

Coniferyl aldehyde 5-hydroxylation and methylation direct syringyl lignin biosynthesis in angiosperms

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ABSTRACT A central question in lignin biosynthesis is how guaiacyl intermediates are hydroxylated and methylated to the syringyl monolignol in angiosperms. To address this question, we cloned cDNAs encoding a cytochrome P450 monooxygenase (LsM88) and a caffeate *O*-methyltransferase (COMT) from sweetgum (*Liquidambar styraciflua*) xylem. Mass spectrometry-based functional analysis of LsM88 in yeast identified it as coniferyl aldehyde 5-hydroxylase (CALd5H). COMT expressed in *Escherichia coli* methylated 5-hydroxyconiferyl aldehyde to sinapyl aldehyde. Together, CALd5H and COMT converted coniferyl aldehyde to sinapyl aldehyde, suggesting a CALd5H/COMT-mediated pathway from guaiacyl to syringyl monolignol biosynthesis via coniferyl aldehyde that contrasts with the generally accepted route to sinapate via ferulate. Although the CALd5H/COMT enzyme system can mediate the biosynthesis of syringyl monolignol intermediates through either route, k_{cat}/K_m of CALd5H for coniferyl aldehyde was ≈ 140 times greater than that for ferulate. More significantly, when coniferyl aldehyde and ferulate were present together, coniferyl aldehyde was a noncompetitive inhibitor ($K_i = 0.59 \mu\text{M}$) of ferulate 5-hydroxylation, thereby eliminating the entire reaction sequence from ferulate to sinapate. In contrast, ferulate had no effect on coniferyl aldehyde 5-hydroxylation. 5-Hydroxylation also could not be detected for feruloyl-CoA or coniferyl alcohol. Therefore, in the presence of coniferyl aldehyde, ferulate 5-hydroxylation does not occur, and the syringyl monolignol can be synthesized only from coniferyl aldehyde. Endogenous coniferyl, 5-hydroxyconiferyl, and sinapyl aldehydes were detected, consistent with *in vivo* operation of the CALd5H/COMT pathway from coniferyl to sinapyl aldehydes via 5-hydroxyconiferyl aldehyde for syringyl monolignol biosynthesis.

Lignin in angiosperms is composed of guaiacyl and syringyl monomers, whereas gymnosperm lignin consists almost entirely of guaiacyl moieties (1). The importance of the syringyl constituent in facilitating overall lignin degradation for more efficient materials and energy production from angiosperm than from gymnosperm wood has long been established (2–4). In contrast, the biosynthesis of syringyl lignin is not well understood.

It has been thought that syringyl lignin biosynthesis involves a cytochrome P450 ferulate 5-hydroxylase (F5H)-catalyzed conversion of guaiacyl intermediate ferulate to 5-hydroxyferulate followed by a caffeate *O*-methyltransferase (COMT)-mediated reaction to sinapate (1, 5–9). Current understanding of F5H function in plants is based solely on the *in vitro* enzymatic activity of proteins from *Populus euramericana* (8). Ferulate was believed to be converted into a product that was “tentatively proposed” as 5-hydroxyferulate (8), but the struc-

ture of this product must yet be corroborated to demonstrate F5H activity. In fact, 5-hydroxyferulate as an intermediate for monolignol biosynthesis has not been reported *in planta*. Although a putative F5H cDNA was recently cloned from *Arabidopsis*, its biochemical function remains unknown (10, 11). Overexpression of this cDNA in *Arabidopsis* mutant (*fah1*) lines deficient in syringyl lignin (12) restored the accumulation of syringyl-enriched lignin, but did not result in detectable F5H enzymatic activity (11). It is also known that, based on *in vitro* studies, proteins from various angiosperm species cannot activate sinapate into its CoA derivative for syringyl lignin biosynthesis (13–15). Taken together, these results challenge the conventional concept of a ferulate 5-hydroxylation/methylation-regulated biosynthesis of syringyl lignin in angiosperms. Based on this and on the general lack of evidence that ferulate 5-hydroxylation is involved in syringyl monolignol biosynthesis, we hypothesize that F5H may encode an enzyme that catalyzes 5-hydroxylation of guaiacyl intermediates other than ferulate to initiate the biosynthesis of the syringyl monolignol. We therefore examined the 5-hydroxylation and methylation reactions in lignifying xylem of an angiosperm tree species, sweetgum (*Liquidambar styraciflua*), to investigate the entrance pathways to syringyl lignin and thereby test the validity of the traditionally accepted pathway.

MATERIALS AND METHODS

Plant Material. Differentiating stem xylem was collected from vegetatively propagated 3-yr-old sweetgum trees (Forest Experimental Station of International Paper Co., Bainbridge, GA) and stored in liquid nitrogen before protein, RNA, and DNA isolation, as described (15).

cDNA Cloning of Sweetgum Monooxygenases and COMT, and Northern and Southern Blotting. Poly(A)⁺ RNA isolated from xylem was used to construct a cDNA library in λ ZAP II vector (Stratagene), as described (16). A pool of phagemid cDNAs rescued from the cDNA library was used as a template for PCR amplification of P450 cDNAs. A degenerate primer (5'-CTAGTCTAGACCATTCGGNDCNGGNMGNMG-3') for the conserved P450 heme-binding domain (PF-GXGRR) with an introduced 5' *Xba*I site and an oligo-dT

Abbreviations: F5H, ferulate 5-hydroxylase; CPR, cytochrome P450 reductase; CALd5H, coniferyl aldehyde 5-hydroxylase; COMT, caffeate *O*-methyltransferase.

Data deposition: The sequences reported in this paper have been deposited in the GenBank database (accession nos. AF139532 and AF139533).

