Transparent testaglabral (ttg1), along with gl1 mutant allele, have greater than normal numbers of clustered trichomes; that is, lateral inhibition appears to be reduced (Marks, 1997). Larkin *et al.* (1994) found that plants heterozygous for TTG (TTG/ttg) and one or two copies of the 35SGL1 construct have a greater number of leaf trichomes than plants that have one or two copies of 35 SGL1 in a homozygous TTG background.

CONCLUSION

The present study on the evaluation of functional genes in sugarcane had given enormous information of type of gene function that governs the productivity, quality and yield of sugarcane varieties. Further, showed that the gene function will alter in varied environmental conditions.

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REFERENCES

- [1] J., Daniels, and Roach.B.T. Germplasm collection, maintenance and use, p. 25, *In* H. DJ, ed. Sugarcane Improvement through Breeding, Elsevier, New York. **1987**. Vol. 11.
- [2] GRIN. The Germplasm Resources Information Network (GRIN) [Online] <http://www.arsgrin.gov/cgi-bin/npgs/html/genform.pl>. **2004**.
- [3] K.M., Naidu, and T.V. Sreenivasan Conservation of the sugarcane germplasm, Copesucar International Sugarcane Breeding Workshop, Copersucar, Sao Paulo, Brazil. **1987**. p. 33-53
- [4] A., P.S. Rao, D'hont, P. Feldmann, L. Grivet, N. Islamfaridi, P. Taylor, and J.C. Glaszmann. *TheorAppl Genet* **1995**, 91, 320-326.
- [5] S., Ha, P.H. Moore, D. Heinz, S. Kato, N. Ohmido, and K. Fukui. *Plant Mol Biol* **1999**, 39, 1165-1173.
- [6] R., Ming, S.C. Liu, P.H. Moore, J.E. Irvine, and A.H. Paterson. *Genome Res* **2001**, 11, 2075-2084.
- [7] D'hont, A., L. Grivet, P. Feldmann, S. Rao, N. Berding, and J.C. Glaszmann. *Mol Gen Genet* **1996**, 250, 405-413.
- [8] D.J., Heinz and T.L. Tew. Hybridization Procedures, *In* D. J. Heinz, ed. Sugarcane Improvement through Breeding, Elsevier, New York. **1987**. Vol. 11.
- [9] C.A., Kimbeng C. LaBorde, K. Bischoff, and K.A. Gravois. Genetic diversity and relationship among parents in the LSU Agcenter sugarcane crossing program. LSU Agcenter. **2004**.
- [10] C. Grof, Molecular manipulation of sucrose metabolism, p. 586-587 Proc Int Soc Sugarcane Tech, **2001**, Vol. 24.
- [11] W.E., Schafer, J.M. Rohwer, and F.C. Botha. *Physiol Plant* **2004**, 121, 187-195.
- [12] H., Winter, and S.C. Huber. *Crit Rev Biochem Mol Biol*, **2000**, 35, 253-289.
- [13] J.S., Hawker, C.F. Jenner, and C.M. Niemietz. *Aust J Plant Physiol* **1991**, 18, 227-237.
- [14] Y.J., Zhu, E. Komor, and P.H. Moore. *Plant Physiol* **1997**, 115, 609-616.
- [15] Minorsky, P. *Plant Physiol* **2002**, 128, 1163-1164.
- [16] Q., Liu, M. Kasuga, Y. Sakuma, H. Abe, S. Miura, K. Yamaguchi-Shinozaki, and K. Shinozaki. *Plant Cell* **1998**, 10, 1391-1406.
- [17] E.J., Stockinger, S.J. Gilmour, and M.F. Thomashow. Arabidopsis thaliana CBF1 encodes an AP2 domain-containing transcriptional activator that binds to the C-repeat/DRE, a cisacting DNA regulatory element that stimulates transcription in response to low temperature and water deficit. Proc Natl Acad Sci U S A **1997**, 94:1035-1040.
- [18] Thomashow, M.F. *Annu Rev Plant Physiol Plant Mol Biol* **1999**, 50, 571-599.
- [19] N.N., Artus, M. Uemura, P.L. Steponkus, S.J. Gilmour, C.T. Lin, and M.F. Thomashow. Constitutive expression of the cold-regulated Arabidopsis thaliana COR15a gene affects both chloroplast and protoplast freezing tolerance. Proc Natl Acad Sci U S A **1996**, 93, 13404-13409.
- [20] Bioenergy Information Network. **1999**. Miscanthus Factoid [Online]. <http://bioenergy.ornl.gov/papers/miscanthus/miscanthus.html>.
- [21] Naidu, S.L., and S.P. Long. *Planta* **2004**, 220, 145-155.
- [22] Naidu, S.L., S.P. Moose, A.K. Al-Shoaibi, C.A. Raines, and S.P. Long. *Plant Physiol* **2003**, 132, 1688-1697.
- [23] Casu, R.E., C.M. Dimmock, S.C. Chapman, C.P.L. Grof, C.L. McIntyre, G.D. Bonnett, and J.M. Manners. *Plant Mol Biol* **2004**, 54, 503-517.
- [24] Harmon, A.C., M. Gribskov, E. Gubrium, and J.F. Harper. *New Phytol* **2000**, 151, 175-183.
- [25] H., Winter, and S.C. Huber. *Crit Rev Biochem Mol Biol* **2000**, 35:253-289.
- [26] G.G. Kennedy, *Annu Rev Entomol* **2003**, 48:51-72.
- [27] M., Lahtinen, J.P. Salminen, L. Kapari, K. Lempa, V. Ossipov, J. Sinkkonen, E. Valkama, E. Haukioja, and K. Pihlaja. **2004**. *J Chem Ecol* 30:2257-2268.
- [28] R.J., Wright, P.M. Thaxton, K.H. El-Zik, and A.H. Paterson. *J Hered* **1999**, 90, 215-219.
- [29] M.D. Marks, *Annu Rev Plant Physiol Plant Mol Biol* 48, **1997**, 137-163.
- [30] J.C., Larkin, D.G. Oppenheimer, A.M. Lloyd, E.T. Pappozzi, and M.D. Marks. *Plant Cell* **1994**, 6, 1065-1076.