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Liu, Bohan, Gómez, Leonardo D orcid.org/0000-0001-6382-9447, Hua, Cangmei et al. (8 more authors) (2016) Linkage Mapping of Stem Saccharification Digestibility in Rice. PLoS ONE. e0159117. ISSN: 1932-6203

<https://doi.org/10.1371/journal.pone.0159117>

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Linkage mapping of stem saccharification digestibility in rice

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Abstract

Rice is the staple food of almost half of the world population, and in excess 90% of it is grown and consumed in Asia, but the disposal of rice straw poses a problem for farmers, who often burn it in the fields, causing health and environmental problems. However, with increased focus on the development of sustainable biofuel production, rice straw has been recognized as a potential feedstock for non-food derived biofuel production. Currently, the commercial realization of rice as a biofuel feedstock is constrained by the high cost of industrial saccharification processes needed to release sugar for fermentation. This study is focused on the alteration of lignin content, and cell wall chemotypes and structures, and their effects on the saccharification potential of rice lignocellulosic biomass. A recombinant inbred lines (RILs) population derived from a cross between the lowland rice variety IR1552 and the upland rice variety Azucena with 271 molecular markers for quantitative trait SNP (QTS) analyses was used. After association analysis of 271 markers for saccharification potential, 1 locus and 4 pairs of epistatic loci were found to contribute to the enzymatic digestibility phenotype, and an inverse relationship between reducing sugar and lignin content in these recombinant inbred lines was identified. As a result of QTS analyses, several cell-wall associated candidate genes are proposed that may be useful for marker-assisted breeding and may aid breeders to produce potential high saccharification rice varieties.

Keywords: rice; cell wall; saccharification; lignin; biofuel; QTS; RIL

Introduction

Rice is one of the most important staple crops in the world, with the potential to feed more than two billion people [1, 2]. Asia, China and India produce and consume more than half of the world's total rice supply [3]. Until recently, rice straw, which represents approximately half of the total biomass of the plant, was considered a waste stream of rice production with little or no value, depending on the country or region of production [4]. The practice of burning rice straw represents not only a waste of

biomass resources, but also a series of challenges to the environment [5, 6]. In response to concerns about greenhouse-gas emissions and the sustainability of fossil fuel supplies, global biofuel production has expanded rapidly in recent years[7]. Many countries are starting to consider the use of rice straw for second generation biofuel production, and this previously underestimated lignocellulosic biomass is now viewed as a potential feedstock rather than a waste product [8].

Rice straw is composed mainly of lignocellulosic biomass, which is approximately 2/3 sugars with the potential for fermentation into biofuels[9]. However, the inherent recalcitrance of plant biomass to hydrolysis is an obstacle to saccharification [10]. This recalcitrance is conferred by the complexity and the crystallinity of the polysaccharides and lignin in the plant cell wall. Thus, facilitating the saccharification or improving the yield of digestible biomass could reduce the cost of industrial biofuel production [11]. Therefore, one approach is to screen rice varieties for cell wall components that are more susceptible to hydrolysis, without compromising the field performance of the crop [12]. There are many studies that focus on the molecular mechanism between cell wall polymers, chemotypes and biomass digestibility, and most of them demonstrate that altering either lignin content or the polysaccharide structure in the cell wall can affect saccharification potential of lignocellulosic biomass [13-18]. Linkage analyses in maize have shown that quantitative trait loci (QTL) associated with saccharification are independent of lignin abundance, suggesting that lignin is not the only factor determining saccharification potential[19]. Indeed, wider research has shown that changes in cellulose production, deposition, and crystallinity will also significantly affect saccharification [20-22]. Hemicelluloses are the second most abundant fraction in the cell wall, and they covalently link with lignin via ferulic acid ester linkages[23]. Changes in the structure of hemicelluloses, as well as the reduction of the covalent links with lignin can significantly affect saccharification of biomass[15, 24].

In order to move towards improved cell-wall digestibility, a RIL population derived from a cross between the lowland rice variety IR1552 and the upland rice variety Azucena was used in this study to research the genetic basis, candidate genes, and molecular markers that can be used in the identification of genes governing

saccharification potential, to further the breeding of high saccharification rice varieties. These recombinant inbred lines were previously studied to analyze root architecture and cell wall expansion traits [25]. In the present work, we performed quantitative trait SNP (QTS) analyses with 271 molecular markers bases with saccharification potential, and further studied the relationship between reducing sugar and lignin content in these inbred lines. These results provide first hand genetic resources and potentially indispensable data for further research of cell-wall digestibility in *Oryza sativa*.

Material and methods

Plant material

The RIL population was generated from a cross between IR1552, an irrigated lowland *indica* variety, and Azucena, an upland tropical *japonica* variety, by single-seed descent in the F₁₀ generation (The seeds were kindly provided by Prof. Wu Ping). The rice plants were cultivated for two independent seasons (2012 summer and 2012 winter) in Changxing, Zhejiang Province (119°39' E, 30°54' N) and Sanya, Hainan province (109°31' E, 18°18' N) in China, respectively. There were no specific permissions required for these locations/activities, because all of the field test was conducted with permission of Zhejiang University's authority. The seedlings were arranged in single rows with 15cm spacing between plants and 30cm between rows, then they were grown under standard lowland rice field parameters [25]. Stem samples were taken between the third and the fourth node of mature and dried plants from these two independent seasons. All stem samples were cut into 4-mm lengths and ground using a custom-made robotic platform as previously described [26].

