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Lignin bioengineering

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Lignin is one of the most abundant aromatic biopolymers and a major component of plant cell walls. It occurs via oxidative coupling of monolignols, which are synthesized from the phenylpropanoid pathway. Lignin is the primary material responsible for biomass recalcitrance, has almost no industrial utility, and cannot be simply removed from growing plants without causing serious developmental defects. Fortunately, recent studies report that lignin composition and distribution can be manipulated to a certain extent by using tissue-specific promoters to reduce its recalcitrance, change its biophysical properties, and increase its commercial value. Moreover, the emergence of novel synthetic biology tools to achieve biological control using genome bioediting technologies and tight regulation of transgene expression opens new doors for engineering. This review focuses on lignin bioengineering strategies and describes emerging technologies that could be used to generate tomorrow's bioenergy and biochemical crops.

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Introduction

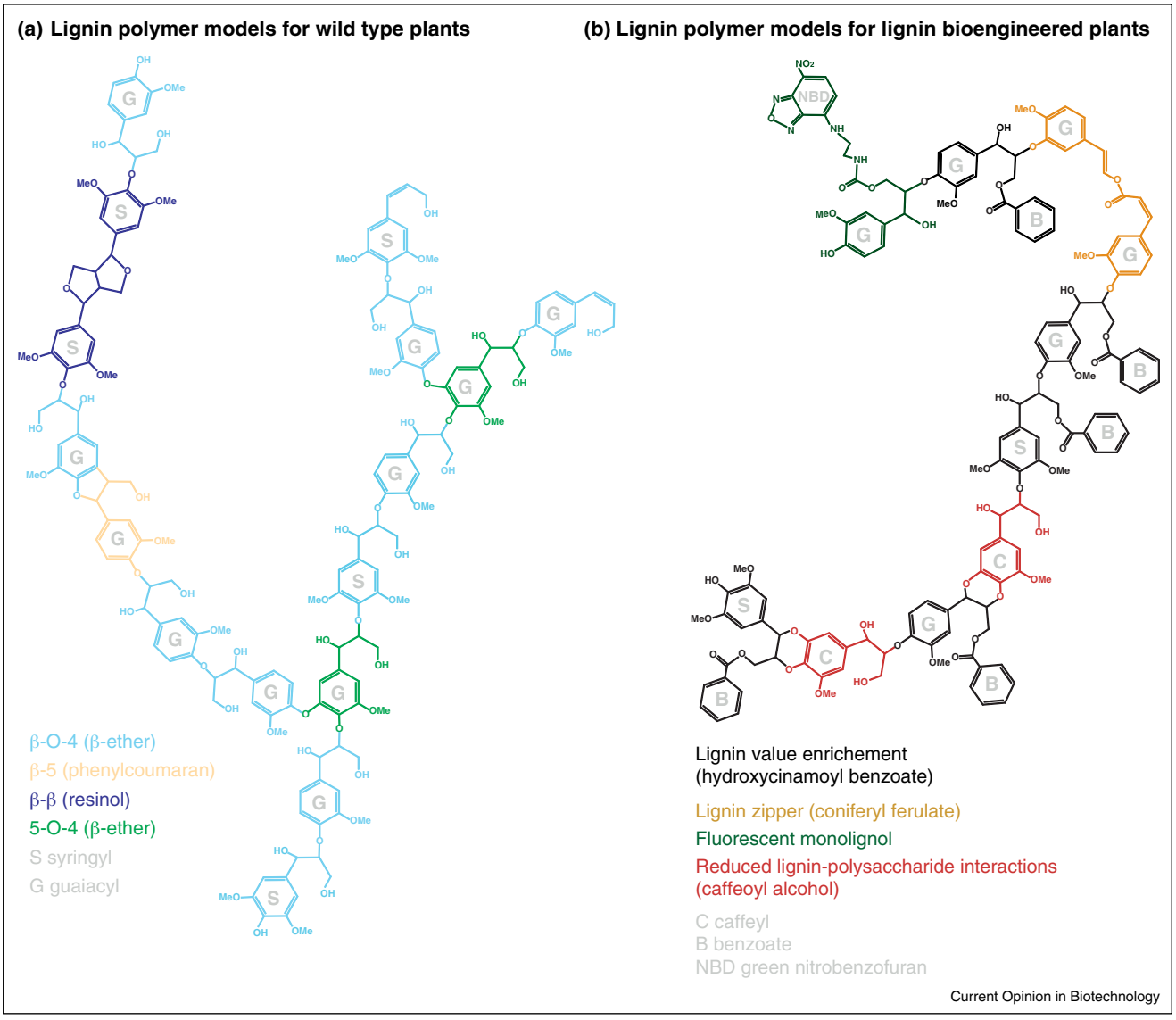
In its effort to make cellulosic biofuel production more cost-effective, the bioenergy field has necessarily focused much of its attention on plant cell walls. Lignin, a major component of cell walls, is the third most-abundant biopolymer and the largest available resource of natural aromatic polymers (Figure 1a). It is mainly composed of the monolignols *p*-coumaryl, coniferyl, and sinapyl alcohols which give rise to the *p*-hydroxyphenyl (H), guaiacyl (G) and syringyl (S) lignin units [1]. Unfortunately, it is also the primary contributor to the high cost of lignocellulosic sugar production, because cell wall polysaccharides are encrusted with lignin which make them highly resistant to extraction and enzymatic hydrolysis [1,2]. Moreover, lignin has almost no commercial value aside from its role as a source of heat, and it is generally treated as a waste product [3].