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primer were used for PCR. The amplified cDNAs were cloned into a pCRII vector (Invitrogen) and sequenced. Sequencing of 24 independent clones classified them into five separate groups, of which three, namely *LsM4*, *LsM7*, and *LsM8*, could be assigned to the *CYP73*, *CYP98*, and *CYP84* gene families, respectively. *LsM8* was used to screen the cDNA library to obtain a full length cDNA, designated *LsM88*, and sequenced (GenBank AF139532). By using an aspen (*Populus tremuloides*) COMT-encoding cDNA (*PtOMT1*) (17) to screen the same sweetgum cDNA library, a full-length cDNA, designated *LsCOMT*, was cloned and sequenced (GenBank AF139533), and exhibited 80% amino acid sequence identity to *PtOMT1*. The GCG software package (Genetics Computer Group, Madison, WI) was used for sequence analysis. Northern and Southern blotting were performed according to Tsai *et al.* (18).

Expression of Recombinant *LsM88* and *LsCOMT* in *Escherichia coli*, Preparation of Anti-*LsM88* Polyclonal Antibodies, and Western Blotting. The plasmid vector pQE30 (Qiagen, Chatsworth, CA) was used for the expression of *LsM88* cDNA in *E. coli*. The first 30 amino acids of *LsM88* consisting of many hydrophobic residues involved in endoplasmic reticulum targeting were replaced by an alanine codon (GCT) for high expression of the transgene (19) in *E. coli*. This modification was achieved by PCR mutagenesis by using a pair of *LsM88*-specific primers that introduced *Bam*HI sites at the 5' and 3' ends of the PCR product that was cloned at the *Bam*HI site of the pQE30 vector to give the expression plasmid pQEΔ*LsM88*. This expression plasmid, in which the *LsM88* cDNA was sequenced and confirmed to have no PCR errors, was used to transform *E. coli* strain M15 for expression according to Li *et al.* (20). The truncated *LsM88* protein was harvested from bacterial cells and affinity purified by using a Ni²⁺-NTA-agarose column (Qiagen) according to the manufacturer's protocol. Anti-*LsM88* polyclonal antibodies were raised in rabbits (Alpha Diagnostic, San Antonio, TX) and used for Western blotting, as described (20). *E. coli*-expressed *LsCOMT* was prepared according to Li *et al.* (20).

Coexpression of Sweetgum *LsM88* with *Arabidopsis* NADPH-Cytochrome P450 Reductase (CPR) in Yeast. To use adenine as a selection marker, we altered the *ADE2* gene (21) of the INVSc1 host strain of yeast *Saccharomyces cerevisiae* (Invitrogen) and designated the mutated form as INVSc2. The *Arabidopsis* CPR cDNA (EST clone G8A6, ABRC) driven by a GAL promoter was then integrated into the INVSc2 genome by homologous recombination, giving rise to the INVSc2(CPR) strain. *LsM88* cDNA driven by a GAL promoter was placed into the autonomously replicating vector pYAL by cloning the *ADE2* gene into the pYX243 vector (Novagen/R & D Systems) and then selected by using adenine and leucine as the markers. This *LsM88* expression vector (pYAL-*LsM88*) was transferred into INVSc2(CPR) to create the INVSc2(CPR)/pYAL-*LsM88* yeast strain for coexpressing CPR and *LsM88* cDNAs. The expression of INVSc2(CPR)/pYAL-*LsM88* and control cells transformed with pYAL alone [INVSc2(CPR)/pYAL], and the preparation of microsomal fractions from these cells was carried out as described (22). P450 was measured from the reduced-CO difference spectrum (23). Microsomal NADPH-cytochrome *c* reductase activity was determined as described (24). Protein concentrations were determined by using the Bradford dye-binding reagent (Bio-Rad) with BSA as the standard.

Chemicals. 5-Hydroxyferulate, feruloyl-CoA, and 5-hydroxyferuloyl-CoA thioesters were synthesized as described (20, 25). 5-Hydroxyconiferyl aldehyde was synthesized from 5-hydroxyvanillin by first condensing it with monoethyl malonate to give ethyl 5-hydroxyferulate, which was ethoxyethylated with ethyl vinyl ether and DL-10-camphorsulfonic acid in CH₂Cl₂/tetrahydrofuran (10/1) to yield ethyl 5-hydroxyferulate diethoxyethyl ether. This ether was reduced by diisobutylaluminum hydride in CH₂Cl₂ to give 5-hydroxyconiferyl

alcohol diethoxyethyl ether, followed by oxidation with activated MnO₂ in CH₂Cl₂ to afford 5-hydroxyconiferyl aldehyde diethoxyethyl ether, of which the ethoxyethyl groups were hydrolyzed by HCl in acetone to produce 5-hydroxyconiferyl aldehyde, and its structure was confirmed by ¹H- and ¹³C-NMR, C,H-correlation spectroscopy, and heteronuclear multiple bond connectivity, and MS. NMR spectra were recorded with a JNM-LA400MK FT-NMR System (JEOL). Electron impact mass spectrometry (70eV) was recorded with a JMS-DX303HF mass spectrometer equipped with a JMA-DA5000 Mass Data System (JEOL). 5-Hydroxyconiferyl aldehyde: ¹H-NMR (acetone-*d*₆, carbon numbers are shown in Fig. 2A), δ 3.88 (3H, s, OCH₃), 6.60 (1H, dd, *J* = 15.6, *J* = 7.8, C₈H), 6.88 (1H, d, *J* = 1.7, C₆H), 6.95 (1H, d, *J* = 1.7, C₂H), 7.50 (1H, d, *J* = 15.6, C₇H), 9.61 (1H, d, *J* = 7.8, C₉H); ¹³C-NMR (acetone-*d*₆), δ 56.6 (OCH₃), 104.7 (C₂), 111.2 (C₆), 126.5 (C₁), 127.2 (C₈), 138.3 (C₄), 146.5 (C₅), 149.3 (C₃), 154.4 (C₇), 193.8 (C₉); MS *m/z* (%), 194 (M⁺, 100), 177 (10.8), 166 (24.4), 151 (53.9), 133 (8.0), 123 (21.1), 105 (7.0). All other chemicals used were obtained from Sigma/Aldrich.