Saccharification Analysis

Ground rice straw (4mg, 4 replicates per plant) was weighed into 96-deep-well plates, using a robotic platform [26]. A pre-treatment solution (0.5M NaOH, 350μL)

was added and plates were sealed before incubation at 90°C for -30 min, followed by five washes with 500µL 25mM sodium acetate buffer, before incubation with 500µL of industrial enzyme mixture (solution of cellulases and hemicellulases) at 50°C with agitation. Aliquots(-45µL) of the resulting biomass hydrolysate were used for the determination of reducing sugars released by hydrolysis, using a modified 3-methyl-2-benzothiazolinone hydrozone (MTBH) method with robotic platform (Tecan Evo200; Tecan Group Ltd.), as previously described [26].

Lignin content analysis

Ground rice straw was sieved to fine fraction (150 or 180µm sieve) before weighed into 200mg per plant, followed by 3 washes with 4mL CHCl₃:MeOH (1:1) solution, 80% MeOH and 100%MeOH respectively (250rpm agitation for 30min, 10 min centrifuge at 2500g and 4 °C), till powder turn into colorless. The washed powder were weighed to 3.5mg for each replicate before 4h incubation at 45°C with 0.3mL 25% (v/v) acetyl bromide/glacial acetic acid, then the mixture was cooled down to 15 °C for adding 0.3mL glacial acetic acid, followed by a 5 min vortex. A 0.5mL of reaction mixture above were added to a tube containing 0.1mL of 0.5M hydroxylamine and 1mL of 2M NaOH solution. Tubes were gently shaken after acetic acid was added to give a final volume of 10 mL. The final solutions were read in spectrophotometer at 280 nm, the percentage of total lignin content in dry sample was calculated as $L\% = A_{280}/17.2 \times 6/5 \times 10/3.5 \times 100\%$.

Association Mapping

The QTX Network software (<http://ibi.zju.edu.cn/software/QTXNetwork/>) was used to perform the quantitative trait SNP (QTS) analyses and dissect the genetic architecture of saccharification potential. Individual locus detection was conducted using a mixed linear model, and epistasis interacting loci were performed using a 2D genome scan with statistical model described before[27]. In total, 271 markers were

used in the association mapping of 121 representative RIL plants (data from two seasons) with saccharification potential. Significant molecular markers were screened by the estimation of genetic main effects (additive A, dominance D) and prediction of epistasis effects (additive by additive AA, additive by dominance AD, dominance by dominance DD). The results were verified by estimation of superior genotypes (positive and negative) in general as well as in different environments and with reference to heritability for individual effects.

Candidate genes mapping and localization

The candidate genes associated with QTS were selected by establishing the location of the marker in the rice genome and locating cell wall associated genes and transcription factors of selected superfamilies within a range 200Kb upstream and downstream of the marker using the Rice Genome Browser (<http://rice.plantbiology.msu.edu/cgi-bin/gbrowse/rice/>).

Results

Saccharification potential variation of RIL population.

To understand further the mechanism behind the saccharification potential of rice straw, a population of 121 F₁₀ RIL plants was grown to maturity, and the third internodes were collected to ascertain saccharification potential. The whole saccharification process was performed using a robotic platform, and the saccharification potential was measured by reducing sugar equivalents as described previously (Fig 1) [26]. Reliable results from the QTS studies require a wide distribution of the trait within the population. The saccharification data of the RILs from two seasons (four independent runs), shows a normal distribution across the population (Fig 1B) ($P = 0.159$, Shapiro-Wilk test), with a maximum/minimum reducing sugar content that is 55.87% higher / 25.81% lower than the median of the population, respectively. A wide range of

saccharification values were observed, ranging from 59 nmol/mg.h to 116 nmol/mg.h, with the highest saccharification plant stems producing 97% more reducing sugar than the lowest saccharification line in this population. However, the two parental lines IR1552 and Azucena show 91.18% and 100.96% of the median, thereby showing a large diversity in saccharification potential in the 121 RIL population that we used in this study (Fig 1A & S1 Table).

Figure 1. Sugar release from rice straws after 0.5M NaOH pretreatment at 90°C and hydrolysis of industrial enzyme mixture.

(A) The saccharification potential (reducing sugar content) of 121 RIL lines. (B) Histogram showing normal distribution in saccharification of whole RIL population in first season dataset.

Lignin content is negatively correlated with saccharification potential

In order to investigate how the cell-wall composition affects the saccharification potential, the lignin content of 24 different plants at different ends of the saccharification spectrum were analyzed by measuring the lignin content of the twelve lines with the highest/lowest yield of reducing sugars after hydrolysis. The results indicate that straw from lines with high saccharification potential has lower lignin content, suggesting that saccharification potential is negatively correlated with lignin content in rice (Fig 2). In lines with high saccharification (above 90 nmol/mg.h), the correlation between lignin and reducing sugars shows a tight linear correlation ($r=0.907$, $p<0.05$), suggesting that high saccharification potential in rice straw is due mainly to low lignin content. Conversely, the data from rice lines with lower reducing sugar release (below 90nmol/mg.h) shows more variation in lignin content ($r=0.342$, $p=0.231$), indicating a more complex set of determinants of saccharification potential ($19\%< \text{lignin content}< 28\%$). Combined together, these results indicate that lines with high saccharification potential in this population were due, mainly, to a reduced lignin

content, while higher recalcitrance is controlled by other cell wall features (Fig 2). This suggests that saccharification is a trait controlled by multiple functional genes combined together to modulate the composition and interaction of the cell wall polymers.

Figure 2. Lineal regression analysis of lignin content of 25 plants which have different saccharification potential from high to low.

(a=155.426, b=-3.231, $R^2=0.646$; a, b and R^2 represents the regression line intercept, the regression line slope and the coefficient of determination, 99% were used for confidence interval estimate)

QTS Loci Associated with Saccharification Potential.