Lignin has been a target of genetic manipulation for several decades because its content in biomass is inversely correlated with its forage digestibility and kappa value in the pulping industry [4,5]. Lignin biosynthesis is well-characterized and all the enzymes required for the synthesis of its three major building blocks — called monolignols — are well-known and highly-conserved in all vascular plants [6,7]. Unfortunately, lignin cannot be simply removed from growing plants without causing deleterious developmental effects [8]. Genetic manipulation trials using natural mutants or silencing strategies have failed because they drastically reduced lignin content in a non-selective way. Nevertheless, there are cases in which mild genetic manipulations have been used to moderately reduce lignin content or modify its composition in biomass, modestly improving saccharification efficiency, forage digestibility, and pulping yield [9]. These approaches are still rather limited.

Novel strategies need to be developed to reduce lignin content further, without altering plant development or causing undesirable effects. Classical lignin-modification methods typically repress the expression or activity of lignin biosynthetic genes. They require identification of natural defective alleles, the screening of single-nucleotide polymorphisms (SNPs) from mutant populations (usually a labor-intensive process) or the development of RNAi-based gene-silencing approaches. The limit of all these approaches is the lack of tissue specificity because every cell carries the same defective allele or silenced gene since RNAi move from cell-to-cell and affect most of the tissues in the plant [10]. Moreover, they affect not only the lignin biosynthesis pathway, but also have indirect effects on other metabolic routes connected to the phenylpropanoid and monolignol pathways. The phenylpropanoid pathway, for example, generates a wide array of secondary metabolites that contribute to all aspects of plant development and plant responses to biotic and abiotic stresses [11].

Recently, researchers have developed more elaborate approaches for lignin modification and employed tissue-specific promoters to reduce the risk of disturbing other phenylpropanoid-derived pathways in non-lignified tissues [12••,13••]. The utilization of such promoters is

Figure 1



Lignin polymer models. **(a)** Lignin polymer models for wild type plants; **(b)** lignin polymer models for lignin bioengineered plants. Bioengineered lignin is exclusively composed of representative unusual monolignols to increase lignin value; to facilitate lignin degradation (lignin zipper); to reduce lignin–polysaccharide interactions; or to fluorescently label lignin.

challenging because most of the lignin genes (PAL, C4H, 4CL, HCT, C3H, among others) belong to the phenylpropanoid pathway [14•]. Use of the corresponding promoters for engineering purposes may affect the biosynthesis of associated metabolites such as flavonoids, suberin, coumarins, phenolic volatiles, or hydrolyzable tannins. On the other hand, most promoters of secondary cell-wall biosynthetic genes (CesAs, GTs, or lignin genes) [15] are expressed in both vascular bundles and interfascicular xylem fibers, raising concerns that lignin modification would affect the integrity of vessels. Vessel-specific and fiber-specific genes (and corresponding promoters) were identified in few species and their number remains limited (VNDs, NSTs, SNDs, WNDs, Lac17 [16–20]). Single-promoter-driven transgene expression, which can confer both adequate spatio-temporal expression and transcription strength for optimal engineering, is consequently difficult to achieve. Furthermore, using several copies of the same promoters for engineering may lead to silencing issues, including the silencing of endogenous promoters if they share high sequence similarities. However, adjusting transgene expression to optimal levels and restricting it to specific cells at particular developmental stages will reduce undesirable side effects. Ideally, newly emerging techniques will be combined with tissue-specific promoters to meet the challenges associated with plant

metabolic engineering, particularly those involving manipulation of the phenylpropanoid pathway. In this review, we will address important aspects in the engineering of lignin that involve the manipulation of its content, composition, and distribution. First we will focus on emerging synthetic biology tools that can fine-tune transgene expression and improve their spatio-temporal expression. We will conclude with the presentation of novel approaches for manipulation of lignin to make it more suitable for various applications such as bioenergy and biochemical production (Figure 1b).