Hydroxylase and *O*-Methyltransferase Enzyme Assays and HPLC-UV/Mass Spectrometer Detector (MSD) Analysis of Reaction Products. For hydroxylase activity, 500 μl of reaction mixture (saturated with oxygen) containing 50 mM NaH₂PO₄ (pH 7.5), 1 mM β-mercaptoethanol, 200 nM P450 from transformed yeast cells or 720 μg microsomal proteins from xylem, 0.5 mM substrate, and 1 mM NADPH was incubated at 30°C for 15 min followed by the addition of 20 μl 6N HCl to terminate the reaction and 1 μg sinapate as internal standard. For kinetic analyses, the reaction time was 5 min with 15 nM P450 from transformed yeast and varying concentrations of coniferyl aldehyde (1 to 32 μM) or ferulate (100 to 3,200 μM) to measure the *K_m*, *V_{max}*, and *k_{cat}*. To measure the *K_i* for coniferyl aldehyde, hydroxylation of ferulate (100 to 3,200 μM) was assayed in the presence of coniferyl aldehyde at various concentrations (0.25 to 5 μM). *O*-methyltransferase activity was assayed according to Li *et al.* (20), except nonradioactive *S*-adenosyl-L-methionine was used and 1 μg *o*-coumarate as internal standard. The ethyl acetate extracted and dried reaction mixtures were dissolved in 30 μl of HPLC mobile phase (20% acetonitrile in 10 mM formic acid, pH 2.7). Samples of 15 μl were injected automatically onto a Supelcosil LC-ABZ column (15 cm × 4.6 mm × 5 μm, Supelco), and compounds were separated isocratically at 40°C and a flow rate of 1 ml/min with an HP 1100 LC system and detected by an HP 1100 diode array detector and an HP 1100 LC-MSD with an Atmospheric Pressure Ionization-electrospray source in negative ion mode (Hewlett Packard). The reaction products were identified and quantified based on the authentic standards. 5-Hydroxyconiferyl aldehyde; UV (HPLC mobile phase) λ_{max} I 244 nm, λ_{max} II 344 nm, λ_{min} 273 nm; MS (150 V) *m/z* (%), 194 (5.9), 193 ([M-H]⁻, 55), 178 (100), 150 (18.1); retention time (Rt) 4.41 min/UV, 4.47 min/MS. 5-Hydroxyferulate; UV, λ_{max} I 236 nm, λ_{max} II 322 nm, λ_{min} 263 nm; MS (150 V) *m/z* (%), 210 (9.8), 209 ([M-H]⁻, 71.9), 194 (100), 150 (79.3); Rt 3.79 min/UV, 3.85 min/MS. Sinapyl aldehyde; UV, λ_{max} I 244 nm, λ_{max} II 344 nm, λ_{min} 275 nm; MS (150 V) *m/z* (%), 208 (7.9), 207 ([M-H]⁻, 44), 192 (77), 177(100), 149 (13); Rt 6.64 min/UV, 6.70 min/MS. Sinapate; UV, λ_{max} I 238 nm, λ_{max} II 324 nm, λ_{min} 264 nm; MS (150 V) *m/z* (%), 224 (11.3), 223 ([M-H]⁻, 100), 208 (44.5), 193 (59); Rt 5.92 min/UV, 5.98 min/MS.

Measurement of Kinetic Constants. *K_m* and *V_{max}* values were determined from Lineweaver-Burk plots, and *k_{cat}* values by dividing *V_{max}* by the enzyme concentration, based on three to four independent assays. *K_i* was derived from a Dixon plot.

RESULTS AND DISCUSSION

Cloning of a Sweetgum Cytochrome P450 Monooxygenase *LsM88* and Coexpression with *Arabidopsis* CPR cDNA. We

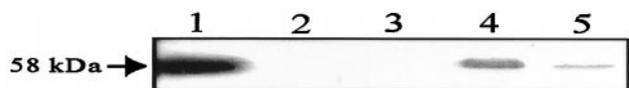


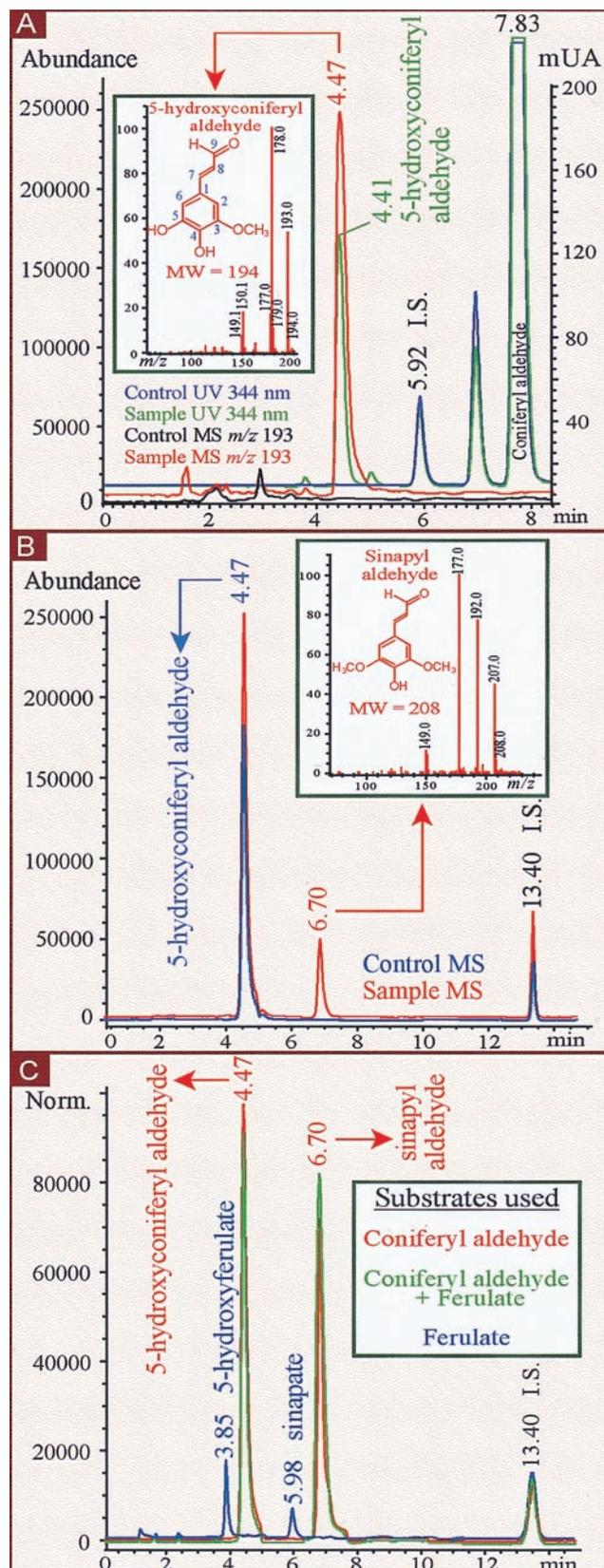
FIG. 1. Western blot analysis of 1 µg of purified *E. coli*-expressed LsM88 recombinant protein (lane 1) and 10 µg microsomal proteins each from leaves (without midveins, lane 2), stem internodes 1 to 4 (primary growth tissue, lane 3), internodes 6 to 10 (secondary growth tissue, lane 4), and stem xylem (lane 5) of sweetgum.