The identification of QTS loci associated with saccharification potential requires the use of a population with a large number of markers. Among 121 lines, the population mean of reducing sugar equivalent is 78.36, with total heritability ($h_{G+GE}^2 \triangleq 40.32\%$). The genetic effect and genetic-environment interaction effect are large contributors to the saccharification potential in this population. In total, 271 markers, 1 phenotypic data with two environments and 121 individuals were used in this study. After analyses of two seasons of saccharification potential with marker set, one main additive effect locus RG264-120 ($h_A^2 \triangleq 11.78\%$, $A = 4.45 \pm 0.65$) and 4 pairs of epistasis loci (RZ70-114 \times RM72-155, $h_{AA}^2 \triangleq 3.80\%$, $AA = 2.59 \pm 0.70$), (AAG-CAG4-137 \times AGG-CAG11-183, $h_{AA}^2 \triangleq 6.14\%$, $AA = -3.29 \pm 0.66$), (RG146-148 \times RM144-198, $h_{AA}^2 \triangleq 10.71\%$, $AA = -4.34 \pm 0.68$), (AGG-CTG3-243 \times RG341-248, $h_{AA}^2 \triangleq 7.91\%$, $AA = -3.73 \pm 0.71$) were identified (S2 Table). The results demonstrated that there were no significant environment effects (Fig 3), which indicates that saccharification potential is determined, in the main, by genetic effect. The data suggested that only one main effect locus (RG264-120) and one pair of additive loci (RZ70-114 \times RM72-155) have a positive effect on the saccharification potential of this RIL population, and that three

pairs of additive loci (AAG-CAG4-137 × AGG-CAG11-183), (RG146-148 × RM144-198), (AGG-CTG3-243 × RG341-248) showed a negative effect on the saccharification potential of rice plants. These markers were distributed, in the main, on chromosomes 6,7,8,9,11 and 12 (Table 1)[25]. An investigation of the functional genes near these markers is required to provide more information on the detailed molecular mechanism behind these loci.

Figure3. QTS linkage and association analyses of rice stem digestion potential.

(A) GxE plot generated by QTX mapping. The left axis is the values of genetic effects, and the bottom axis is the SNP ID for loci; Red column= main effect, green line= environment-specific effect; A= additive effect; AA= additive-by-additive epistasis effect; (B) GxG plot generated by QTX mapping. Circle= additive effect locus; Line between two circles= epistasis effect of two loci; Red color= main effect; Black color= involving epistasis but with no individual locus effect.

Table 1. Genetic position of Main QTLs Marker.

Marker No.	Name	Type	Chromosome	Genetic positon(cM)
114	*RZ70	RFLP	8	60.00
120	*RG264	RFLP	6	53.70
137	*AAG-CAG4	AFLP	7	0.00
148	*RG146	RFLP	7	154.70
155	*RM72	SSR	8	44.30
183	*AGG-CAG11	AFLP	9	186.90
198	*RM144	SSR	11	17.60
243	*AGG-CTG3	AFLP	12	170.30
248	*RG341	RFLP	12	48.70

Putative cell-wall associated gene associated with saccharification potential

The results presented indicate that lignin content is one of the main factors in establishing the saccharification potential of rice straw, especially in those lines with

the highest digestibility. Traditional linkage analysis would provide QTL located between two markers within a centi-Morgan (cM) scale and this would cover hundreds or even thousands of candidate genes in the region, but exploiting the primer sequences and reference sequences of markers that were used in this study, and the availability of a reference genome in rice, it is possible to locate the exact position of the markers in the genome. Using these positions, cell wall associated genes in the region of the markers were identified (Table 2). (Due to the lack of information about the physical position of 4 of these markers, the candidate genes for 5 markers were investigated. Interestingly, 5 copies of UDP-glucuronosyl and UDP-glucosyl transferase genes were located close to only main effect locus (RG264). The glucosyl transferases may participate in the synthesis of polysaccharides during the cell-wall synthesis. The genes topologically associated with the other 4 markers, are involved in diverse cell wall processes in different cell wall fractions, and whilst the proximity of these cell wall genes to identified markers does not represent a definite proof of their role in determining the saccharification potential, these candidate genes will be investigated further using molecular tools.

Table 2. Putative cell wall associated genes in the regions of the genetic markers linked to saccharification potential.

Marker	Locus	Annotation
RZ70	Os05g41240	Myb-like DNA-binding containing protein
	Os05g41610	glucan endo-1,3-beta-glucosidase
	Os05g41760	AP2 domain containing protein
	Os05g41780	AP2 domain containing protein
	Os05g41870	glycine-rich cell wall protein
	Os05g41990	peroxidase extracellular
RG264	Os06g17090	UDP-glucuronosyl and UDP-glucosyl transferase
	Os06g17110	UDP-glucuronosyl and UDP-glucosyl transferase
	Os06g17120	UDP-glucuronosyl and UDP-glucosyl transferase
	Os06g17220	UDP-glucuronosyl and UDP-glucosyl

		transferase
	Os06g17260	UDP-glucuronosyl and UDP-glucosyl transferase
	Os06g17410	Dof zinc finger domain containing protein
RG146	Os07g43420	MYB family transcription factor
	Os07g43530	Helix-loop-helix DNA-binding domain containing protein
	Os07g43710	CSLA7 - cellulose synthase-like family A
	Os07g43820	glycosyl hydrolase
	Os07g44070	pectinacylesterase
RM72	Os08g34280	cinnamoyl-CoA reductase, CCR1
	Os08g34360	AP2 domain containing protein
	Os08g34900	pectinesterase
	Os08g34910	pectinesterase
	Os08g34960	MYB family transcription factor
RM144	Os11g47350	beta-D-xylosidase
	Os11g47390	laccase
	Os11g47460	MYB family transcription factor
	Os11g47500-610	glycosyl hydrolase
	Os11g47820	glucan endo-1,3-beta-glucosidase

*The physical position of Markers AAG-CAG4, AAG-CAG11, AAG-CTG3, and RG341 is not determined.

