We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

6,900
Open access books available

185,000
International authors and editors

200M
Downloads

Our authors are among the

154
Countries delivered to

TOP 1%
most cited scientists

12.2%
Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com



Chapter

Breeding Rice for Sustainable Bioenergy Production

Manasi Dash, Abinash Mishra and Mahendra Kumar Mohanty

Abstract

Bioenergy including biofuels from lignocellulosic biomass has immense potential to meet growing energy demand of the ever-growing world population. Bioenergy will help to mitigate the environmental problems arising due to burning of fossil fuels. Rice is the staple food for more than half of the world population and is grown in more than 100 countries. Rice straw is rich in lignocellulose and several technologies are available for efficient extraction and conversion of cellulose to ethanol. Thus, the surplus rice straw can be utilised to produce biofuel, so as to replace conventional fossil fuel sources. But it is reported that the present-day rice varieties showing high lignocellulosic straw biomass have low grain yield potential. Hence, it is important to re orient the breeding strategies for developing dual purpose rice varieties that are bioenergy efficient without compromising grain yield.

Keywords: Rice, Bioenergy, Cellulose, Lignin, Cell wall architecture, Genomics, QTLs

1. Introduction

After the Paris climate change agreement in 2016, its signatories are making considerable efforts towards reducing carbon emissions into the atmosphere. Production of biofuel also called as 'green energy' will be a key target to achieve this by reducing the use of petrochemicals. Now focus is to harness ethanol from the existing ample quantity of lignocellulosic feedstocks such as rice and wheat straws, which are usually burnt in the fields thereby causing air pollution and health hazards [1]. The bioenergy crops have tremendous potential to address the twin issues of climate change and energy security by eliminating the 'food verses fuel' disputes.

Of the various crops grown worldwide, rice has an immense potential to be used as a dual-purpose crop, due to it's wide geographical distribution, covering entire tropical, subtropical and Mediterranean region of the globe [2]. High amount of cellulose (32–47%) and hemicellulose (19–27%) in rice straw, which can be converted to biofuel, has made it a potential future bioenergy crop [3–6]. But the cell wall polymers (cellulose, hemicellulose and lignin) form a complex network by crosslinking with each other. Hence, various pre-treatments are employed in order to break this complex to ensure higher amount of cellulose availability for the activity of cellulosic enzymes to yield considerable sugars. These pre-treatments are costly and environment unfriendly, so various genetic approaches can be utilised to enhance cellulose availability. Lignin, comprising three main types of monolignols, serves as a promising target to

alter the cell wall architecture in different ways in rice [7–9]. Cellulose synthases genes particularly, OsCesA4, OsCesA7 and OsCesA9, associating with specific phenotypes, can also be suitably engineered to enhance cellulose content without changing lignin and other polymers in cell wall [10]. So, breeding approaches that can alter plant cell wall architecture can be used to develop bioenergy efficient rice variety but, subjected to one condition that it should not affect yield contributing traits negatively.

Usually, a negative correlation has been observed between grain yield and biomass traits. Breeding for high grain yield is associated with developing cultivars with reduced plant height and short leaves and thereby, reducing the plant biomass as a whole. The plant breeding strategies have to be reoriented towards selection of higher yielding plants with moderate biomass traits including lesser ash & potassium content in vegetative biomass. Also, the role of stay green traits, fostering greater decomposition of vegetative biomass as well as rewarding higher yield, can never be underestimated in this regard. This chapter will deal with the above said issues and measures, with the prime focus on methods for developing rice genotypes for higher yield and greater biofuel production, in subsequent heads.

2. Ethanol production from rice straw

Ethanol production is primarily centered around the lignocellulosic fraction of the plant biomass. Among all the left-over waste of crop species, rice straw is the cheapest and most abundant source of lignocellulosic feed stock. Rice straw, possessing considerable amount of cellulose (32–47%), hemicellulose (19–27%), with relatively less lignin (5–24%), is considered as one of the potent bioenergy sources [3, 5]. Various enzymes have been identified in the biosynthesis of these polymers (**Figures 1**–**3**) which determine the type and amount of polymer production in the plant cells. The cell wall polymers form a complex network by crosslinking with each other inside the cell walls. Hence, various pre-treatments are employed in order to break these complexes, to reduce crystallinity of cellulose (crt), degree of polymerisation (DP), increase in

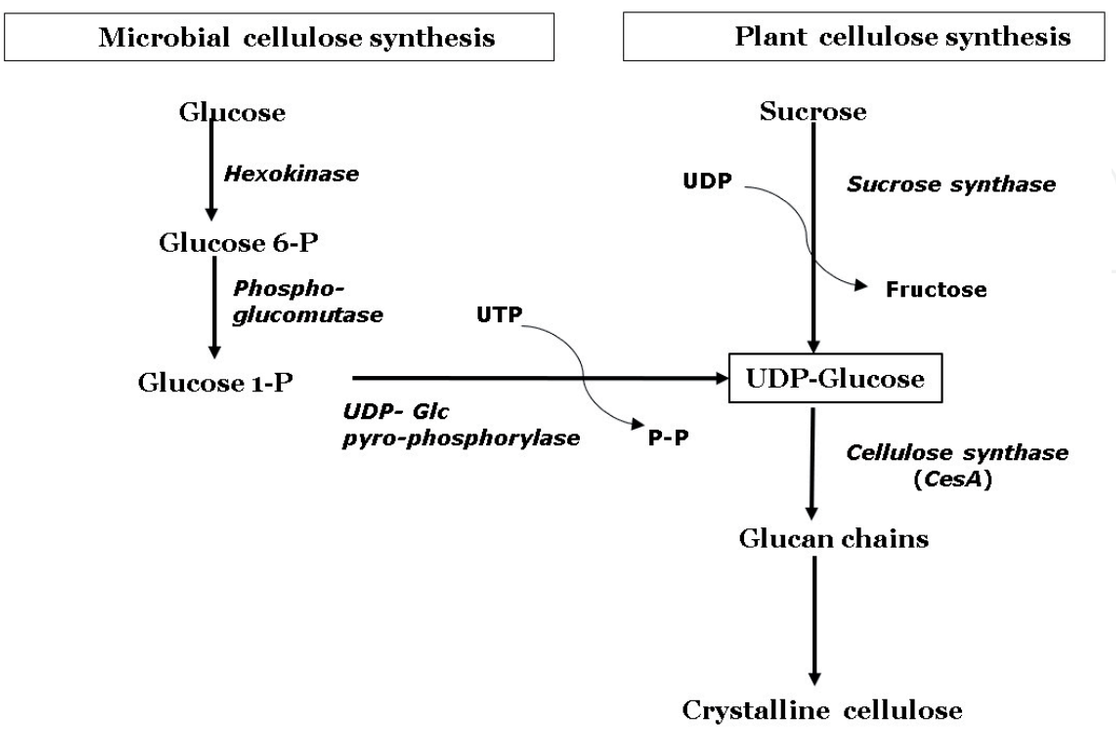


Figure 1.
Cellulose biosynthesis pathway in microbes and plants.