focused on the 5-hydroxylation of guaiacyl monolignol precursors by first cloning cytochrome P450 monooxygenases from lignifying stem xylem of sweetgum. A full-length cDNA *LsM88* (GenBank AF139532) was isolated and was 1,883-bp long, encoding an ORF of 511 amino acids with a calculated M_r of 57,503 and a pI of 5.94. *LsM88* has a 75% amino acid sequence identity (82% similarity) to the *Arabidopsis* putative *F5H* (10), suggesting that *LsM88* encodes a plant CYP84. However, the N-terminal 34-aa sequence of LsM88 is highly divergent from *Arabidopsis* F5H and contains the hydrophobic region typical of the uncleavable signal peptide for anchoring P450 protein to the endoplasmic reticulum membrane (26). A proline-rich region following the putative signal peptide and a cytochrome P450 heme-binding signature (PFGXGRR) toward the C terminus, which is typical of plant P450 proteins, were also identified in LsM88. Northern blot analysis of sweetgum xylem mRNA showed a 1.9-Kb transcript matching well with the length of the *LsM88* clone, and Southern blot analysis indicated that a small *LsM88* gene family of two to three members may be present in the sweetgum genome (data not shown). Western blotting showed that LsM88 protein is present in syringyl lignin-forming secondary growth tissue, including developing stem xylem, but not in leaves or the guaiacyl lignin-enriched primary growth tissue (15, 18, 27) (Fig. 1), suggesting a role for LsM88 enzyme in the biosynthesis of the syringyl monolignol.

To investigate LsM88 enzyme function, we used a yeast expression system. Yeast strain INVSc2 (CPR) exhibited a 5-fold higher microsomal NADPH-cytochrome *c* reductase activity (500 nmol/minute per mg) than INVSc2 without the CPR transgene. INVSc2(CPR)/pYAL-LsM88 yeast cells expressed a ~58-kDa protein that localized to the microsomal fraction and crossreacted strongly with the anti-LsM88 antibody, whereas no such crossreaction could be detected in microsomes of control INVSc2(CPR)/pYAL cells (data not shown). P450 expression levels in INVSc2(CPR)/pYAL-LsM88 were typically ~300 pmol P450 per mg of microsomal proteins. No P450 protein was detectable in control INVSc2(CPR)/pYAL.

LsM88 Is a Coniferyl Aldehyde 5-Hydroxylase (CALd5H). We focused on monolignol biosynthetic pathways starting from

FIG. 2. HPLC separation of products from enzymatic reactions with recombinant proteins. (A) HPLC-UV (344 nm) and HPLC-MS [Selected Ion Monitoring (SIM), 70 V; m/z 193] chromatograms of reaction mixture after incubating 0.5 mM coniferaldehyde (Rt 7.83 min/UV) with 100 pmol LsM88 (CALd5H)-containing (Sample) or 500 µg vector-only (Control) yeast microsomes. Internal standard (I.S.) was sinapate. Negative ion electrospray (NI-ES) mass spectrum (Inset, scanning mode at 150 V) of the reaction product 5-hydroxyconiferyl aldehyde (Rt 4.47 min/MS, 4.41 min/UV) is identical to that of the authentic standard. (B) HPLC-MS [SIM, 70 V; m/z 193 (0–5.50 min), m/z 207 (5.50–10.00 min), m/z 163 (10.00–15.00 min)] chromatograms of reaction mixture after incubating 0.05 mM 5-hydroxyconiferyl aldehyde with 9.5 µg protein extract from LsCOMT-containing (Sample) *E. coli* cells or with boiled (Control) LsCOMT recombinant proteins. NI-ES mass spectrum (Inset, scanning mode at 150 V) of product sinapyl aldehyde (Rt 6.70 min) is identical to that of the authentic standard. (C) HPLC-MS [SIM, 70 V; m/z 209 (0–4.10 min), m/z 193 (4.10–5.20 min), m/z 223 (5.20–6.30 min), m/z 207 (6.30–10.00 min), m/z 163 (10.00–15.00 min)] chromatograms of



reaction mixture after incubating either 0.5 mM coniferyl aldehyde, 0.5 mM ferulate, or 0.5 mM of both with a mixture of 100 pmol CALd5H-containing yeast microsomes and 9.5 µg protein extract from LsCOMT-containing *E. coli* cells. 5-Hydroxyconiferyl aldehyde and sinapyl aldehyde were products (red or green) from coniferyl aldehyde or a mixture of coniferyl aldehyde and ferulate. 5-Hydroxyferulate (Rt 3.85 min) and sinapate (Rt 5.98 min) were products (blue) from ferulate. I.S. was *o*-coumarate in B and C.