Discussion

Rice straw represents an abundant source of lignocellulosic biomass, which is cheap and widely available in Asia. The utilization of this rice straw for the production of second generation biofuel would supplant the environmental problem of straw burning with an environmentally favorable alternative that also reduces dependency on fossil fuels. However, the recalcitrance of rice straw to digestibility is a significant barrier to the realization of large scale industrial conversion of rice straw into biofuel. Lignin has been widely considered as the major determinant of cell-wall digestibility, and in poplar, alfalfa and tobacco, it has been demonstrated that down-regulation of catalases involved in lignin synthesis pathway can lead to a reduction in lignin content

and an increase in saccharification compared with wildtype [28-31]. However, it has also been established that the modification of cellulose, matrix polysaccharides, or cell architecture will also affect the saccharification of lignocellulosic biomass[13, 15, 22, 24, 32]. Nonetheless, lignin appears as the main determinant of the saccharification potential only in rice lines with low lignin content. The negative correlation between lignin content and saccharification potential in lines with lower lignin content is not observed when lignin content is high, supporting the hypothesis that whilst lignin content is a key factor, it is not the only obstacle preventing the hydrolysis of polysaccharides. The saccharification potential of cellulosic biomass is also affected by transcription factors that modify the expression of genes directly involved in the modification and biosynthesis of cell wall content. A group of secondary wall NACs (SND1, VND6/7 and AtNST1-3 in Arabidopsis[33-35], PtrWNDs in poplar[36], MtNST1 in Medicago[37]) and MYBs (AtMYB46/83, AtMYB58/63, AtMYB61 and AtMYB85 in Arabidopsis[38-42], ZmMYB31, ZmMYB42 and ZmMYB46 in maize[43, 44], OsMYB46 in rice[45]) transcription factors have been well characterized. As secondary wall and lignin associated transcription factors, the SWNs (Secondary wall NACs) can bind to an 19bp consensus sequence called SNBE (Secondary wall NAC binding element), which is widely found in promoters of cell wall biosynthesis and modification genes[45]. The SWMs (Secondary wall MYBs), involved in the regulation of lignin biosynthesis were found to be expressed specifically in the metaxylem. [46]. Taken together, the SWNs and SWMs present a complex and coordinated regulatory network between lignin biosynthesis and other plant physiological pathways. In addition, transcription factors in other superfamilies were also found to be involved in the regulation of lignin biosynthesis. These include PtrWRKY19 in *Populus trichocarpa*, PpDof5 in *Pinus pinaster*, SbbHLH1 in *Sorghum bicolor*, EjAP2-1 in *Eriobotrya japonica*, BpMADS12 in *Betula platyphylla* Suk. Since digestibility is a trait determined by genes that affect the physical structure and chemo-types of the secondary cell-wall, finding markers and identifying the genes involved in conferring recalcitrance is a major step towards improving biomass feedstocks.

In a study of the genetic basis of high saccharification potential in rice, a QTS analysis of a RIL population that was generated from a cross between IR1552 and Azucena was performed. This population has been used previously for root traits under different water supply conditions [25]. After saccharification analyses of rice straw from this population during two independent growth seasons, the saccharification data showed a normal distribution, within a large range of values. This indicates that the cross between IR1552 and Azucena generated widely and randomly distributed values for saccharification potential and will be a useful tool to find markers associated with this trait. Further QTS analyses demonstrate that there is one main additive effect locus (RG264-120) and one pair of additive loci (RZ70-114 × RM72-155) that can enhance the saccharification potential in this RIL population, and three pairs of additive loci (AAG-CAG4-137 × AGG-CAG11-183), (RG146-148 × RM144-198), (AGG-CTG3-243 × RG341-248) that can reduce the saccharification potential of these rice plants. These results demonstrate that there are more interacting loci pairs involved in the modification of saccharification potential than single dominant loci. This may be due to the distant consanguineous relationship between IR1552 and Azucena even the saccharification of the two parents were not deviate far from the median of the population. In contrast the lowest and highest individuals showed a much wider deviation from median, suggesting that the new combination of interacting locus generated by the hybridization of this two varieties may contribute most to this phenomenon. In the F10 generation of hybrid progeny, most loci were well segregated, but few QTLs locus were detected, due to the density and type of molecular markers in this population. Nonetheless, it was established that the genetic location and sequences of these markers are widely distributed in the rice genome, in combination with reference genome databases, our results provide new genetic information regarding the combined regulation of saccharification potential.