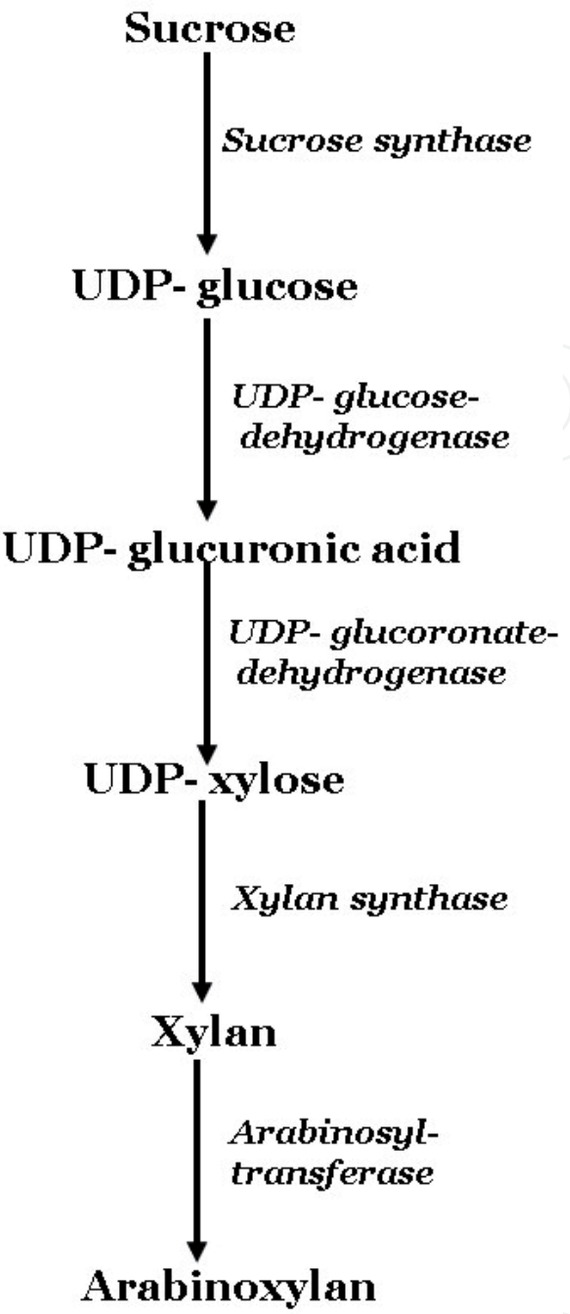


Figure 2.
Hemicellulose monomer biosynthesis pathway.

biomass surface area, and breaking the lignin seal. Chemical pre-treatment of rice straw is practiced to enable enzymatic saccharification for ethanol production [13–26].

Biological pretreatment, an eco-friendly method, overcomes the disadvantages of chemical pretreatment. White-rot fungi (*Pleurotus ostreatus*) of class Basidiomycetes are most promising microorganisms [27]. Basidiomycetes degrades lignin fraction in lignocellulosic biomass in rice straw. Patel and co-workers [28] in a study on rice straw reported that pretreatment involving *Aspergillus niger* and *Aspergillus awamori*, followed by *Saccharomyces cerevisiae* aided fermentation and recorded highest ethanol yield of 2.2 g/l. Cellulose upon hydrolysis produces glucose while hemicellulose produces hexose and pentoses [29]. Use of steam pretreatment or hydrolysis of rice straw using H_2SO_4 has also been reported [30, 31]. Pretreatment with *Aspergillus niger* increased the glucose yield from 43 to 87% [32].

Cellulose contain glucans while hemicellulose is composed of polymers of xylan, mannan, glucan, galactan and arabinan. The general process of ethanol

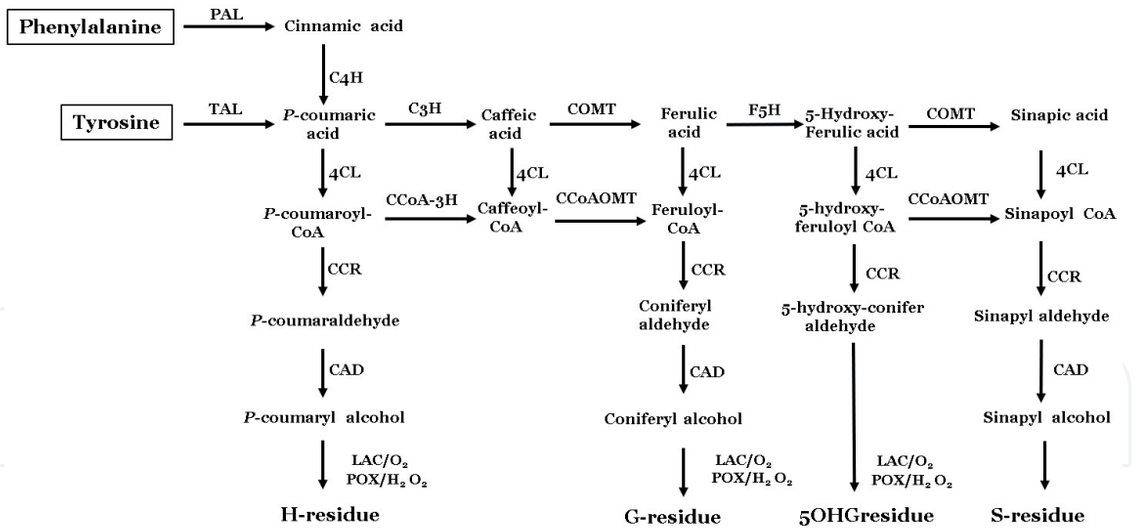


Figure 3.
Lignin biosynthesis pathways. The various enzymes are PAL [phenylalanine ammonia-lyase]; TAL [tyrosine ammonia-lyase]; C4H [cinnamate 4-hydroxylase]; C3H [4-hydroxycinnamate 3-hydroxylase]; COMT [caffeic acid 3-O- methyltransferase]; F5H [ferulate 5-hydroxylase]; 4CL [4-coumarate: CoA ligase]; CCoA-3H [coumaroyl-CoA 3-hydroxylase]; CCoAOMT [caffeoyl-CoA O-methyltransferase]; CCR [cinnamoyl-CoA reductase]; CAD [cinnamyl alcohol dehydrogenase]; LAC [laccase]; and PDX [peroxidase] (modified from Furtado et al. [11]; Vermerris and Abril [12]).

production involves conversion of cellobiose to ethanol by a series of steps of involving pre-treatment, enzymatic saccharification and fermentation as described earlier. These steps may include simultaneous saccharification and fermentation (SSF) or separate enzymatic hydrolysis and fermentation (SHF). SSF is generally used as cost incurred in the process is less [33]. In this process also, higher yield of ethanol is obtained. However, some drawbacks are observed in this process such as requirement of optimum temperature (40-50°C) for enzymatic hydrolysis, which the microorganisms cannot tolerate. This problem can be tackled by using thermophilic microorganisms such as *Kluyveromyces marxianus, Candida lusitamiae and Zymomonas mobilos* or mixed culture of *Bettanomyces clausenii* and *Saccharomyces cereviseae* [34, 35]. Shengdong and co-workers [36] employed the SSF of alkali and alkali/microwave pretreatment to generate ethanol using cellulase from *Trichoderma reesei* and *Saccharomyces cereviseae*. The ethanol concentration was 29.1 g/l and yield were 61.3% under optimum condition. Chada and co-workers [37] mentioned that SSF was superior to traditional saccharification in production of ethanol as it can improve the ethanol content by removal of end product inhibition by saccharification process. In the fermentation process alcohol is mixed with the straw to produce fermentable sugars and this is referred to as mash. This mash is fed into fractional distillation unit which differentiates alcohol from other components. The alcohol thus produced is cleaned and dehydrated to remove the water content. After cleaning and drying bioethanol is produced with a purity of 99.7% V/V.

These chemical processes for saccharification are harmful to the environment. Hence now research should be focused towards minimising or eliminating these steps by developing rice genotypes with higher saccharification efficiency (SE).

3. Role of plant breeding and biotechnology to enhance SE

As mentioned earlier the lignocellulosic biomass is primarily a complex network of various cellular constituents including cellulose, hemicellulose, lignin and interaction of a wide array of compounds like chlorophyll, waxes, oils, terpenes

and phenolics, called extractives [38, 39]. It is beneficial to have knowledge on the genetics as well as correlation between biomass traits and these cellular constituents. A greater insight into the composition, structure and the synthesis of cellular constituents will help in designing suitable breeding strategies for the genetic modification of cell wall architecture and in turn development of high energy efficient rice genotypes.