Table 1. Substrate specificity of recombinant sweetgum LsM88 (CAld5H) and LsCOMT (COMT) proteins and of sweetgum xylem proteins

Substrate	Substrate specificity (pmol/min per mg protein)					
	Recombinant proteins			Xylem proteins		
	CAld5H	COMT	CAld5H + COMT	Microsome	Soluble	Microsome + soluble
Coniferyl aldehyde	723.9 ± 24.0 (5-OH-CAld)		382.2 ± 15.2 (SAld)	114.0 ± 3.6 (5-OH-CAld)		13.8 ± 1.2 (SAld)
Ferulate	60.7 ± 3.2 (5-OH-FA)		32.2 ± 2.4 (SA)	26.3 ± 1.2 (5-OH-FA)		12.0 ± 1.4 (SA)
5-Hydroxyconiferyl aldehyde		14,370 ± 200 (SAld)			5,900 ± 35 (SAld)	
5-Hydroxyferulate		12,710 ± 70 (SA)			5,700 ± 90 (SA)	
Coniferyl aldehyde + ferulate	526.5 ± 30.0 (5-OH-CAld)		247.5 ± 17.2 (SAld)	8.8 ± 1.4 (5-OH-CAld)		4.8 ± 1.9 (SAld)
	0 (5-OH-FA)		0 (SA)	0 (5-OH-FA)		0 (SA)

Substrate and recombinant protein concentrations and the control experiments were the same as described in Fig. 2. For assaying xylem proteins, 9.5 and 720 μg of soluble and microsome proteins were used, respectively, with the same substrate concentrations as for recombinant proteins and boiled plant proteins as control. Specific activities were mean \pm SD ($n =$ two to three independent assays). Reaction products: 5-OH-CAld, 5-hydroxyconiferyl aldehyde; 5-OH-FA, 5-hydroxyferulate; SAld, sinapyl aldehyde; SA, sinapate.

ferulate. After HPLC separation, all enzymatic reaction products were confirmed for their purity and identity and were quantified based on the authentic compounds. In preliminary experiments, plant protein extracts were used to test the enzymatic 5-hydroxylation of ferulate and its downstream derivatives, feruloyl-CoA, coniferyl aldehyde, and coniferyl alcohol. To mimic an *in vivo* situation, a mixture of these four monolignol intermediates was incubated with microsomal proteins from lignifying stem xylem of sweetgum. This experiment should result in the formation of 5-hydroxyferulate according to the traditional ferulate 5-hydroxylation pathway for syringyl monolignol biosynthesis. But no 5-hydroxyferulate was detected. Instead, the single product formed exhibited the UV and MS spectral profiles of 5-hydroxyconiferyl aldehyde. To verify this reaction and to test whether it is mediated by LsM88, the assays were repeated by using microsomes from xylem and *LsM88*-transformed yeast cells with coniferyl aldehyde as the lone substrate. In both cases, the single product formed coeluted with authentic 5-hydroxyconiferyl aldehyde and exhibited UV and MS spectral properties identical to those of authentic 5-hydroxyconiferyl aldehyde (Fig. 2A). This identifies LsM88 as a protein that hydroxylates coniferyl aldehyde, instead of ferulate, to initiate the biosynthesis of the syringyl monolignol from the guaiacyl pathway. These results confirm a 5-hydroxylation function involved in monolignol metabolism (Table 1). We therefore designated LsM88 as CAld5H and propose that *CYP84* genes also encode a coniferyl aldehyde 5-hydroxylase.

Coniferyl Aldehyde Is 5-Hydroxylated and Methylated in Series by CAld5H and COMT to Form Sinapyl Aldehyde. To support the proposed model of coniferyl aldehyde-initiated syringyl monolignol biosynthesis, methylation of 5-hydroxyconiferyl aldehyde to sinapyl aldehyde, as suggested by Higuchi (28), must be demonstrated. The results from two sets of experiments attested to such a model. First, 5-hydroxyco-

niferyl aldehyde was converted exclusively into sinapyl aldehyde when incubated with *E. coli*-expressed LsCOMT (Fig. 2B and Table 1), providing the first evidence that the aldehyde precursor is methylated during monolignol biosynthesis and that COMT can catalyze this reaction. Second, when coniferyl aldehyde was incubated with a mixture of CAld5H-containing yeast P450 and *E. coli*-expressed COMT, it was converted into sinapyl aldehyde via 5-hydroxyconiferyl aldehyde (Fig. 2C, in red, and Table 1). Thus, CAld5H catalyzes 5-hydroxylation of coniferyl aldehyde into 5-hydroxyconiferyl aldehyde, which in turn is methylated by COMT to sinapyl aldehyde, supporting the idea of a hydroxylation/methylation flux *in vivo* from guaiacyl to syringyl monolignol biosynthesis via coniferyl aldehyde. This finding stands in sharp contrast to the generally accepted idea that regulation of syringyl and guaiacyl lignin composition occurs upstream at the ferulate 5-hydroxylation step (1, 9, 10).