Based on annotation of genes adjacent to these loci candidate genes with a role in cell wall and lignin synthesis were selected. (Table 2). Among the 39 cell wall associated candidate genes that were selected some showed tandem copies. Among the candidates, the glucan endo-1,3-β-glucosidases (Os05g41610, Os11g47820) have been

associated with cell expansion processes [47, 48]. The glycine-rich cell wall protein (Os05g41870) has been reported to influence the plasticity of the cell wall, and is expressed in xylem and phloem, playing an important role in early cell wall development [49-51]. OsPRX74 (Os05g41990) is an extracellular peroxidase that might be involved in the biosynthesis and degradation of lignin, and has also been reported to be involved in responding to stress and pathogens [52-54]. OsCSLA7 (Os07g43710) is a cellulose synthase-like A family member genes, and may play an important role in mannan synthesis, mannan being a component of the non-cellulosic polysaccharides in cell-walls [55, 56]. CCR1 (Os08g34280), encodes a Cinnamoyl-CoA reductase as one of the key enzymes involved in the biosynthesis of monolignols and downregulation of its expression can lead an enhanced saccharification potential in *Medicago sativa* [28]. Pectin acetyltransferase (Os07g44070) is involved in pectin deacetylation in primary cell wall of higher plants, which will influence the composition and structure of cell wall polysaccharides [57, 58]. UDP-glucuronosyl and UDP-glucosyl transferase (Os06g17090, Os06g17110, Os06g17120, Os06g17220, Os06g17260) are glycosyltransferases, that have been associated with the modulation of glycosylation and polymerization of polysaccharides during secondary cell wall formation processes [59, 60]. Pectinesterases (Os08g34900, Os08g34910) are involved in pectin modification during fruit softening and cell wall pectin metabolism [61, 62]. Beta-D-xylosidase (Os11g47350) takes part in remodeling processes [63, 64]. Laccases (Os11g47390) are a key component of the lignin synthesis process [65]. Glycosyl hydrolases (Os11g47500-610, Os07g43820) are part of a large family involved in cellulose and hemicellulose degradation [66]. Furthermore, there are also 4 MYBs (Os05g41240, Os07g43420, Os08g34960, Os11g47460), 3 AP2s (Os05g41760, Os05g41780, Os08g34360), 1 bHLH (Os07g43530) and 1 Dof-like (Os06g17410) transcription factors found near the QTLs markers, but their function and role in the regulation of lignin and cell wall biosynthesis remains unknown.

The direct involvement of these candidate genes in altering the cell wall recalcitrance requires further research, including a study of the interaction of these genes and epistatic effects observed. Although QTS studies fall short of establishing the

genes involved in cell wall recalcitrance, the results presented provide initial and valuable information on markers to assist in the selection of more digestible rice straw, which will be of benefit for further breeding of high saccharification potential rice varieties and their utilization for sustainable biofuel production.

Acknowledgments

The research was funded by Major State Basic Research Development Program (973 Program, grant no. 2015CB150200); Zhejiang Provincial Natural Science Foundation of China (Grant No. LZ15C020001); National Natural Science Foundation of China (Grant No. 31570183; 31529001) and UK-China partnering award from BBSRC of UK (Grant No BB/H531419).

References:

1. Seck PA, Diagne A, Mohanty S, Wopereis MCS. Crops that feed the world 7: Rice. *Food Secur.* 2012;4(1):7-24. PubMed PMID: WOS:000303380000002.
2. Khush GS. What it will take to Feed 5.0 Billion Rice consumers in 2030. *Plant Mol Biol.* 2005;59(1):1-6. PubMed PMID: WOS:000232498000001.
3. Bi Y, Gao C, Wang y, Li B. Estimation of straw resources in China. *Transactions of the Chinese Society of Agricultural Engineering.* 2009;25(12):211-7. PubMed PMID: CSCD:3780899.
4. Zhang HF, Ye XN, Cheng TT, Chen JM, Yang X, Wang L, et al. A laboratory study of agricultural crop residue combustion in China: Emission factors and emission inventory. *Atmospheric Environment.* 2008;42(36):8432-41. doi: 10.1016/j.atmosenv.2008.08.015. PubMed PMID: WOS:000261266900008.
5. Cao GL, Zhang XY, Wang YQ, Zheng FC. Estimation of emissions from field burning of crop straw in China. *Chinese Science Bulletin.* 2008;53(5):784-90. doi: 10.1007/s11434-008-0145-4. PubMed PMID: WOS:000254402000023.
6. Gadde B, Bonnet S, Menke C, Garivait S. Air pollutant emissions from rice straw open field burning in India, Thailand and the Philippines. *Environ Pollut.* 2009;157(5):1554-8. PubMed PMID: WOS:000265802900021.
7. Kim S, Dale BE. Global potential bioethanol production from wasted crops and crop residues. *Biomass & Bioenergy.* 2004;26(4):361-75. doi: 10.1016/j.biombioe.2003.08.002. PubMed PMID: WOS:000189133200006.
8. Gadde B, Menke C, Wassmann R. Rice straw as a renewable energy source in India, Thailand, and the Philippines: Overall potential and limitations for energy contribution and

greenhouse gas mitigation. *Biomass & Bioenergy*. 2009;33(11):1532-46. doi: 10.1016/j.biombioe.2009.07.018. PubMed PMID: WOS:000271454700006.

9. Chen F, Dixon RA. Lignin modification improves fermentable sugar yields for biofuel production. *Nat Biotechnol*. 2007;25(7):759-61. PubMed PMID: WOS:000247994000026.

10. Harris D, DeBolt S. Synthesis, regulation and utilization of lignocellulosic biomass. *Plant Biotechnol J*. 2010;8(3):244-62. PubMed PMID: WOS:000275145800002.

11. Mansfield SD, Kang KY, Chapple C. Designed for deconstruction - poplar trees altered in cell wall lignification improve the efficacy of bioethanol production. *New Phytol*. 2012;194(1):91-101. PubMed PMID: WOS:000300719400012.

12. Marriott PE, Gómez LD, McQueen-Mason SJ. Unlocking the potential of lignocellulosic biomass through plant science. *New Phytol*. 2016;209(4):1366-81. doi: 10.1111/nph.13684.

13. Abramson M, Shoseyov O, Shani Z. Plant cell wall reconstruction toward improved lignocellulosic production and processability. *Plant Sci*. 2010;178(2):61-72. PubMed PMID: WOS:000274877700001.