Synthetic biology tools for lignin engineering

Genome bioediting tools

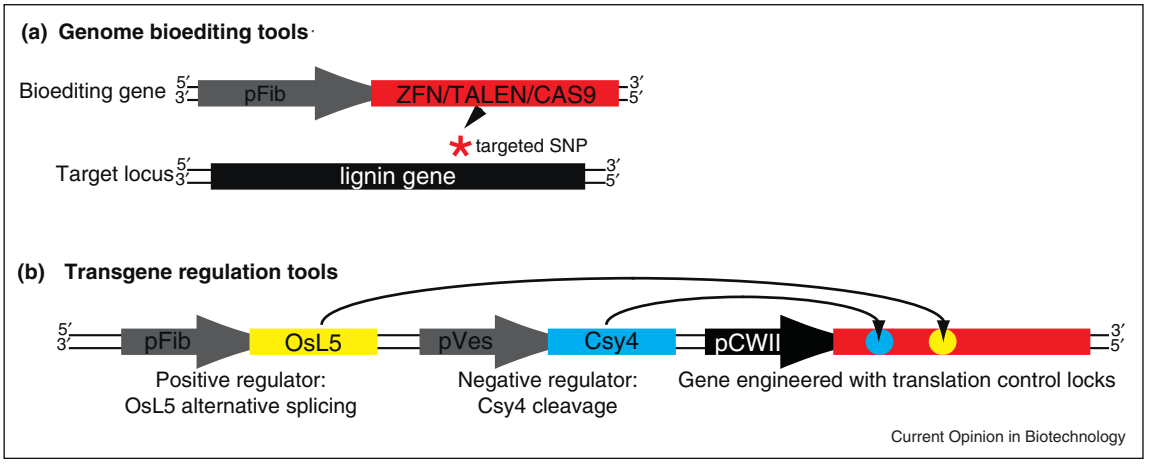
Creation of biological tools for targeted genome manipulation is an important goal in molecular biology. Such tools have an essential role in reverse genetics, and their development will have fundamental implications in biotechnology applications ranging from gene therapy to the production of chimeric plants. For example, tissue-specific promoters could be used to express these novel biological tools to create SNPs in key genes to render them defective only in target tissues. Using such an approach, the target genes present in meristematic and meiotic cells would be SNP-free. Major progress has been made in the development of crucially important genome bioediting tools, as exemplified by zinc-finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and the clustered, regularly interspaced, short palindromic repeats (CRISPR)/CRISPR-associated (CAS) system [21•]. These various genome bioediting tools share a common principle: the utilization of engineered endonucleases is associated with customizable DNA binding elements. Directed by the DNA binding elements, endonucleases cleave at the target loci and generate DNA double-strand breaks (DSBs). DSBs are subsequently repaired by one of the two cellular DNA repair mechanisms: non-homologous end joining (NHEJ), or homologous recombination (HR). Repair by NHEJ frequently introduces mutations, resulting in gene interruption at the target locus.

DNA-binding elements in ZFNs and TALENs are composed of modular protein motifs [22–24]. An individual ZF primarily recognizes DNA sites of 3 bp. To establish recognition specificity, arrays of ZF units connected by linker sequences recognize DNA sequences 9–18 bp in length [23]. The DNA-binding motifs in TALEs present as near-perfect repeats, typically 34 amino acids in length. Repeat-variable di-residues (RVDs), usually occurring at residues 12 and 13, designate the base pair or nucleotide recognition code in a one-to-one manner [22–24]. Since the first demonstration of *yellow* gene interruption in *Drosophila melanogaster* in 2002 [25], various ZF-effector combinations have been applied in genome bioediting of diverse organisms including flies, moths, zebrafish, rats, and humans [21•,26]. Following the pioneering work done with ZF-effectors, genome bioediting using TALE-effectors advanced rapidly since the first TALENs were reported in 2010 [27]. ZFNs and TALENs are also applied to generate genetically engineered crop plants, such as herbicide-tolerant *Zea mays* [28] and disease-resistant rice [29•].

Some bacteria and archaea genomes contain the CAS protein operon followed by CRISPR arrays, which are composed of direct repeats interspersed by small segments (protospacers) adopted from invading DNAs. Transcription of a CRISPR array, followed by enzymatic cleavage, yields short mature CRISPR RNA (crRNA). Through base pairing with a protospacer sequence in the invading DNA, crRNA guides the targeted degradation of invading DNA by recruiting CAS nucleases. A CRISPR/CAS genome bioediting system was developed based on the Type II CRISPR system from *Streptococcus pyogenes*, which contains the minimal CRISPR machinery composed of a single CAS9 protein, a crRNA with complementary sequence to the target site, and a trans-activating RNA (tracrRNA) that forms a hairpin with crRNA. A modified CRISPR/CAS9 system has been shown to drive targeted DNA cleavage *in vitro* [30,31••] and was also used to induce mutations and edit genetic loci of interest in eukaryotes such as mouse and human cell lines [32,33••], but thus far not in plants. RNA-guided genome editing avoids intrinsic limitations in protein-guided genome editing, such as off-target mutagenesis activity due to imperfect protein-DNA recognition. RNA-guiding sequence in crRNA is readily programmable compared to the substantial effort required to generate customized DNA binding proteins. CRISPR/CAS9 also offers the possibility of multiplex genome bioediting. In addition, the CAS9 protein can be mutated to DNA nickase [30] to promote precise genome editing through HR. Cong *et al.* [32,33••] consistently detected no indels induced by a CRISPR/CAS nickase system [32,33••]. When a homology repair template was provided, a pair of restriction sites was inserted precisely into the target loci with the CRISPR/CAS nickase system [30]. Despite the apparent benefit of RNA-guided genome bioediting and its broad application potential, the CRISPR/CAS9 bioediting system is still in its infancy. To date, no application of CRISPR/CAS9 has been reported in plants. Extensive studies are required to evaluate its targeting specificity and effectiveness.