Coniferyl Aldehyde Inhibits Ferulate 5-Hydroxylation, Eliminating the Reaction Sequence from Ferulate to Sinapate. Consistent with the reaction observed in xylem microsomes, recombinant CAld5H also selectively mediated the conversion of coniferyl aldehyde into 5-hydroxyconiferyl aldehyde from a substrate mixture of ferulate, feruloyl-CoA, coniferyl aldehyde, and coniferyl alcohol. Interestingly, when these substrates were incubated individually with either recombinant CAld5H or xylem microsomes, both coniferyl aldehyde and ferulate were 5-hydroxylated (Table 1). Although the catalytic efficiency with ferulate is considerably lower than that with coniferyl aldehyde (Table 1), a bifunctional 5-hydroxylase activity is implied. This bifunctional activity, however, is inconsistent with the exclusive detection of 5-hydroxyconiferyl aldehyde in mixed substrate reactions mediated either by xylem or CAld5H-containing yeast microsomes. This surprising discovery prompted us to determine whether coniferyl aldehyde inhibits the 5-hydroxylation of ferulate. Equal molar

Table 2. Kinetic constants for CAld5H enzyme

Substrate	K_m , μM	V_{max} , $\text{nM}\cdot\text{min}^{-1}$	k_{cat} , min^{-1}	k_{cat}/K_m , $\text{min}^{-1}\cdot\mu\text{M}^{-1}$
Coniferyl aldehyde	2.77 ± 0.04	64.58 ± 2.08	4.31 ± 0.14	1.56
Ferulate	286.05 ± 0.35	46.50 ± 1.10	3.10 ± 0.07	0.0108

Values were mean \pm SD ($n =$ three or four independent assays).

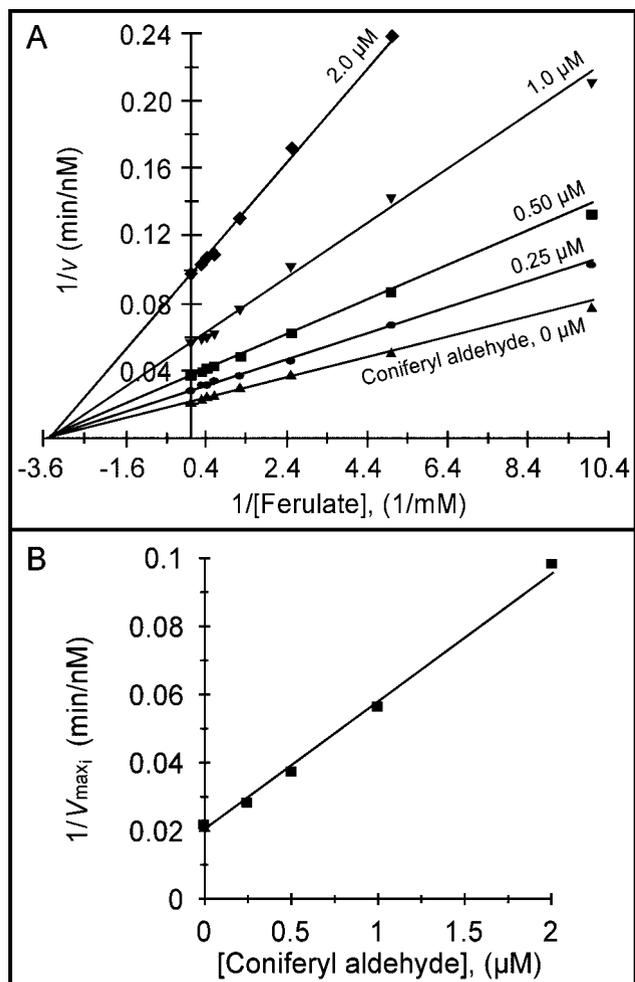


Fig. 3. (A) Lineweaver-Burk plot of CAld5H-catalyzed ferulate 5-hydroxylation in the presence of conferyl aldehyde at different concentrations (as shown). Ferulate concentrations: 100 to 3,200 μM . (B) A replot of $1/V_{\text{max}_i}$ for each reciprocal plot (in A) vs. the corresponding conferyl aldehyde (inhibitor) concentration at which it was obtained. Slope = $1/V_{\text{max}} K_i$.

conferyl aldehyde and ferulate were incubated with recombinant CAld5H. This mixed substrate reaction resulted in a complete inhibition of ferulate 5-hydroxylation, but the conversion of conferyl aldehyde into 5-hydroxyconferyl aldehyde was conserved (Table 1). Similarly, incubation of such mixed substrates with a mixture of yeast CAld5H and *E. coli* LsCOMT recombinant proteins resulted in the production of 5-hydroxyconferyl aldehyde and sinapyl aldehyde, but not of 5-hydroxyferulate and sinapate (Fig. 2C, in green). Elimination of conferyl aldehyde from the substrate mixture restored the production of 5-hydroxyferulate and sinapate (Fig. 2C, in blue). Thus, these results provide unambiguous evidence that conferyl aldehyde inhibits ferulate 5-hydroxylation, thereby eliminating the entire reaction sequence from ferulate to sinapate, the traditionally accepted branch to syringyl lignin biosynthesis (1, 9).

Conferyl Aldehyde Is Both a Noncompetitive Inhibitor of Ferulate 5-Hydroxylation and the Substrate for 5-Hydroxylation Initiating Syringyl Monolignol Biosynthesis. To understand how conferyl aldehyde may inhibit ferulate 5-hydroxylation *in vivo*, we studied the kinetics of CAld5H reaction. The specificity constant (k_{cat}/K_m) values indicated that conferyl aldehyde 5-hydroxylation is ≈ 140 times more efficient than ferulate 5-hydroxylation (Table 2), suggesting that conferyl aldehyde 5-hydroxylation would be the dominant reaction