14. Fu CX, Mielenz JR, Xiao XR, Ge YX, Hamilton CY, Rodriguez M, et al. Genetic manipulation of lignin reduces recalcitrance and improves ethanol production from switchgrass. *P Natl Acad Sci USA*. 2011;108(9):3803-8. PubMed PMID: WOS:000287844400066.

15. Bartley LE, Peck ML, Kim SR, Ebert B, Manisseri C, Chiniquy DM, et al. Overexpression of a BAHD Acyltransferase, OsAt10, Alters Rice Cell Wall Hydroxycinnamic Acid Content and Saccharification. *Plant Physiol*. 2013;161(4):1615-33. PubMed PMID: WOS:000316987900004.

16. d'Yvoire MB, Bouchabke-Coussa O, Voorend W, Antelme S, Cezard L, Legee F, et al. Disrupting the cinnamyl alcohol dehydrogenase 1 gene (BdCAD1) leads to altered lignification and improved saccharification in *Brachypodium distachyon*. *Plant J*. 2013;73(3):496-508. PubMed PMID: WOS:000314184600012.

17. DeMartini JD, Pattathil S, Miller JS, Li HJ, Hahn MG, Wyman CE. Investigating plant cell wall components that affect biomass recalcitrance in poplar and switchgrass. *Energ Environ Sci*. 2013;6(3):898-909. PubMed PMID: WOS:000315165700025.

18. Marriott PE, Sibout R, Lapierre C, Fangel JU, Willats WGT, Hofte H, et al. Range of cell-wall alterations enhance saccharification in *Brachypodium distachyon* mutants. *P Natl Acad Sci USA*. 2014;111(40):14601-6. PubMed PMID: WOS:000342633900070.

19. Penning BW, Sykes RW, Babcock NC, Dugard CK, Held MA, Klimek JF, et al. Genetic Determinants for Enzymatic Digestion of Lignocellulosic Biomass Are Independent of Those for Lignin Abundance in a Maize Recombinant Inbred Population. *Plant Physiol*. 2014;165(4):1475-87. PubMed PMID: WOS:000341648600008.

20. Gomez LD, Steele-King CG, McQueen-Mason SJ. Sustainable liquid biofuels from biomass: the writing's on the walls. *New Phytol*. 2008;178(3):473-85. PubMed PMID: WOS:000255061500005.

21. Harris D, Stork J, Debolt S. Genetic modification in cellulose-synthase reduces crystallinity and improves biochemical conversion to fermentable sugar. *Gcb Bioenergy*. 2009;1(1):51-61. PubMed PMID: WOS:000278036000005.

22. Sahoo DK, Stork J, DeBolt S, Maiti IB. Manipulating cellulose biosynthesis by expression of mutant Arabidopsis gene in transgenic tobacco. *Plant Biotechnol J*. 2013;11(3):362-72. PubMed PMID: WOS:000316825400010.

23. Buanaфина MMD. Feruloylation in Grasses: Current and Future Perspectives. *Mol Plant*.

2009;2(5):861–72. PubMed PMID: WOS:000270218900004.

24. Buanaфина MMDO, Langdon T, Hauck B, Dalton S, Morris P. Expression of a fungal ferulic acid esterase increases cell wall digestibility of tall fescue (*Festuca arundinacea*). *Plant Biotechnol J*. 2008;6(3):264–80. PubMed PMID: WOS:000253760500005.

25. Zheng BS, Yang L, Zhang WP, Mao CZ, Wu YR, Yi KK, et al. Mapping QTLs and candidate genes for rice root traits under different water-supply conditions and comparative analysis across three populations. *Theor Appl Genet*. 2003;107(8):1505–15. PubMed PMID: WOS:000187196900020.

26. Gomez LD, Whitehead C, Barakate A, Halpin C, McQueen-Mason SJ. Automated saccharification assay for determination of digestibility in plant materials. *Biotechnol Biofuels*. 2010;3:23. doi: 10.1186/1754-6834-3-23. PubMed PMID: 20979637; PubMed Central PMCID: PMC2974669.

27. Zhang FT, Zhu ZH, Tong XR, Zhu ZX, Qi T, Zhu J. Mixed Linear Model Approaches of Association Mapping for Complex Traits Based on Omics Variants. *Sci Rep*. 2015;5:10298. doi: 10.1038/srep10298. PubMed PMID: 26223539.

28. Jackson LA, Shadle GL, Zhou R, Nakashima J, Chen F, Dixon RA. Improving Saccharification Efficiency of Alfalfa Stems Through Modification of the Terminal Stages of Monolignol Biosynthesis. *Bioenerg Res*. 2008;1(3–4):180–92. PubMed PMID: WOS:000207576300002.

29. Kavousi B, Daudi A, Cook CM, Joseleau JP, Ruel K, Devoto A, et al. Consequences of antisense down-regulation of a lignification-specific peroxidase on leaf and vascular tissue in tobacco lines demonstrating enhanced enzymic saccharification. *Phytochemistry*. 2010;71(5–6):531–42. PubMed PMID: WOS:000277223100006.

30. Min DY, Li QZ, Jameel H, Chiang V, Chang HM. The Cellulase-Mediated Saccharification on Wood Derived from Transgenic Low-Lignin Lines of Black Cottonwood (*Populus trichocarpa*). *Appl Biochem Biotech*. 2012;168(4):947–55. PubMed PMID: WOS:000309870500020.