3.1 Morphological and biochemical characterisation of biomass traits

In simple term, it refers to the study of various morphological, physiological, biochemical traits, associated with grain and biomass yield. Rigorous phenotyping is essential for the success of any crop improvement programme. In breeding for biofuel, although some noticeable work has been done in case of bioenergy crops like sorghum, maize and sugarcane, very limited information is available with respect to rice, which is considered as a hinderance in effective phenotyping in this regard.

It is reported that culm length, stem girth, tiller length and diameter, leaf characteristics such as leaf length, width and angle as well as leaf, stem, tiller dry weight are few key biomass traits that can be used for indirect selection [40, 41]. These traits recorded at different developmental stages will help to decipher the genetic basis of biomass partitioning and accumulation in vegetative parts.

Biochemical characterisation of rice straw cell wall polymers (cellulose, lignin and hemicellulose) is an integral part of biomass phenotyping. Many methods like use of ultrasonicator, HPLC, microarrays, Infrared absorption spectroscopy, X- ray diffraction (XRD), transmission electron microscopy (TEM) and carbon-13 nuclear magnetic resonance (C-NMR) spectroscopy can be used for quantitative estimation of cell wall polymers [42, 43].

3.2 Polymer composition of rice biomass

Cellulose is the utmost abundant organic compound available on earth. It is a linear polymer of repeating units of cellobiose molecule. Cellobiose, a β (1–4)-linked residue, is produced when two glucose molecules (one in 180 deg. rotation) are in proximity to yield a β (1–4)-linkage. These cellulose fibres impart a greater rigidity and strength to the cell wall and hence, enabling plants to exhibit a wide spectrum resistance to various biotic and abiotic factors [12]. The non-cellulosic polysaccharides further enhance the rigidity and strength of plant cell walls by cross-linking with cellulose and lignin. Various reports have suggested this cellular constituent as a mixture of various monosaccharides such as xylose, arabinose, glucose, galactose and rhamnose as well as certain acids [44, 45]. This complex nature of non-cellulosic polysaccharides as well as their involvement in cross linking with cellulose, possesses a major setback in the efficient enzymatic degradation of cellulose to produce biofuel.

Lignin, the second most abundant biopolymer after cellulose, is polymerised with three main types of monolignols namely, Syringyl alcohol (S), Coniferyl alcohol (H) and p-Coumaryl alcohol (H) [46, 47]. As a complex phenolic compound, it improves cell wall rigidity and strength, imparts resistance to a wide array of microbes [48], fosters transporting of minerals through vascular bundles [49], involves in resistance against lodging as well as abiotic anomalies [50–52].

Cellulose and hemicellulose in rice straw can be subjected to fermentation for production of biofuels. However, their efficient conversion into fermentable sugars is hindered by presence of higher amount of lignin (5–24%), ash (10–17%), silica (75% of ash) and potassium [53].

In rice, silica comprises 74.67% of the stem ash content. Both high ash and high silica (SiO2) silica content of ash negatively affect biochemical conversion of lignocellulosic feedstock [11, 53]. High silica content reduces the availability of cellulose to enzymatic digestion and thus, reducing saccharification efficiency. Besides this, high silica accumulation in the cell walls disrupts the cellulosic microfibrils and such aberration hinders overall sugar release and ultimately, ethanol yields in subsequent stages. Therefore, considerable efforts are required to engineer silica content along with lignin and non-carbohydrate polysaccharides content to develop rice genotypes, amenable to greater enzymatic digestibility.

Although, different enzymatic and chemical pre-treatment methods are being employed for the disruption of this complex network but these procedures are energy intensive, costly and harmful to the environment. Hence, genetically modifying the cell wall architecture by employing conventional and modern breeding methods are beneficial for sustainable biofuel production [11, 54].

3.3 Modifications in polymer composition for elevating cellulose utilisation

As discussed earlier, lignin serves as a key element in cross linking of cellulose and hemicellulosic polysaccharides. This feature is beneficial to the rice plant as it helps it to counteract biotic and abiotic stress but it is a limiting feature for biofuel production. The cross linking creates a barrier for the cellulose degrading enzymes to freely access cellulose for conversion. So, efforts are being made towards reducing the degree of lignification and cross linking through various approaches so as to enhance the efficiency of cellulose degrading enzymes.

3.3.1 Modification of lignin

Some noticeable work has been done to alter the plant cell wall architecture with the help of biotechnology in model dicot plants such as Arabidopsis and tobacco (**Table 1**). The purpose behind these experiments has been the downregulation of key genes involved in monolignol biosynthesis, as well as the essential enzymes involving in polymerisation thereof. Nearly 40% reduction in total lignin content was achieved by downregulating laccases and peroxidases in the Arabidopsis [61] and tobacco mutants [62], respectively. So, these available reports documenting successful reduction of lignin composition in model dicot plants can be judiciously used by the researchers to favourably alter the cell wall architecture of the less exploited prospective biofuel crops such as rice. The *japonica* rice 'Nipponbare' harbouring an Arabidopsis TF (SHN), was found to be deficient in total lignin content. Expression of essential genes such as *CAD* (cinnamyl alcohol dehydrogenase) and 4-CL (4- coumarate- CoA ligase) were reported to be repressed, which might have contributed in producing lower lignin content [9].

Alternatively, there is another way of altering the plant cell wall architecture, by curbing the expression of essential genes involved in lignin monomers synthesis (**Figure 3**). In rice, flexible culm (*fc1*) mutant with repressed *CAD* gene, a cinnamyl alcohol dehydrogenase gene, was reported to synthesise reduced level of H and G lignin monomers [7]. Zhang and co-workers, [60] were able to produce some transgenics with improved saccharification efficiency as compared to wildtype by targeting same *OsCAD2* gene in rice. Apart from these genes, few other genes including caffeoyl-CoA- methyl transferase (*CCoAOMT*) and caffeic acid o-methyl transferase (*COMT*) were genetically engineered in different species such as alfalfa, canola, maize, poplar, tobacco and sugarcane, to alter the lignin monomers composition [63–66, 70–74]. Several reports enumerating the modifications of some key TFs such as *OsMYB103L* are also available for improved plant architecture in rice [58, 59].

Cell wall polymer regulation	Genes	Approach	Phenotypes	Reference(s)
Cellulose synthesis	*OsCesA4*	Bc11 (G858R), NE1031, ND5658 (TOS17)	Reduce cellulose; affect growth	[10]
	OsCesA7	NC0258, ND8759 (TOS17)	Reduce cellulose; affect growth	[10]
	OsCesA9	ND2359 (TOS17)	Reduce cellulose; affect growth	[10]
	OsGH9B	Osfc4; Osfc11 (T-DNA)	Reduced Cr1(Cellulose crystallinity)	[55]
	OsGH9B 1; OsGH9B 3	pCAMBIAI11300: *OsGH9B*	Reduced Cr1; DP (Degree of Polymerisation)	[56]
	Fc17 (OsCESA4)	F_2 (fc17 × MH 63)	Reduced Cr1	[57]
Cellulose regulation	*OsMYB103L*	pUbi:: OsMYB103L (OE)	Increased secondary cell wall	[58]
	OsMYB103L: NAC29,31	pUbi:: OsMYB61; NAC29, 31 (OE)	Increased secondary cell wall	[59]
Lignin synthesis	*OsCAD2*	CRISPR/Cas9	Altered H and G residues; reduced lignin	[60]
	Fc1 (Cinnamyl-alcohol dehydrogenase)	Fc1 (T-DNA)	Reduced H and G residues; reduced lignin	[8]
	4CL; CAD	p35S::AtSHN2 (OE)	Reduced lignin	[9]
	Bc1 (COBRA like protein)	bc1 ($_{\gamma}$-rays)	Reduced lignin	[7]
	Laccases	LAC4/LAC7 (T- DNA)	Reduced lignin; hinderance in deposition of G subunits	[61]
	Peroxidases	TP60 (RNAi)	Reduced lignin; reduced G and S residues	[62]
	COMT	pWFOsC4H::Bg4CLi (RNAi)	Reduced lignin; reduced S/G ratio	[63]
	CCoAOMT	*CCoAOMT (RNAi)*	Altered lignin subunit composition	[64–66]
Hemicellulose synthesis	*OsXAX1 (GT61)*	axa1 (T-DNA)	Reduced xylose, ferulic acid, coumaric acid	[67]
	BAHD acetyl transferase	pUbi: OsAt10	Reduction in matrix bound ferulic acid	[68]
	OsIRX10 (GT47)	*OsIRX10* (RGT6229D)	Reduced X/A; affect growth	[69]

Table 1.
Candidate genes for preferable altering the cell wall polymers (cellulose, hemicellulose and lignin) in plant system.