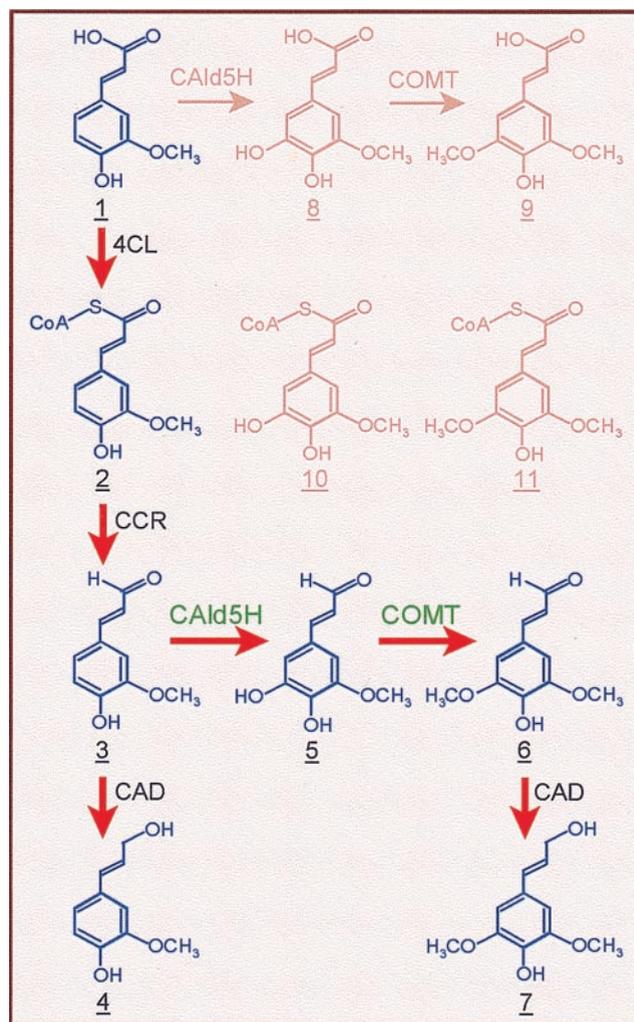


Fig. 4. Biosynthetic pathway from ferulate to conferyl alcohol and sinapyl alcohol for the formation of guaiacyl-syringyl lignin in angiosperms. 4CL, 4-coumarate:CoA ligase; CCR, cinnamoyl-CoA reductase; CAld5H, conferyl aldehyde 5-hydroxylase; COMT, caffeate O-methyltransferase; CAD, cinnamyl alcohol dehydrogenase.

leading to syringyl monolignol biosynthesis. In fact, when conferyl aldehyde and ferulate are used as substrates together, conferyl aldehyde is both the favored substrate for 5-hydroxylation and a noncompetitive inhibitor of ferulate 5-hydroxylation (Fig. 3A), with a K_i of $0.59 \pm 0.01 \mu\text{M}$ (Fig. 3B). Consistent with the predicted degree of inhibition based on the K_i value, no ferulate 5-hydroxylation activity could be detected at conferyl aldehyde concentrations $\geq 4 \mu\text{M}$, regardless of ferulate concentrations (100 to 3,200 μM). Various concentrations (0.02 to 2 μM) of product 5-hydroxyconferyl aldehyde had no effect on the CAld5H reaction with ferulate, confirming that substrate conferyl aldehyde is solely responsible for the observed inhibition. In contrast, ferulate did not inhibit conferyl aldehyde 5-hydroxylation at any concentrations tested. Based on the K_i for conferyl aldehyde and k_{cat}/K_m values for conferyl aldehyde and ferulate, we concluded that ferulate 5-hydroxylation is unlikely to take place in the presence of conferyl aldehyde *in vivo*.

Enzymatic reactions analogous to those of CAld5H and COMT recombinant proteins, including the conferyl aldehyde-induced elimination of ferulate 5-hydroxylation and methylation, were obtained by using xylem proteins (Table 1). Furthermore, by using HPLC-mass spectrometer detector analysis of methanol extracts from sweetgum xylem cells, we report detection of endogenous conferyl, 5-hydroxyconferyl,

and sinapyl aldehydes, at 12, 4, and 110 ng/g fresh weight, respectively. The detection of these aldehydes in xylem cells and the kinetic results are consistent with a reaction sequence *in planta* from coniferyl aldehyde (**3**; in Fig. 4) to sinapyl aldehyde (**6**) via 5-hydroxyconiferyl aldehyde (**5**) catalyzed by CALd5H and COMT that diverts guaiacyl intermediates into syringyl monolignol biosynthesis. Proteins from aspen stem xylem catalyzed reactions (data not shown) similar to those catalyzed by sweetgum proteins, suggesting that coniferyl aldehyde-modulated CALd5H function for mediating syringyl monolignol biosynthesis may be common to angiosperm tree species.

To our knowledge, this is the first observation that non-competitive inhibition among substrates may modulate a plant P450 activity. Our current results indicate a coniferyl aldehyde-sensitive 5-hydroxylation activity that regulates ferulate metabolism in angiosperms. In the absence of coniferyl aldehyde, CALd5H-catalyzed conversion of ferulate is possible, leading to the formation of 5-hydroxyferulate (**8**, Fig. 4) and sinapate (**9**) as the intermediates, for instance, for sinapoyl malate for UV protection in leaf epidermis (12, 29), or as donors of acyl groups for esterification to the cell wall (30). In its presence because of lignification in tissues such as developing xylem, coniferyl aldehyde, which interrupts ferulate 5-hydroxylation/methylation to divert the carbon flow toward biosynthesis of lignin, becomes 5-hydroxylated to initiate syringyl monolignol biosynthesis. This finding may also suggest that 5-hydroxylation of ferulate and coniferyl aldehyde are developmentally regulated and that coniferyl aldehyde 5-hydroxylation is specific to lignifying tissues.

CONCLUSION

Our finding that coniferyl aldehyde in cooperation with CALd5H can block the ferulate 5-hydroxylation/methylation reaction sequence challenges those ferulate-initiated branch pathways placing **8–11** (in Fig. 4) as the intermediates for monolignol biosynthesis. Another proposed branch from feruloyl CoA (**2**) to 5-hydroxyferuloyl CoA (**10**) for syringyl monolignol (**31**) also could not be substantiated, because there was no detectable hydroxylation of feruloyl CoA by either soluble or microsomal proteins from sweetgum lignifying xylem. Our results, supported by chemical, biochemical, and enzyme kinetic evidence, led us to conclude that CALd5H/COMT regulates the diversion of guaiacyl intermediates toward synthesis of syringyl monolignol. The CALd5H/COMT pathway (**3** to **6**) also provides clarification as to (i) why syringyl lignin is formed when sinapate is not activated to its CoA ester by 4CL (13–15); (ii) why enrichment of syringyl lignin biosynthesis in transgenic *Arabidopsis* is not associated with detectable ferulate 5-hydroxylation activity (11); and (iii) why abnormal 5-hydroxyconiferyl aldehyde-derived monolignols accumulate in lignin of COMT-suppressed transgenic trees (18, 32). Thus, based on the previously identified substrate preference of 4CL (13–15), CCR (33, 34), and CAD (35), these proteins, together with CALd5H and COMT, constitute a dynamic enzyme system (red arrows in Fig. 4) that efficiently mediates conversion of ferulate into the guaiacyl and syringyl monolignols, coniferyl alcohol (**4**), and sinapyl alcohol (**7**), respectively, for the biosynthesis of guaiacyl-syringyl lignin in angiosperms.