These genetically encoded bioediting tools could be used to introduce SNPs into essential lignin genes exclusively in targeted tissue such as fiber (Figure 2). Using a fiber-specific promoter (e.g. *pNST*, *pLAC17*) to drive the expression of ZFNs, TALENs or CAS9 designed to recognize the genomic sequence of a key lignin biosynthetic gene (e.g. C4H, C3H, HCT, or CCR1) would repress lignin biosynthesis only in fiber cells without affecting the lignification of vessel cells and other

Figure 2



New strategies enable mutifaceted genetic engineering of plants. **(a)** Genome bioediting tools. Black box, endogenous lignin locus (target of editing); grey arrow, fiber specific promoter used to drive the expression of the bioediting gene; red box, bioediting gene: ZFNs, TALENs or CRISPR/CAS9; red star, SNP generated when the genome bioediting gene is expressed. **(b)** Transgene regulation tools. Grey arrow, fiber (pFib) or vessel (pVes) specific promoter; yellow box, gene encoding the OsL5 protein with the alternative splicing cassette shown in the same color inserted in transgenes (yellow circle); blue box, gene encoding the Cys4 protein with its cognition sequence shown in the same color inserted in transgenes (blue circle); black arrow, secondary cell wall promoter (pCWII); red box, engineered gene: gene used to manipulate lignin composition which has been engineered with transgene regulation tool (yellow circle, OsL5 alternative splicing cassette; blue circle, Cys4 cognition sequence).

phenylpropanoid-derived pathways active in non-lignified tissues. Such approach would offer greater potentials than the approach developed by Yang *et al.* [34] that consists of complementing a lignin mutant with a vessel specific promoter which restored the phenylpropanoid pathway only in vessels. However, it is also important to note that expression of biological editing systems has to be tightly controlled, as editing is irreversible and a leaky expression could be lethal to the engineered organism. Therefore, it will be important to use these tools with additional regulatory controls such as those described below.

Transgene regulation at the post-transcriptional level

The ability to control stringently the spatial and temporal expression of a transgene, as well as its expression level, is an important requirement for successful genetic engineering. It allows optimal tradeoffs such plant fitness versus trait performance (e.g. cell-wall recalcitrance). To attain such perfection, utilization of tissue-specific promoters is rarely sufficient, and additional transcriptional or translation controls typically need to be implemented. The rapid emergence of new technologies will likely offer new opportunities to further optimize transgene expression that will be worthy of further exploration.

In diverse plant lineages, the expression of transcription factor IIIA (TFIIIA) is controlled by a splicing cassette, which includes a regulatory exon flanked by two introns [35]. The regulatory exon encodes a premature termination codon that targets the transcript for nonsense-mediated decay. Binding of ribosomal protein L5 to the splicing cassette triggers exon skipping and allows the expression of the full-length TFIIIA protein. The alternative splicing machinery controlling TFIIIA expression has been adopted to regulate transgene expression [36••]. The splicing cassette is structurally modified to interact specifically with rice L5 protein (OsL5) but not endogenous L5 proteins in dicots (such as tobacco or *Arabidopsis*). The insertion of the modified splicing cassette in the encoding sequence of GFP reporter protein showed traceless expression when expressed alone and a ~97-fold expression activation in the presence of OsL5 protein. This result indicates that the expression of a transgene with the splicing cassette inserted in the exon is strictly controlled by the presence of OsL5. This system could be readily adopted as a promoter stacking strategy, that is, when the transgene and OsL5 are expressed under promoters with different characteristics. The resulting expression of the transgene is defined by the activities of both promoters.

In CRISPR/CAS machinery, maturation of crRNA requires cleavage in each repeat sequence of the precursor crRNA by dedicated endoRNase [37]. In *Pseudomonas aeruginosa* strain UCBPP-PA14, endoRNase Cys4 selectively recognizes and cleaves a 28-nucleotide (nt) repetitive sequence in the CRISPR repeats [38,39]. Qi *et al.* [40••] utilized the Cys4 cleavage system in *Escherichia coli* to achieve physical separation of genetic elements of transgenes at the transcript level. In addition, when Cys4 cognition sequence is inserted in frame with a reporter gene, Cys4-controlled transgene silencing was demonstrated in both bacteria and yeast systems [40••].