3.3.2 Modification of hemicellulose

A general trade-off has been discovered between saccharification efficiency and ferulic acid [75, 76]. Bartley and co-workers, [68] reported the possible role of OsAt10, a BAHD acetyltransferase gene in achieving higher sugar release by favourably modifying glucuronoarabinoxylan (GAX) in rice. Young leaf tissues of the genetically engineered plants were found to be deficient in ferulic acid (FA). The possible role of other genes such as OsXAX1 and OsIRX10 were known to reciprocate similar results in rice [67, 68].

3.4 Role of cellulose synthase genes

Cellulose synthase enzymes are pivotal for cellulose synthesis. These proteins organise to form a hexameric 'rosette' structure approx. 25–30 nm diameter [77]. The plant cellulose synthase (*Ces A*) genes were first identified during random sequencing of cotton ESTs [78] and its role in cellulose synthesis was first reported in Arabidopsis Ces *A* mutants [10, 79]. The Ces *A* gene family was also identified in rice, maize, barely and poplar [57, 80–92].

Tanaka and co-workers [10] generated four different introgressed lines, showing brittle culm phenotypes by suitably introgressing Tos17, a retroposons in the genetic background of rice wildtype. They identified three cellulose synthase genes namely, *OsCesA4*, *OsCesA7* and *OsCesA9* on three different chromosomes. The mutant *Osfc16* with a mutation on *CesA9*- conserved sequence was found with altered cellulose crystallinity (crt1), which possibly enhanced the saccharification efficiency [93]. In a similar experiment, conserved site of another potential cellulose synthase CesA4 is mutated to alter cellulose crystallinity (crt1) for enhanced cellulose synthesis in *fc17* mutants [57]. Considerable efforts have been made to alter various structural properties of cell wall constituents including cellulose crystallinity (crt1) and degree of polymerisation (DP) which usually negatively affect the saccharification potential. In this regard, some noticeable work has been done to identify and characterise few genes of glycoside hydrolase family (*OsGH9B 1, 3 and 16*), promising candidate genes for favourably modifying structural properties of cell wall polymers as well as cellulose synthesis in rice [55, 56]. Beside cellulose synthase genes, other genes including KORRIGN [94–96], COBRA-like protein [7] and KOBITO [80] need to be explored properly to develop energy efficient elite cultigens in rice.

3.5 Genomics and QTL identification for biomass traits

Correlation between biomass traits and grain yield in rice is negative. Breeding varieties for high grain yield usually involves designing the varieties for medium plant height with short erect flag leaves which in turn affect the total biomass yield. This can be addressed to some extent by crossing rice cultivars, showing high polymorphism for grain yield potential as well as biomass traits and identify the candidate genes or QTLs involved. After the successful mapping of genes or, QTLs, the linked markers can be used for marker assisted selection (MAS) as well as can be used to screen the existing wild types or landraces for dual characteristics. As we have discussed earlier, cell wall polymers i.e., cellulose, hemicellulose and lignin composition can be altered for improved saccharification traits, hence, it is essential to search for the genetic link between cell-wall polymer composition and grain yield in order to breed dual purpose rice cultigens [97–103]. Gui- Fu and co-workers [97] identified few major QTLs associated with three plant traits namely, total biomass yield, straw yield and grain yield by developing suitable doubled haploid population. A QTL co-associated with both cell wall polymer composition and heading

date (HD17) has also been identified by crossing parents with considerable polymorphism for the dual characters [102]. Recently, Genome wide association survey (GWAS) involving high throughput molecular markers (SNPs) were employed to identify the genomic regions exhibiting significant association between markers and phenotypic trait and characterise the candidate genes involved [101]. Dissecting the genomic fragments involving lignin and cellulose biosynthesis is possible now with the application of GWAS technique [100].

3.6 Plant breeding strategies for improving biomass traits

Pre- existence of variability is of paramount importance in any crop improvement programme. Selection, being the core stone of plant breeding activities, is employed to harness the existing variability present in various germplasms including wild types and landraces, before creating additional variability by mutation.

A preferred high HI for good yield reduces the vegetative biomass of the rice as a whole including reduction in plant height. There is a trade-off for plant height vs. biomass yield. Hence, the role of long- culm rice cultivars in breeding high energy efficient varieties has been given due consideration [104–108]. However, an increase in culm length may increase the risk of plant lodging, which is a major factor influencing rice grain yield stability especially in direct-seeded rice. A thick culm with tolerable lignin content in cell wall will decrease the risk of plant lodging. So, there should be a balance between the cell wall constitution and morphological characters. Hence, judicious selection of genotypes for increased plant height with thick culm along with high grain yield can address the negative impact exerted by short culm height on overall biomass production. Few researches have enumerated the importance of selecting certain traits such as stem girth, plant height, leaf, sheath and stem weight for higher biomass yield in rice [40, 108, 109].

Another way for breeding dual purpose cultigens is to incorporate 'stay green' traits in cultivated type [110, 111]. Varieties possessing these traits are able to maintain higher photosynthetic activity at post-flowering stage, increasing yield thereof. At the same time, higher decomposability of these traits could serve the dual objectives as discussed above. Hence, there is a possible opportunity to exploit this stay green character in developing dual purpose rice genotypes as it has been exploited in other biofuel/bioenergy crops. Also, this character genetically enhances the photosynthetic efficiency, there may be no need to apply extra N inputs. Nevertheless, more research is required in this aspect. As of till date there are no reports of this strategy being exploited in breeding rice varieties for dual purpose.

Next it is important to identify the genetic loci (QTL) associated with these stay green trait and the markers flanking those regions [112–115]. Various biotechnological tools can then be employed for their successful integration into the plant genome or alternatively, marker aided selection (MAS) can be employed for varietal improvement. Also, heterosis breeding can be used to exploit the possible heterotic gene combinations in remodelling the plant architecture for higher biomass yield in rice, as it has been done in sorghum which possesses similar architectural traits [116–119].

4. Conclusion

There is an urgent need to address greenhouse gas emissions (GHGs) and climate changes occurring due to rampant use of fossil fuels. Rice straw, being an abundant source of lignocellulosic feedstock, has the potential to produce green energy to address the above said global concerns. Lignin and hemicellulose

complexes act as hinderance to produce energy efficient cultigens and hence, various studies are being made to down regulate the gene involved in their biosynthesis without affecting the plant system and cellulose concentration. Directly engineering cellulose synthase genes also provides an alternative opportunity in designing plant cell wall architecture. Stay green traits and heterosis breeding enhance the opportunity of developing energy efficient varieties to a greater extent. Thus, the role of plant breeding can never be bypassed as careful selection of individuals for dual traits will be highly rewarding in achieving the goal of growing dual-purpose rice varieties.

Acknowledgements

The authors thank Professor, Biofuel Chair, BPCL-OUAT project, Odisha, India for his guidance and encouragement to write this chapter. The authors also acknowledge the funding provided by the BPCL-OUAT Biofuel project implemented in OUAT, Bhubaneswar, India for the research work.

Conflict of interest

The authors declare no conflict of interest.