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- Higuchi, T. (1997) in *Biochemistry and Molecular Biology of Wood* (Springer, New York), pp. 131–233.
- Sarkanen, K. V. (1971) in *Lignins: Occurrence, Formation, Structure and Reaction*, eds. Sarkanen, K. V. & Ludwig, C. H. (Wiley Interscience, New York), pp. 639–694.
- Chang, H. M. & Sarkanen, K. V. (1973) *Tappi* **56**, 132–136.
- Chiang, V. L. & Funaoaka, M. (1990) *Holzforchung* **44**, 309–313.
- Higuchi, T. & Brown, S. A. (1963) *Can. J. Biochem. Physiol.* **41**, 65–76.
- Higuchi, T. & Brown, S. A. (1963) *Can. J. Biochem. Physiol.* **41**, 613–620.
- Higuchi, T. & Brown, S. A. (1963) *Can. J. Biochem. Physiol.* **41**, 621–627.
- Grand, C. (1984) *FEBS Lett.* **169**, 7–11.
- Whetten, R. W., MacKay, J. J. & Sederoff, R. R. (1998) *Annu. Rev. Plant Physiol. Plant Mol. Biol.* **49**, 585–609.
- Meyer, K., Cusumano, J. C., Somerville, C. & Chapple, C. C. S. (1996) *Proc. Natl. Acad. Sci. USA* **93**, 6869–6874.
- Meyer, K., Shirley, A. M., Cusumano, J. C., Bell-Lelong, D. A. & Chapple, C. C. S. (1998) *Proc. Natl. Acad. Sci. USA* **95**, 6619–6623.
- Chapple, C. C. S., Vogt, T., Ellis, B. E. & Somerville, C. (1992) *Plant Cell* **4**, 1413–1424.
- Kutsuki, H., Shimada, M. & Higuchi, T. (1982) *Phytochemistry* **21**, 267–271.
- Gross, G. G., Mansell, R. L. & Zenk, M. H. (1975) *Biochem. Physiol. Pflanz.* **168**, 41–51.
- Hu, W. J., Kawaoka, A., Tsai, C. J., Lung, J., Osakabe, K., Ebinuma, H. & Chiang, V. L. (1998) *Proc. Natl. Acad. Sci. USA* **95**, 5407–5412.
- Zhang, X.-H. & Chiang, V. L. (1997) *Plant Physiol.* **113**, 65–74.
- Bugos, R. C., Chiang, V. L. & Campbell, W. H. (1991) *Plant Mol. Biol.* **17**, 1203–1215.
- Tsai, C. J., Popko, J. L., Mielke, M. R., Hu, W. J., Podila, G. K. & Chiang, V. L. (1998) *Plant Physiol.* **117**, 101–112.
- Looman, A. C., Bodlaender, J., Comstock, L. J., Eaton, D., Thurani, R., deBoer, H. R. & Van Knippenberg, P. H. (1987) *EMBO J.* **6**, 2489–2492.
- Li, L., Popko, J. L., Zhang, X.-H., Osakabe, K., Tsai, C. J., Joshi, C. P. & Chiang, V. L. (1997) *Proc. Natl. Acad. Sci. USA* **94**, 5461–5466.
- Stotz, A. & Linder, P. (1990) *Gene* **95**, 91–98.
- Pompon, D., Louerat, B., Bronine, A. & Urban, P. (1996) *Methods Enzymol.* **272**, 51–64.
- Omura, T. & Sato, R. (1964) *J. Biol. Chem.* **239**, 2370–2378.
- Yasukochi, Y. & Masters, B. S. S. (1976) *J. Biol. Chem.* **251**, 5337–5344.
- Stockigt, J. & Zenk, M. H. (1975) *Z. Naturforsch.* **30**, 352–358.
- Mizutani, M. & Ohta, D. (1998) *Plant Physiol.* **116**, 357–367.
- Bland, D. E. (1966) *Holzforchung* **20**, 12–18.
- Higuchi, T. (1985) in *Biosynthesis and Biodegradation of Wood Components*, ed. Higuchi, T. (Academic, New York), pp. 141–160.
- Ruegger, M., Meyer, K., Cusumano, J. C. & Chapple, C. C. S. (1999) *Plant Physiol.* **119**, 101–110.
- Mock, H. P. & Strack, D. (1993) *Phytochemistry* **32**, 575–579.
- Ye, Z. H., Kneusel, R. E., Matern, U. & Varner, J. E. (1994) *Plant Cell* **6**, 1427–1439.
- Van Doorselaere, L., Baucher, M., Chognot, E., Chabbert, B., Tollier, M. T., Petit-Conil, M., Leple, J. C., Pilate, G., Cornu, D., Monties, B., *et al.* (1995) *Plant J.* **8**, 855–864.
- Sarni, F., Grand, C. & Boudet, A. M. (1984) *Eur. J. Biochem.* **139**, 259–265.
- Lacombe, E., Hawkins, S., Van Doorselaere, J., Piquemal, J., Goffner, D., Poeydomenge, O., Boudet, A. M. & Grima-Pettenati, J. (1997) *Plant J.* **11**, 429–441.
- Kutsuki, H., Shimada, M. & Higuchi, T. (1982) *Phytochemistry* **21**, 19–23.