31. Van Acker R, Leple JC, Aerts D, Storme V, Goeminne G, Ivens B, et al. Improved saccharification and ethanol yield from field-grown transgenic poplar deficient in cinnamoyl-CoA reductase. *P Natl Acad Sci USA*. 2014;111(2):845–50. PubMed PMID: WOS:000329614500064.

32. Mewalal R, Mizrahi E, Mansfield SD, Myburg AA. Cell Wall-Related Proteins of Unknown Function: Missing Links in Plant Cell Wall Development. *Plant Cell Physiol*. 2014;55(6):1031–43. PubMed PMID: WOS:000338127800001.

33. Zhong RQ, Demura T, Ye ZH. SND1, a NAC domain transcription factor, is a key regulator of secondary wall synthesis in fibers of *Arabidopsis*. *Plant Cell*. 2006;18(11):3158–70. PubMed PMID: WOS:000243093700024.

34. Kubo M, Udagawa M, Nishikubo N, Horiguchi G, Yamaguchi M, Ito J, et al. Transcription switches for protoxylem and metaxylem vessel formation. *Gene Dev*. 2005;19(16):1855–60. PubMed PMID: WOS:000231277600005.

35. Mitsuda N, Iwase A, Yamamoto H, Yoshida M, Seki M, Shinozaki K, et al. NAC transcription factors, NST1 and NST3, are key regulators of the formation of secondary walls in woody tissues of *Arabidopsis*. *Plant Cell*. 2007;19(1):270–80. PubMed PMID: WOS:000244757400023.

36. Zhong R, Ye Z-H. The poplar PtrWNDs are transcriptional activators of secondary cell wall biosynthesis. *Plant signaling & behavior*. 2010;5(4):469–72. PubMed PMID:

MEDLINE:20383071.

37. Zhao QA, Gallego-Giraldo L, Wang HZ, Zeng YN, Ding SY, Chen F, et al. An NAC transcription factor orchestrates multiple features of cell wall development in *Medicago truncatula*. *Plant J*. 2010;63(1):100-14. doi: 10.1111/j.1365-313X.2010.04223.x. PubMed PMID: WOS:000279406400008.

38. McCarthy RL, Zhong RQ, Ye ZH. MYB83 Is a Direct Target of SND1 and Acts Redundantly with MYB46 in the Regulation of Secondary Cell Wall Biosynthesis in *Arabidopsis*. *Plant Cell Physiol*. 2009;50(11):1950-64. doi: 10.1093/pcp/pcp139. PubMed PMID: WOS:000271820300009.

39. Zhong R, Richardson EA, Ye ZH. The MYB46 transcription factor is a direct target of SND1 and regulates secondary wall biosynthesis in *Arabidopsis*. *Plant Cell*. 2007;19(9):2776-92. doi: 10.1105/tpc.107.053678. PubMed PMID: WOS:000250507300008.

40. Zhou JL, Lee CH, Zhong RQ, Ye ZH. MYB58 and MYB63 Are Transcriptional Activators of the Lignin Biosynthetic Pathway during Secondary Cell Wall Formation in *Arabidopsis*. *Plant Cell*. 2009;21(1):248-66. doi: 10.1105/tpc.108.063321. PubMed PMID: WOS:000263842600023.

41. Zhong RQ, Lee CH, Zhou JL, McCarthy RL, Ye ZH. A Battery of Transcription Factors Involved in the Regulation of Secondary Cell Wall Biosynthesis in *Arabidopsis*. *Plant Cell*. 2008;20(10):2763-82. doi: 10.1105/tpc.108.061325. PubMed PMID: WOS:000261378600022.

42. Newman LJ, Perazza DE, Juda L, Campbell MM. Involvement of the R2R3-MYB, AtMYB61, in the ectopic lignification and dark-photomorphogenic components of the *det3* mutant phenotype. *Plant J*. 2004;37(2):239-50. doi: 10.1046/j.1365-313X.2003.01953.x. PubMed PMID: WOS:000187452800009.

43. Fornale S, Shi XH, Chai CL, Encina A, Irar S, Capellades M, et al. ZmMYB31 directly represses maize lignin genes and redirects the phenylpropanoid metabolic flux. *Plant J*. 2010;64(4):633-44. doi: 10.1111/j.1365-313X.2010.04363.x. PubMed PMID: WOS:000284122400007.

44. Sonbol FM, Fornale S, Capellades M, Encina A, Tourino S, Torres JL, et al. The maize ZmMYB42 represses the phenylpropanoid pathway and affects the cell wall structure, composition and degradability in *Arabidopsis thaliana*. *Plant Mol Biol*. 2009;70(3):283-96. doi: 10.1007/s11103-009-9473-2. PubMed PMID: WOS:000265827000006.

45. Zhong RQ, Lee C, McCarthy RL, Reeves CK, Jones EG, Ye ZH. Transcriptional Activation of Secondary Wall Biosynthesis by Rice and Maize NAC and MYB Transcription Factors. *Plant Cell Physiol*. 2011;52(10):1856-71. doi: 10.1093/pcp/pcr123. PubMed PMID: WOS:000295932800013.

46. Zhong RQ, Ye ZH. Secondary Cell Walls: Biosynthesis, Patterned Deposition and Transcriptional Regulation. *Plant Cell Physiol*. 2015;56(2):195-214. doi: 10.1093/pcp/pcu140. PubMed PMID: WOS:000351514000003.

47. Beffa RS, Neuhaus JM, Meins F. Physiological Compensation in Antisense Transformants - Specific Induction of an Ersatz Glucan Endo-1,3-Beta-Glucosidase in Plants Infected with Necrotizing Viruses. *P Natl Acad Sci USA*. 1993;90(19):8792-6. PubMed PMID: WOS:A1993MA59500009.