Author details

Manasi Dash[1*], Abinash Mishra[1] and Mahendra Kumar Mohanty[2]

1 Department of Plant Breeding and Genetics, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

2 College of Agricultural Engineering, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India

*Address all correspondence to: mdpbgouat@gmail.com

IntechOpen

© 2021 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. CC BY

References

[1] Mussatto SI, Roberto IC. Optimal experimental condition for hemicellulosic hydrolyzate treatment with activated charcoal for xylitol production. Biotechnology progress. 2004; 20(1): 134-139.

[2] Abraham A, Mathew AK, Sindhu R, Pandey A, Binod P. Potential of rice straw for bio-refining: an overview. Bioresource Technology. 2016 Sep 1; 215:29-36.

[3] Maiorella BI. Ethanol industrial chemicals. Biochem Fuels.

[4] Zamora R, JA SC. Production of an acid extract of rice straw. Acta cientifica venezolana. 1995 Jan 1;46(2):135-139.

[5] Garrote G, Domínguez H, Parajó JC. Autohydrolysis of corncob: study of non-isothermal operation for xylooligosaccharide production. Journal of Food Engineering. 2002 May 1;52(3):211-218.

[6] Saha BC. Hemicellulose bioconversion. Journal of industrial microbiology and biotechnology. 2003 May 1;30(5):279-291.

[7] Li Y, Qian Q, Zhou Y, Yan M, Sun L, Zhang M, Fu Z, Wang Y, Han B, Pang X, Chen M. BRITTLE CULM1, which encodes a COBRA-like protein, affects the mechanical properties of rice plants. The Plant Cell. 2003 Sep 1;15(9): 2020-2031.

[8] Li X, Yang Y, Yao J, Chen G, Li X, Zhang Q, Wu C. FLEXIBLE CULM 1 encoding a cinnamyl-alcohol dehydrogenase controls culm mechanical strength in rice. Plant molecular biology. 2009 Apr;69(6): 685-697.

[9] Ambavaram MM, Krishnan A, Trijatmiko KR, Pereira A. Coordinated activation of cellulose and repression of lignin biosynthesis pathways in rice. Plant physiology. 2011 Feb 1;155(2): 916-931.

[10] Tanaka K, Murata K, Yamazaki M, Onosato K, Miyao A, Hirochika H. Three distinct rice cellulose synthase catalytic subunit genes required for cellulose synthesis in the secondary wall. Plant physiology. 2003 Sep 1;133(1):73-83.

[11] Furtado A, Lupoi JS, Hoang NV, Healey A, Singh S, Simmons BA, Henry RJ. Modifying plants for biofuel and biomaterial production. Plant biotechnology journal. 2014 Dec;12(9):1246-1258.

[12] Vermerris W, Abril A. Enhancing cellulose utilization for fuels and chemicals by genetic modification of plant cell wall architecture. Current opinion in biotechnology. 2015 Apr 1;32:104-112.

[13] Hideno A, Inoue H, Tsukahara K, Fujimoto S, Minowa T, Inoue S, Endo T, Sawayama S. Wet disk milling pretreatment without sulfuric acid for enzymatic hydrolysis of rice straw. Bioresource Technology. 2009 May 1;100(10):2706-2711.

[14] Bak JS, Ko JK, Han YH, Lee BC, Choi IG, Kim KH. Improved enzymatic hydrolysis yield of rice straw using electron beam irradiation pretreatment. Bioresource Technology. 2009 Feb 1;100(3):1285-1290.

[15] Xiong J, Ye J, Liang WZ, Fan PM. Influence of microwave on the ultrastructure of cellulose I. Journal of South China University Technology. 2000;28(1):84-89.

[16] Azuma JI, Higashino J, Isaka M, Koshijima T. < Original> Microwave Irradiation of Lignocellulosic Materials: IV. Enhancement of Enzymatic

Susceptibility of Microwave-irradiated Softwoods. Wood research: bulletin of the Wood Research Institute Kyoto University. 1985 Feb 28;71:13-24.

[17] Wongjewboot I, Kangsadan T, Kongruang S, Burapatana V, Pripanapong P. Ethanol production from rice straw using ultrasonic pretreatment. In2010 International Conference on Chemistry and Chemical Engineering 2010 Aug 1 (pp. 16-19). IEEE.

[18] Wi SG, Choi IS, Kim KH, Kim HM, Bae HJ. Bioethanol production from rice straw by popping pretreatment. Biotechnology for biofuels. 2013 Dec;6(1):1-7.

[19] Gáspár M, Kálmán G, Réczey K. Corn fiber as a raw material for hemicellulose and ethanol production. Process Biochemistry. 2007 Jul 1;42(7):1135-1139.

[20] Zhang Q, Cai W. Enzymatic hydrolysis of alkali-pretreated rice straw by Trichoderma reesei ZM4-F3. Biomass and Bioenergy. 2008 Dec 1;32(12):1130-1135.

[21] Cha YL, Yang J, Ahn JW, Moon YH, Yoon YM, Yu GD, An GH, Choi IH. The optimized CO 2-added ammonia explosion pretreatment for bioethanol production from rice straw. Bioprocess and biosystems engineering. 2014 Sep;37(9):1907-1915.

[22] Harun S, Geok SK. Effect of sodium hydroxide pretreatment on rice straw composition. Indian J Sci Technol. 2016 Jun;9(21):1-9.

[23] Kim SB, Lee SJ, Lee JH, Jung YR, Thapa LP, Kim JS, Um Y, Park C, Kim SW. Pretreatment of rice straw with combined process using dilute sulfuric acid and aqueous ammonia. Biotechnology for biofuels. 2013 Dec;6(1):1-1.

[24] Chiranjeevi T, Mattam AJ, Vishwakarma KK, Uma A, Peddy VR, Gandham S, Ravindra Velankar H. Assisted single-step acid pretreatment process for enhanced delignification of rice straw for bioethanol production. ACS Sustainable Chemistry & Engineering. 2018 Jun 5;6(7):8762-8774.

[25] Hon DN, Shiraishi N. Wood and cellulosic chemistry, revised, and expanded. CRC press; 2000 Nov 8.

[26] Wei CJ, Cheng CY. Effect of hydrogen peroxide pretreatment on the structural features and the enzymatic hydrolysis of rice straw. Biotechnology and bioengineering. 1985 Oct;27(10):1418-1426.

[27] Taniguchi M, Suzuki H, Watanabe D, Sakai K, Hoshino K, Tanaka T. Evaluation of pretreatment with Pleurotus ostreatus for enzymatic hydrolysis of rice straw. Journal of bioscience and bioengineering. 2005 Dec 1;100(6):637-643.

[28] Patel SJ, Onkarappa R, Shobha KS. Comparative study of ethanol production from microbial pretreated agricultural residues. Journal of Applied Sciences and Environmental Management. 2007;11(4):137-141.

[29] Taherzadeh MJ, Niklasson C. Ethanol from lignocellulosic materials: pretreatment, acid and enzymatic hydrolyses, and fermentation.

[30] Gonzalez Valdes I, Lopez Planes R. Study of the hydrolysis of rice straw with sulfuric acid under moderate conditions. Rev. Cienc. Quim.;(Cuba). 1983 Jan 1;14(1).

[31] Abedinifar S, Karimi K, Khanahmadi M, Taherzadeh MJ. Ethanol production by Mucor indicus and Rhizopus oryzae from rice straw by separate hydrolysis and fermentation. Biomass and bioenergy. 2009 May 1;33(5):828-833.

[32] Aderemi BO, Abu E, Highina BK. The kinetics of glucose production from rice straw by Aspergillus niger. African journal of Biotechnology. 2008; 7(11).

[33] Wyman CE. Ethanol from lignocellulosic biomass: technology, economics, and opportunities. Bioresource Technology. 1994 Jan 1;50(1):3-15.

[34] Spindler DD, Wyman CE, Mohagheghi A, Grohmann K. Thermotolerant yeast for simultaneous saccharification and fermentation of cellulose to ethanol. Applied Biochemistry and Biotechnology. 1988 Apr;17(1):279-293.