The various lignin manipulation strategies discussed later may be broadly classified into two categories: novel lignin generation and lignin reduction. Generation of novel lignin or monolignol replacement may be introduced into both vessel and fiber tissues by using promoters of lignin biosynthetic genes or secondary cell wall genes to drive transgene expression. However, a promoter-stacking strategy with the OsL5 system may be applied to add strength control for transgene expression. By contrast, lignin reduction strategies using either genome bioediting or transgene expression require a more stringent control, that is, one that is restricted to fiber cells so that vessel lignification occurs normally and the general phenylpropanoid will not be affected constitutively. Such cell-type specificity can be achieved by utilization of the OsL5 or Cys4 systems. With the OsL5 system, the splicing cassette will be introduced into the transgene (e.g. encoding an enzyme that depletes monolignol biosynthesis intermediates) whose expression is driven by lignin (*pC4H*, *pHCT*) or other secondary cell wall (*pIRX8*, *pIRX5*) promoters of different strengths. OsL5 can be expressed under the control of a fiber-specific promoter (*pNST*) to further restrict the transgene expression in fiber cells. With the Cys4 system, expression of the transgene (harboring the Cys4 cognition sequence) driven by lignin or other secondary cell wall promoters can be eliminated from vessel cells by expressing Cys4 in vessel cells. Furthermore, it is envisioned that the OsL5 and Cys4 systems can be used to regulate complex multigenic pathways by incorporating the regulatory sequence (the splicing cassette or the Cys4 cognition sequence) into each of the genes to be regulated. In such cases, a single switch for multiple gene regulation would be necessary. A simplified model summarizing the emerging techniques for plant engineering is presented in Figure 2.

Rerouting the lignin pathway and lignin replacement by novel monolignols

Rerouting of the lignin pathway

The various strategies described previously can be employed to reduce lignin in specific tissues (i.e. fibers) by expressing enzymes that use intermediates from the lignin pathway. For example, the recently described monolignol 4-O-methyltransferase is a promising case study of enzyme engineering conducted specifically to reduce the availability of polymerizable monolignols [13••]. More generally, fungi and bacteria are great sources for the discovery of new enzymes active on lignin intermediates, such as the newly characterized caffeoyl-CoA dioxygenase [41].

In a similar fashion, known biosynthetic enzymes could be used to produce several phenylpropanoid-derived metabolites at the expense of lignin. These metabolites includes flavonoids, stilbenes, coumarins, curcuminoids, benzalacetones, hydoxycinnamate esters, and amides synthesized from hydroxycinnamoyl-CoAs; lignans, neolignans, and phenylpropene volatiles such as eugenol and isoeugenol produced from coniferyl alcohol; and benzenoid/phenylpropanoid volatiles derived from phenylalanine and cinnamate. Interestingly, increasing these metabolites may offer other potential benefits in addition to lignin reduction, such as improving resistance to various biotic and abiotic stresses or enhancing a plant's nutritional value. Identification of transport mechanisms for apoplast targeting of some of these phenylpropanoid-derived metabolites should be investigated further. Several biomimetic studies showed their possible coupling with lignin, which, in some cases, resulted in improved cell-wall digestibility or fermentation [42–46]. These observations can be explained by the structure of these metabolites, which have the characteristics of 'novel monolignol candidates' for reducing lignin recalcitrance.