48. Wan LL, Zha WJ, Cheng XY, Liu CA, Lv L, Liu CX, et al. A rice beta-1,3-glucanase gene *Osg1* is required for callose degradation in pollen development. *Planta*. 2011;233(2):309-23. PubMed PMID: WOS:000286613200009.

49. Condit CM, Meagher RB. Expression of a Gene Encoding a Glycine-Rich Protein in *Petunia*. *Mol Cell Biol*. 1987;7(12):4273-9. PubMed PMID: WOS:A1987K958600015.

-
50. Xu DP, Lei M, Wu R. Expression of the Rice Osgrp1 Promoter-Gus Reporter Gene Is Specifically Associated with Cell Elongation Expansion and Differentiation. *Plant Mol Biol*. 1995;28(3):455-71. PubMed PMID: WOS:A1995RN25300011.
51. Liu ZZ, Wang JL, Huang X, Xu WH, Liu ZM, Fang RX. The promoter of a rice glycine-rich protein gene, Osgrp-2, confers vascular-specific expression in transgenic plants. *Planta*. 2003;216(5):824-33. PubMed PMID: WOS:000182093700012.
52. Gold MH, Wariishi H, Valli K. Extracellular Peroxidases Involved in Lignin Degradation by the White Rot Basidiomycete *Phanerochaete-Chrysosporium*. *ACS Symposium Series*. 1989;389:127-40. PubMed PMID: WOS:A1989AH47800009.
53. Lin CC, Kao CH. Cell wall peroxidase against ferulic acid, lignin, and NaCl-reduced root growth of rice seedlings. *J Plant Physiol*. 2001;158(5):667-71. PubMed PMID: WOS:000168896800017.
54. Mika A, Minibayeva F, Beckett R, Luthje S. Possible functions of extracellular peroxidases in stress-induced generation and detoxification of active oxygen species. *Phytochem Rev*. 2004;3(1-2):173-93. doi: 10.1023/b:phyt.0000047806.21626.49. PubMed PMID: BCI:BCI200500180369.
55. Hazen SP, Scott-Craig JS, Walton JD. Cellulose synthase-like genes of rice. *Plant Physiol*. 2002;128(2):336-40. PubMed PMID: WOS:000173977100005.
56. Wang LQ, Guo K, Li Y, Tu YY, Hu HZ, Wang BR, et al. Expression profiling and integrative analysis of the CESA/CSL superfamily in rice. *Bmc Plant Biol*. 2010;10. PubMed PMID: WOS:000286218700001.
57. Gou JY, Miller LM, Hou GC, Yu XH, Chen XY, Liu CJ. Acetyltransferase-Mediated Deacetylation of Pectin Impairs Cell Elongation, Pollen Germination, and Plant Reproduction. *Plant Cell*. 2012;24(1):50-65. PubMed PMID: WOS:000300881800008.
58. Vercauteren I, Engler JD, De Groodt R, Gheysen G. An *Arabidopsis thaliana* pectin acetyltransferase gene is upregulated in nematode feeding sites induced by root-knot and cyst nematodes. *Mol Plant Microbe In*. 2002;15(4):404-7. PubMed PMID: WOS:000174820200013.
59. Cao PJ, Bartley LE, Jung KH, Ronald PC. Construction of a rice glycosyltransferase phylogenomic database and identification of rice-diverged glycosyltransferases. *Mol Plant*. 2008;1(5):858-77. PubMed PMID: WOS:000259104500014.
60. Zhou YH, Li SB, Qian Q, Zeng DL, Zhang M, Guo LB, et al. BC10, a DUF266-containing and Golgi-located type II membrane protein, is required for cell-wall biosynthesis in rice (*Oryza sativa* L.). *Plant J*. 2009;57(3):446-62. PubMed PMID: WOS:000262695800006.
61. Hall LN, Tucker GA, Smith CJS, Watson CF, Seymour GB, Bundick Y, et al. Antisense Inhibition of Pectin Esterase Gene-Expression in Transgenic Tomatoes. *Plant J*. 1993;3(1):121-9. PubMed PMID: WOS:A1993KJ19500009.
62. Lazan H, Selamat MK, Ali ZM. Beta-Galactosidase, Polygalacturonase and Pectinesterase in Differential Softening and Cell-Wall Modification during Papaya Fruit Ripening. *Physiol Plantarum*. 1995;95(1):106-12. PubMed PMID: WOS:A1995TD52000016.
63. Itai A, Ishihara K, Bewley JD. Characterization of expression, and cloning, of beta-D-xylosidase and alpha-L-arabinofuranosidase in developing and ripening tomato (*Lycopersicon esculentum* Mill.) fruit. *J Exp Bot*. 2003;54(393):2615-22. PubMed PMID: WOS:000187146900003.
64. Arsovski AA, Popma TM, Haughn GW, Carpita NC, McCann MC, Western TL. AtBXL1 Encodes a Bifunctional beta-D-Xylosidase/alpha-L-Arabinofuranosidase Required for Pectic

Arabinan Modification in Arabidopsis Mucilage Secretory Cells. *Plant Physiol.* 2009;150(3):1219-34. PubMed PMID: WOS:000268696800010.

65. Christopher LP, Yao B, Ji Y. Lignin Biodegradation with Laccase-Mediator Systems. *Frontiers in Energy Research.* 2014;2. doi: 10.3389/fenrg.2014.00012.

66. Fry SC. Primary cell wall metabolism: tracking the careers of wall polymers in living plant cells. *New Phytol.* 2004;161(3):641-75. doi: 10.1111/j.1469-8137.2003.00980.x. PubMed PMID: WOS:000188646500004.