[35] Golias H, Dumsday GJ, Stanley GA, Pamment NB. Evaluation of a recombinant Klebsiella oxytoca strain for ethanol production from cellulose by simultaneous saccharification and fermentation: comparison with native cellobiose-utilising yeast strains and performance in co-culture with thermotolerant yeast and Zymomonas mobilis. Journal of biotechnology. 2002 Jun 26;96(2):155-168.

[36] Shengdong Z, Yuanxin W, Yufeng Z, Shaoyong T, Yongping X, Ziniu Y, Xuan Z. Fed-batch simultaneous saccharification and fermentation of microwave/acid/alkali/H2O2 pretreated rice straw for production of ethanol. Chemical Engineering Communications. 2006 May 1;193(5):639-648.

[37] Chadha BS, Kanwar SS, Garcha HS. Simultaneous saccharification and fermentation of rice straw into ethanol. Acta microbiologica et immunologica hungarica. 1995 Jan 1;42(1):71-75.

[38] Browning BL. The wood-water relationship. The chemistry of wood. Interscience Publishers, Willey, New York. 1963.

[39] Carroll A, Somerville C. Cellulosic biofuels. Annual review of plant biology. 2009 Jun 2;60:165-182.

[40] Jahn CE, Mckay JK, Mauleon R, Stephens J, McNally KL, Bush DR, Leung H, Leach JE. Genetic variation in biomass traits among 20 diverse rice varieties. Plant Physiology. 2011 Jan 1;155(1):157-168.

[41] Slavov GT, Nipper R, Robson P, Farrar K, Allison GG, Bosch M, Clifton-Brown JC, Donnison IS, Jensen E. Genome-wide association studies and prediction of 17 traits related to phenology, biomass and cell wall composition in the energy grass Miscanthus sinensis. New phytologist. 2014 Mar;201(4):1227-1239.

[42] Bhattacharyya P, Bhaduri D, Adak T, Munda S, Satapathy BS, Dash PK, Padhy SR, Pattanayak A, Routray S, Chakraborti M, Baig MJ. Characterization of rice straw from major cultivars for best alternative industrial uses to cutoff the menace of straw burning. Industrial Crops and Products. 2020 Jan 1;143:111919.

[43] Harris D, Bulone V, Ding SY, DeBolt S. Tools for cellulose analysis in plant cell walls. Plant physiology. 2010 Jun 1;153(2):420-426.

[44] Esteghlalian AR, Srivastava V, Gilkes N, Gregg DJ, Saddler JN. An overview of factors influencing the enzymatic hydrolysis of lignocellulosic feedstocks.

[45] Wyman CE, Decker SR, Himmel ME, Brady JW, Skopec CE, Viikari L. Hydrolysis of cellulose and hemicellulose. Polysaccharides: Structural diversity and functional versatility. 2005;1:1023-1062.

[46] Miao YC, Liu CJ. ATP-binding cassette-like transporters are involved in the transport of lignin precursors across plasma and vacuolar membranes.

Proceedings of the National Academy of Sciences. 2010 Dec 28;107(52):22728-22733.

[47] Ralph J. Hydroxycinnamates in lignification. Phytochemistry Reviews. 2010 Mar 1;9(1):65-83.

[48] Ithal N, Recknor J, Nettleton D, Maier T, Baum TJ, Mitchum MG. Developmental transcript profiling of cyst nematode feeding cells in soybean roots. Molecular Plant-Microbe Interactions. 2007 May;20(5):510-525.

[49] Schuetz M, Benske A, Smith RA, Watanabe Y, Tobimatsu Y, Ralph J, Demura T, Ellis B, Samuels AL. Laccases direct lignification in the discrete secondary cell wall domains of protoxylem. Plant Physiology. 2014 Oct 1;166(2):798-807.

[50] Tripathi SC, Sayre KD, Kaul JN, Narang RS. Growth and morphology of spring wheat (Triticum aestivum L.) culms and their association with lodging: effects of genotypes, N levels and ethephon. Field Crops Research. 2003 Dec 1;84(3):271-290.

[51] Moura JC, Bonine CA, de Oliveira Fernandes Viana J, Dornelas MC, Mazzafera P. Abiotic and biotic stresses and changes in the lignin content and composition in plants. Journal of integrative plant biology. 2010 Apr;52(4):360-376.

[52] Liu Q, Luo L, Zheng L. Lignins: biosynthesis and biological functions in plants. International journal of molecular sciences. 2018 Feb;19(2):335.

[53] Binod P, Sindhu R, Singhania RR, Vikram S, Devi L, Nagalakshmi S, Kurien N, Sukumaran RK, Pandey A. Bioethanol production from rice straw: an overview. Bioresource technology. 2010 Jul 1;101(13):4767-4774.

[54] Wang P, Dudareva N, Morgan JA, Chapple C. Genetic manipulation of lignocellulosic biomass for bioenergy. Current opinion in chemical biology. 2015 Dec 1;29:32-39.

[55] Xie G, Yang B, Xu Z, Li F, Guo K, Zhang M, Wang L, Zou W, Wang Y, Peng L. Global identification of multiple OsGH9 family members and their involvement in cellulose crystallinity modification in rice. PloS one. 2013 Jan 4;8(1):e50171.

[56] Huang J, Xia T, Li G, Li X, Li Y, Wang Y, Wang Y, Chen Y, Xie G, Bai FW, Peng L. Overproduction of native endo-β-1, 4-glucanases leads to largely enhanced biomass saccharification and bioethanol production by specific modification of cellulose features in transgenic rice. Biotechnology for Biofuels. 2019 Dec;12(1):1-5.

[57] Li F, Liu S, Xu H, Xu Q. A novel FC17/CESA4 mutation causes increased biomass saccharification and lodging resistance by remodeling cell wall in rice. Biotechnology for biofuels. 2018 Dec;11(1):1-13.

[58] Yang C, Li D, Liu X, Ji C, Hao L, Zhao X, Li X, Chen C, Cheng Z, Zhu L. OsMYB103L, an R2R3-MYB transcription factor, influences leaf rolling and mechanical strength in rice (Oryza sativa L.). BMC plant biology. 2014 Dec;14(1):1-5.

[59] Huang D, Wang S, Zhang B, Shang-Guan K, Shi Y, Zhang D, Liu X, Wu K, Xu Z, Fu X, Zhou Y. A gibberellin-mediated DELLA-NAC signaling cascade regulates cellulose synthesis in rice. The Plant Cell. 2015 Jun 1;27(6):1681-1696.

[60] Zhang G, Wang L, Li X, Bai S, Xue Y, Li Z, Tang SW, Wang Y, Wang Y, Hu Z, Li P. Distinctively altered lignin biosynthesis by site-modification of OsCAD2 for enhanced biomass saccharification in rice. GCB Bioenergy. 2021 Feb;13(2):305-319.

[61] Berthet S, Demont-Caulet N, Pollet B, Bidzinski P, Cézard L, Le Bris P, Borrega N, Hervé J, Blondet E, Balzergue S, Lapierre C. Disruption of LACCASE4 and 17 results in tissue-specific alterations to lignification of Arabidopsis thaliana stems. The Plant Cell. 2011 Mar 1;23(3):1124-1137.

[62] Blee KA, Choi JW, O'Connell AP, Schuch W, Lewis NG, Bolwell GP. A lignin-specific peroxidase in tobacco whose antisense suppression leads to vascular tissue modification. Phytochemistry. 2003 Sep 1;64(1):163-176.

[63] Jung JH, Fouad WM, Vermerris W, Gallo M, Altpeter F. RNAi suppression of lignin biosynthesis in sugarcane reduces recalcitrance for biofuel production from lignocellulosic biomass. Plant biotechnology journal. 2012 Dec;10(9):1067-1076.