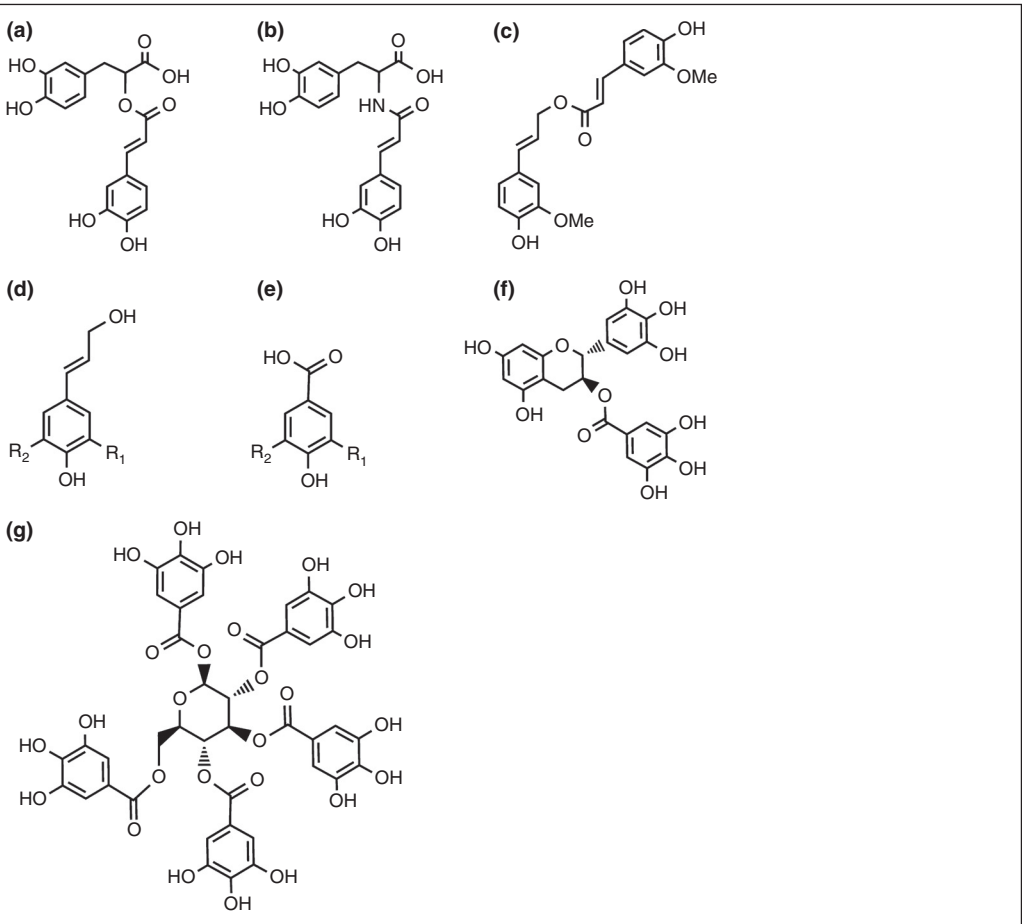
Novel monolignol candidates

Producing in planta alternative lignin monomers to reduce lignin recalcitrance is a concept that has recently emerged. These monomers should possess a phenolic function containing a hydroxyl group, at the C4 position on the ring, for radicalization and coupling to the lignin. Incorporation of the novel monomers could, depending on their structure, introduce cleavable groups inside the polymer (e.g. coniferyl ferulate and rosmarinic acid); reduce interactions between polysaccharides and lignin (e.g. caffeoyl alcohol); or give rise to lignin with reduced chain lengths (e.g. syringaldehyde) [12••,44,46,47•] (Figures 1b and 4).

Hydroxycinnamates esters and amides: Molecules consisting of hydroxycinnamates conjugated to another phenolic group via an ester or amide bond are potentially cleavable monolignols. These types of dimers would fully incorporate into lignin because of their phenolic groups on both ends, and hence would create some internal alkali-and acid-labile ester and amid bonds within lignin. For example, rosmarinic acid (an ester of caffeate with 3,4-dihydroxyphenyl lactate; Figure 3a), clovamide (an amide of caffeate with L-dopa; Figure 3b), and coniferyl ferulate (an ester of ferulate with coniferyl alcohol; Figure 3c) meet these criteria to introduce labile groups into the lignin backbone. Model studies using biomimetic systems have indeed demonstrated peroxidase-catalyzed polymerization of rosmarinic acid and coniferyl ferulate with conventional monolignols, resulting in enhanced cell wall saccharification after incorporation and mild alkali pretreatment [44,46] (Figures 1b and 4).

Monomers that decrease lignin–polysaccharide interactions: The presence of monomers containing catechol or pyrogallol groups would reduce the formation of benzyl ether and ester cross-linking between hemicelluloses and lignin during the β-*O*-4 coupling of monomers, due to internal trapping of the quinone methide intermediate and the formation of benzodioxane structures [48,49] (Figure 1b).

Figure 3



A- Rosmarinic acid.
B- Clovamide.
C- Coniferyl ferulate.
D- Caffeoyl alcohol (R_1 = OH, R_2 = H), 5-Hydroxyconiferyl alcohol (R_1 = OCH_3, R_2 = OH), 3,4,5-trihydroxycinnamyl alcohol (R_1 = R_2 = OH).
E- Protocatechuate (R_1 = OH, R_2 = H), 5-Hydroxyvanillate (R_1 = OCH_3, R_2 = OH), gallate (R_1 = R_2 = OH).
F- Epigallocatechin gallate.
G- Pentagalloylglucose.