[64] Marita JM, Ralph J, Hatfield RD, Guo D, Chen F, Dixon RA. Structural and compositional modifications in lignin of transgenic alfalfa down-regulated in caffeic acid 3-O-methyltransferase and caffeoyl coenzyme A 3-O-methyltransferase. Phytochemistry. 2003 Jan 1;62(1): 53-65.

[65] Chen F, Dixon RA. Lignin modification improves fermentable sugar yields for biofuel production. Nature biotechnology. 2007 Jul;25(7): 759-761.

[66] Pinçon G, Maury S, Hoffmann L, Geoffroy P, Lapierre C, Pollet B, Legrand M. Repression of O-methyltransferase genes in transgenic tobacco affects lignin synthesis and plant growth. Phytochemistry. 2001 Aug 1;57(7):1167-1176.

[67] Chiniquy D, Sharma V, Schultink A, Baidoo EE, Rautengarten C, Cheng K, Carroll A, Ulvskov P, Harholt J, Keasling JD, Pauly M. XAX1 from glycosyltransferase family 61 mediates xylosyltransfer to rice xylan. Proceedings of the National Academy of Sciences. 2012 Oct 16;109(42):17117-17122.

[68] Bartley LE, Peck ML, Kim SR, Ebert B, Manisseri C, Chiniquy DM, Sykes R, Gao L, Rautengarten C, Vega-Sánchez ME, Benke PI. Overexpression of a BAHD acyltransferase, OsAt10, alters rice cell wall hydroxycinnamic acid content and saccharification. Plant Physiology. 2013 Apr 1;161(4):1615-1633.

[69] Chen X, Vega-Sánchez ME, Verhertbruggen Y, Chiniquy D, Canlas PE, Fagerström A, Prak L, Christensen U, Oikawa A, Chern M, Zuo S. Inactivation of OsIRX10 leads to decreased xylan content in rice culm cell walls and improved biomass saccharification. Molecular Plant. 2013 Mar 1;6(2):570-573.

[70] Meyermans H, Morreel K, Lapierre C, Pollet B, De Bruyn A, Busson R, Herdewijn P, Devreese B, Van Beeumen J, Marita JM, Ralph J. Modifications in lignin and accumulation of phenolic glucosides in poplar xylem upon down-regulation of caffeoyl-coenzyme A O-methyltransferase, an enzyme involved in lignin biosynthesis. Journal of Biological Chemistry. 2000 Nov 24;275(47):36899-36909.

[71] Zhong R, Morrison WH, Himmelsbach DS, Poole FL, Ye ZH. Essential role of caffeoyl coenzyme A O-methyltransferase in lignin biosynthesis in woody poplar plants. Plant Physiology. 2000 Oct 1;124(2):563-578.

[72] Chen F, Srinivasa Reddy MS, Temple S, Jackson L, Shadle G, Dixon RA. Multi-site genetic modulation of monolignol biosynthesis suggests new routes for formation of syringyl lignin and wall-bound ferulic

acid in alfalfa (Medicago sativa L.). The Plant Journal. 2006 Oct;48(1):113-124.

[73] Bhinu VS, Li R, Huang J, Kaminskyj S, Sharpe A, Hannoufa A. Perturbation of lignin biosynthesis pathway in Brassica napus (canola) plants using RNAi. Canadian journal of plant science. 2009 May 1;89(3):441-453.

[74] Li X, Chen W, Zhao Y, Xiang Y, Jiang H, Zhu S, Cheng B. Downregulation of caffeoyl-CoA O-methyltransferase (CCoAOMT) by RNA interference leads to reduced lignin production in maize straw. Genetics and molecular biology. 2013;36(4):540-546.

[75] Grabber JH, Ralph J, Hatfield RD. Ferulate cross-links limit the enzymatic degradation of synthetically lignified primary walls of maize. Journal of Agricultural and Food Chemistry. 1998 Jul 20;46(7):2609-2614.

[76] Lam TB, Iiyama K, Stone BA. Hot alkali-labile linkages in the walls of the forage grass Phalaris aquatica and Lolium perenne and their relation to in vitro wall digestibility. Phytochemistry. 2003 Sep 1;64(2):603-607.

[77] Taylor NG. Cellulose biosynthesis and deposition in higher plants. New Phytologist. 2008 Apr;178(2):239-252.

[78] Pear JR, Kawagoe Y, Schreckengost WE, Delmer DP, Stalker DM. Higher plants contain homologs of the bacterial celA genes encoding the catalytic subunit of cellulose synthase. Proceedings of the National Academy of Sciences. 1996 Oct 29;93(22):12637-12642.

[79] Arioli T, Peng L, Betzner AS, Burn J, Wittke W, Herth W, Camilleri C, Höfte H, Plazinski J, Birch R, Cork A. Molecular analysis of cellulose biosynthesis in Arabidopsis. Science. 1998 Jan 30;279(5351):717-720.

[80] Holland N, Holland D, Helentjaris T, Dhugga KS, Xoconostle-Cazares B, Delmer DP. A comparative analysis of the plant cellulose synthase (CesA) gene family. Plant physiology. 2000 Aug 1;123(4):1313-1324.

[81] Taylor NG, Scheible WR, Cutler S, Somerville CR, Turner SR. The irregular xylem3 locus of Arabidopsis encodes a cellulose synthase required for secondary cell wall synthesis. The plant cell. 1999 May 1;11(5):769-779.

[82] Fagard M, Desnos T, Desprez T, Goubet F, Refregier G, Mouille G, McCann M, Rayon C, Vernhettes S, Höfte H. PROCUSTE1 encodes a cellulose synthase required for normal cell elongation specifically in roots and dark-grown hypocotyls of Arabidopsis. The plant cell. 2000 Dec 1;12(12):2409-2423.

[83] Taylor NG, Laurie S, Turner SR. Multiple cellulose synthase catalytic subunits are required for cellulose synthesis in Arabidopsis. The plant cell. 2000 Dec 1;12(12):2529-2539.

[84] Kikuchi S, Satoh K, Nagata T, Kawagashira N, Doi K, Kishimoto N, Yazaki J, Ishikawa M, Yamada H, Ooka H, Hotta I. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice. science. 2003 Jul 18;301(5631):376-379.

[85] Taylor NG, Howells RM, Huttly AK, Vickers K, Turner SR. Interactions among three distinct CesA proteins essential for cellulose synthesis. Proceedings of the National Academy of Sciences. 2003 Feb 4;100(3):1450-1455.

[86] Zhong R, Morrison WH, Freshour GD, Hahn MG, Ye ZH. Expression of a mutant form of cellulose synthase AtCesA7 causes dominant negative effect on cellulose biosynthesis. Plant physiology. 2003 Jun 1;132(2):786-795.

[87] Appenzeller L, Doblin M, Barreiro R, Wang H, Niu X, Kollipara K, Carrigan L, Tomes D, Chapman M, Dhugga KS. Cellulose synthesis in maize: isolation and expression analysis of the cellulose synthase (CesA) gene family. Cellulose. 2004 Sep;11(3): 287-299.

[88] Burton RA, Shirley NJ, King BJ, Harvey AJ, Fincher GB. The CesA gene family of barley. Quantitative analysis of transcripts reveals two groups of co-expressed genes. Plant physiology. 2004 Jan 1;134(1):224-236.

[89] Joshi CP, Bhandari S, Ranjan P, Kalluri UC, Liang X, Fujino T, Samuga A. Genomics of cellulose biosynthesis in poplars. New Phytologist. 2004 Oct;164(1):53-61.

[90] Desprez T, Juraniec M, Crowell EF, Jouy H, Pochylova Z, Parcy F, Höfte H, Gonneau M, Vernhettes S. Organization of cellulose synthase complexes involved in primary cell wall synthesis in Arabidopsis thaliana. Proceedings of the National Academy of Sciences. 2007 Sep 25;104(39):15572-15577.