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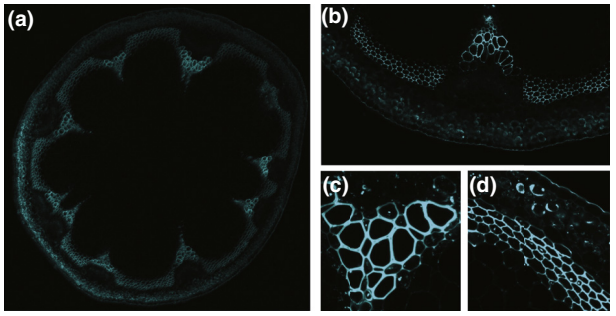
Examples of novel monolignols for lignin bioengineering. **(a)** Rosmarinic acid; **(b)** clovamide; **(c)** coniferyl ferulate; **(d)** caffeoyl alcohol (R_1 = OH, R_2 = H), 5-hydroxyconiferyl alcohol (R_1 = OCH_3, R_2 = OH) and 3,4,5-trihydroxycinnamyl alcohol (R_1 = R_2 = OH); **(e)** protochatechuate (R_1 = OH, R_2 = H), 5-hydroxyvanillate (R_1 = OCH_3, R_2 = OH) and gallate (R_1 = R_2 = OH); **(f)** epigallocatechin gallate; **(g)** pentagalloylglucose.

For example, the β-*O*-4 polymerization of conventional monolignols with benzene diols such as caffeoyl alcohol and 5-hydroxyconiferyl alcohol (Figure 3d); or with triols such as 3,4,5-trihydroxycinnamyl alcohol and derivatives of gallate (Figure 3d and e respectively) should minimize lignin–polysaccharide crosslinkages and enhance cell wall digestibility. Lignins made of caffeoyl alcohol units have been described in seed coats of *Vanilla planifolia* and of several members of the Cactaceae family [50•,51•], whereas 5-hydroxyconiferyl alcohol is found in lignins of COMT-deficient plants that were shown to exhibit increased cell wall digestibility [52,53]. Interestingly, biomimetic studies revealed that incorporation of gallate derivatives such as epigallocatechin gallate and pentagalloylglucose (Figure 3f and g) into lignin enhances the enzymatic digestion or fermentation of cell walls [42,43,45]. Lastly, rosmarinic acid and clovamide, described previously, also fall into the novel monomers category due to their potential to form benzodioxane structures during β-*O*-4 coupling with conventional monolignols.

Monomers that reduce lignin polymerization degree: Overproduction of monomers that initiate or terminate the synthesis of lignin chains should result in a polymer with higher number of shorter molecules. For example,

Figure 4



Incorporation of NBD-tagged monolignol probe 3G into wild type Arabidopsis stems as describe in Tobimatsu *et al.* 2013 [55]. Transverse sections of a wild type Arabidopsis stem fed with NBD-tagged monolignol probe showing exclusive polymerization of the probe in lignifying tissues (interfascicular fibers and xylem cells). Fluorescence in cortical cells comes from cytosolic accumulation of the fluorescent probe. Magnifications: Panel (a): 5×; Panel (b): 10×; Panel (c): 20×; Panels (d) and (e): 40×.

hydroxybenzoates and hydroxybenzaldehydes (C_6C_1 monomers) couple to conventional monolignols only via their phenolic ring to form lignin 'end-groups.' Our recent worked showed that expressing the bacterial hydroxycinnamoyl-CoA hydratase-lyase (HCHL) in *Arabidopsis* allowed the overproduction of such C_6C_1 aromatics, which incorporate into the lignin and reduce its molecular weight [12••]. Notably, cell walls from these transgenics have improved saccharification but with no reduction of lignin content or biomass yield compared to wildtype plants. C_6C_1 aromatics containing catechol and pyrogallol groups such as protocatechuate, 5-hydroxyvanillate and gallate, or their aldehyde forms (Figure 3e) were not detected in the lignin of HCHL plants. Nevertheless, they represent important targets for lignin replacement that would combine the properties of decreasing lignin–polysaccharide interactions and reducing lignin polymerization degree.

Monomers that increase lignin value: Based on the capacity of monolignols to attach various compounds, such as fluorophores, onto their C_9 position without disturbing their ability to polymerize with lignin monomers and polymers [54,55] (Figures 1b and 4), a similar approach could be developed to enrich *in vivo* lignin polymers with free, readily cleavable, and valuable moieties (e.g. benzoate, cinnamate, and tyramine). These lignin 'decorative' moieties would be recovered from lignin after pretreatment during biomass processing and directly used for industrial purposes or as precursors to production of more valuable chemicals. These decorative moieties would be selected based on downstream application, their resistance to polymerization by peroxidase or laccase with other monolignols *in vivo*, and the existence of acyltransferases capable of coupling them to hydroxycinnamoyl-CoAs. The hydroxycinnamoyl moiety would serve as a carrier since it would polymerize as a conventional monolignol and incorporate the valuable chemical moieties into the lignin polymers. Such processes are already occurring naturally in some species, but at very low levels [1,56] (Figure 1b). Alternatively, such monolignol engineering could also be used to change the chemical and physical properties of lignins and facilitate downstream utilization.