[91] Persson S, Paredez A, Carroll A, Palsdottir H, Doblin M, Poindexter P, Khitrov N, Auer M, Somerville CR. Genetic evidence for three unique components in primary cell-wall cellulose synthase complexes in Arabidopsis. Proceedings of the National Academy of Sciences. 2007 Sep 25;104(39):15566-15571.

[92] Harris DM, Corbin K, Wang T, Gutierrez R, Bertolo AL, Petti C, Smilgies DM, Estevez JM, Bonetta D, Urbanowicz BR, Ehrhardt DW. Cellulose microfibril crystallinity is reduced by mutating C-terminal transmembrane region residues CESA1A903V and CESA3T942I of cellulose synthase. Proceedings of the National Academy of Sciences. 2012 Mar 13;109(11):4098-4103.

[93] Li F, Xie G, Huang J, Zhang R, Li Y, Zhang M, Wang Y, Li A, Li X, Xia T, Qu C. Os CESA 9 conserved-site mutation leads to largely enhanced plant lodging resistance and biomass enzymatic saccharification by reducing cellulose DP and crystallinity in rice. Plant biotechnology journal. 2017 Sep;15(9):1093-1104.

[94] Nicol F, His I, Jauneau A, Vernhettes S, Canut H, Höfte H. A plasma membrane-bound putative endo-1, 4-β-d-glucanase is required for normal wall assembly and cell elongation in Arabidopsis. The EMBO journal. 1998 Oct 1;17(19):5563-5576.

[95] Lane DR, Wiedemeier A, Peng L, Höfte H, Vernhettes S, Desprez T, Hocart CH, Birch RJ, Baskin TI, Burn JE, Arioli T. Temperature-sensitive alleles of RSW2 link the KORRIGAN endo-1, 4-β-glucanase to cellulose synthesis and cytokinesis in Arabidopsis. Plant physiology. 2001 May 1;126(1):278-288.

[96] Szyjanowicz PM, McKinnon I, Taylor NG, Gardiner J, Jarvis MC, Turner SR. The irregular xylem 2 mutant is an allele of korrigan that affects the secondary cell wall of Arabidopsis thaliana. The Plant Journal. 2004 Mar;37(5):730-740.

[97] Gui-Fu LI, Jian YA, Jun ZH. Mapping QTL for biomass yield and its components in rice (Oryza sativa L.). Acta Genetica Sinica. 2006 Jul 1;33(7):607-616.

[98] Liu B, Gómez LD, Hua C, Sun L, Ali I, Huang L, Yu C, Simister R, Steele-King C, Gan Y, McQueen-Mason SJ. Linkage mapping of stem saccharification digestibility in rice. PloS one. 2016 Jul 14;11(7):e0159117.

[99] Matsubara K, Yamamoto E, Kobayashi N, Ishii T, Tanaka J, Tsunematsu H, Yoshinaga S, Matsumura O, Yonemaru JI,

Mizobuchi R, Yamamoto T. Improvement of rice biomass yield through QTL-based selection. PloS one. 2016 Mar 17;11(3):e0151830.

[100] Naz AA, Reinert S, Bostanci C, Seperi B, Leon J, Böttger C, Südekum KH, Frei M. Mining the global diversity for bioenergy traits of barley straw: genomewide association study under varying plant water status. Gcb Bioenergy. 2017 Aug;9(8):1356-1369.

[101] Wood IP, Pearson BM, Garcia-Gutierrez E, Havlickova L, He Z, Harper AL, Bancroft I, Waldron KW. Carbohydrate microarrays and their use for the identification of molecular markers for plant cell wall composition. Proceedings of the National Academy of Sciences. 2017 Jun 27;114(26): 6860-6865.

[102] Xu Z, Li S, Zhang C, Zhang B, Zhu K, Zhou Y, Liu Q. Genetic connection between cell-wall composition and grain yield via parallel QTL analysis in indica and japonica subspecies. Scientific reports. 2017 Oct 2;7(1):1-3.

[103] Matsubara K, Yonemaru JI, Kobayashi N, Ishii T, Yamamoto E, Mizobuchi R, Tsunematsu H, Yamamoto T, Kato H, Yano M. A follow-up study for biomass yield QTLs in rice. PloS one. 2018 Oct 23;13(10):e0206054.

[104] Takeda T, Oka M, Agata W. Characteristics of dry matter and grain production of rice cultivars in the Warmer Part of Japan: I. Comparison of dry matter production between old and new types of rice cultivars. Japanese Journal of Crop Science. 1983 Sep 5;52(3):299-306.

[105] Kuroda E, Ookawa T, Ishihara K. Analysis on difference of dry matter production between rice cultivars with different plant height in relation to gas diffusion inside stands. Japanese Journal of Crop Science. 1989 Sep 5;58(3):374-382.

[106] Peng S, Laza RC, Visperas RM, Sanico AL, Cassman KG, Khush GS. Grain yield of rice cultivars and lines developed in the Philippines since 1966. Crop science. 2000 Mar;40(2):307-314.

[107] Yang W, Peng S, Laza RC, Visperas RM, Dionisio-Sese ML. Grain yield and yield attributes of new plant type and hybrid rice. Crop Science. 2007 Jul;47(4):1393-1400.

[108] Ookawa T, Yasuda K, Kato H, Sakai M, Seto M, Sunaga K, Motobayashi T, Tojo S, Hirasawa T. Biomass production and lodging resistance in 'Leaf Star', a new long-culm rice forage cultivar. Plant production science. 2010;13(1):58-66.

[109] Yang XC, Hwa CM. Genetic modification of plant architecture and variety improvement in rice. Heredity. 2008 Nov;101(5):396-404.

[110] Ahlawat S, Chhabra AK, Behl RK, Bisht SS. Genotypic divergence analysis for stay green characters in Wheat (Triticum aestivum L. em. Thell). The South Pacific Journal of Natural and Applied Sciences. 2008;26(1):73-81.

[111] Fu JD, Yan YF, Lee BW. Physiological characteristics of a functional stay-green rice "SNU-SG1" during grain-filling period. Journal of Crop Science and Biotechnology. 2009 Mar;12(1):47-52.

[112] Xu W, Subudhi PK, Crasta OR, Rosenow DT, Mullet JE, Nguyen HT. Molecular mapping of QTLs conferring stay-green in grain sorghum (Sorghum bicolor L. Moench). Genome. 2000 Jun 1;43(3):461-469.

[113] Cha KW, Lee YJ, Koh HJ, Lee BM, Nam YW, Paek NC. Isolation, characterization, and mapping of the

stay green mutant in rice. Theoretical and Applied Genetics. 2002 Mar 1;104(4):526-532.

[114] Jiang GH, He YQ, Xu CG, Li XH, Zhang Q. The genetic basis of stay-green in rice analyzed in a population of doubled haploid lines derived from an indica by japonica cross. Theoretical and Applied Genetics. 2004 Feb 1;108(4):688-698.

[115] Yoo SC, Cho SH, Zhang H, Paik HC, Lee CH, Li J, Yoo JH, Koh HJ, Seo HS, Paek NC. Quantitative trait loci associated with functional stay-green SNU-SG1 in rice. Molecules & Cells (Springer Science & Business Media BV). 2007 Aug 1;24(1).

[116] Meshram MP, Atale SB, Murumkar RD, Raut PB. Heterosis and heterobeltiosis studies in sweet sorghum. Annals of Plant Physiology. 2005;19(1):96.

[117] Corn RJ. *Heterosis and composition of sweet sorghum* (Doctoral dissertation, Texas A & M University).

[118] Pfeiffer TW, Bitzer MJ, Toy JJ, Pedersen JF. Heterosis in sweet sorghum and selection of a new sweet sorghum hybrid for use in syrup production in Appalachia. Crop Science. 2010 Sep;50(5):1788-1794.

[119] Packer DJ, Rooney WL. High-parent heterosis for biomass yield in photoperiod-sensitive sorghum hybrids. Field Crops Research. 2014 Oct 1;1(167): 153-158.