Lignin-engineering pathways

Several type III polyketide synthases have been characterized for the synthesis of flavonoids, stilbenes, coumarins, curcuminoids, and benzalacetones in various plant species [57], but the impact of overexpressing them in tissues developing lignified secondary cell walls has never been investigated. Providing that there is a sufficient amount of the co-substrate malonyl-CoA, these enzymes could be used to reroute hydroxycinnamoyl-CoAs away from the lignin pathway. Similarly, enzymes involved in the synthesis of lignans and neolignans could be used to reroute coniferyl alcohol away from lignin formation [58], and the precursors phenylalanine, cinnamate, and coniferyl alcohol could be converted by different enzymes into benzenoid/phenylpropanoid volatiles at the expense of lignin synthesis [59].

The tissue-specific overexpression of several enzymes from the BAHD acyl-CoA transferase family [60] is of particular interest for the production of cleavable monolignol candidates. For example, several transferases that catalyze the synthesis of hydroxycinnamate esters such as rosmarinic acid and coniferyl ferulate/coumarate have been identified within this family [61–63]. However, besides hydroxycinnamoyl/benzoyl-CoA:anthranilate N-hydroxycinnamoyl/benzoyltransferase (HCBT) from carnation, and hydroxycinnamoyl-CoA:hydroxyanthranilate N-hydroxycinnamoyltransferase (HHT) from oats — which couple hydroxcinnamoyl-CoAs to (hydroxyl)anthranilates [12••,64] — no BAHDs catalyzing the synthesis of hydroxycinnamate amides using aromatic acceptors have been identified. However, several N-phenylpropenoyl-aromatic amino acid amides, such as (deoxy)clovamide, are found in various plant species [65]. Instead, enzymes responsible for the synthesis of hydroxycinnamate amides of tyramine, other potential cleavable monolignols, were found to belong to the GCN5-related N-acyltransferase family (GNAT) [66,67]. More generally, overexpression of monolignol acyltransferases that use (hydroxy)benzoyl-CoA as a donor, which still remain to be discovered, could potentially be used to produce monomers to reduce lignin DP and enrich it with valuable moieties that could be recovered during biomass processing [68].

Biosynthetic enzymes for the production of C_6C_1 compounds have been described in plants. In particular, three

enzymes from the vanilla orchid have been implied in the synthesis of vanillin from coumarate via the intermediates 4-hydroxybenzaldehyde and protocatechualdehyde [69–71]. Therefore, co-expressing theses enzymes in lignifying tissues could reroute coumarate towards the synthesis of these C_6C_1 aromatics. Alternatively, HCHL enzymes can be used for the conversion of hydroxycinnamoyl-CoAs into C_6C_1 hydroxybenzaldehydes. Expression of HCHL in *Arabidopsis* showed that C_6C_1 hydroxybenzaldehydes were efficiently converted by endogenous enzymes to the corresponding C_6C_1 acids and could undergo hydroxylation and methoxylation of their aromatic ring [12••]. Finally, bacterial chorismate pyruvate-lyase such as UbiC from *Escherichia coli* can be used for in-planta accumulation of 4-hydroxybenzoate from chorismate [72,73], whereas bacterial 4-hydroxybenzoate-3-hydroxylases can be used for protocatechuate production [74].

Concerning the synthesis of pyrogallol groups, a study reported a fivefold increase of gallate content in tobacco plants that overexpress the shikimate dehydrogenase from walnut (*Juglans regia*) or from *E. coli* [75]. We recently reported that the bacterial coumarate 3-hydroxylase Sam5 from *Saccharothrix espanaensis* was able to hydroxylate caffeate to produce 3,4,5-trihydroxycinnamate when expressed in *E. coli* [12••]. This discovery opens an opportunity to reroute coumarate from the lignin pathway and to produce in planta molecules with pyrogallol groups.

Conclusion

Although the lignin biosynthesis pathway and its enzymes are well characterized, lignin reduction remains a challenging task. This problem stems from a lack of specificity in traditional lignin-reduction methods, which usually compromise plant growth or impair the plant defense system. Emerging strategies like genome bioediting and transgene regulation provide new options to achieve controlled lignin manipulations in targeted plant tissues when applied in conjunction with tissue-type-specific or cell-type-specific promoters. It will finally give the opportunity to design crops with optimized lignin composition and distribution while retaining all other traits related to the phenylpropanoid pathway. Besides traditional lignin reduction methods that directly target genes from the lignin biosynthetic pathway, novel dominant approaches are currently in development. This new trend for lignin engineering focuses on the redirection of carbon flux to the production of related phenolic compounds and on the replacement of monolignols with novel lignin monomers to improve biophysical and chemical properties of lignins such as recalcitrance, or industrial use. These novel technologies require experimental validation, as several have yet to be tested in plants or crops, but they are worthy of attention because they offer both economic potential and an intellectual challenge to the research community.

Conflict of interest

DL has financial conflicts of interest in Afingen.

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Papers of particular interest, published within the period of review, have been highlighted as:

- • of special interest
- •• of outstanding interest

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