

Original Research Paper

Improved sugar yield upon steam explosion and enzymatic saccharification of field-grown poplar downregulated for cinnamyl alcohol dehydrogenase 1

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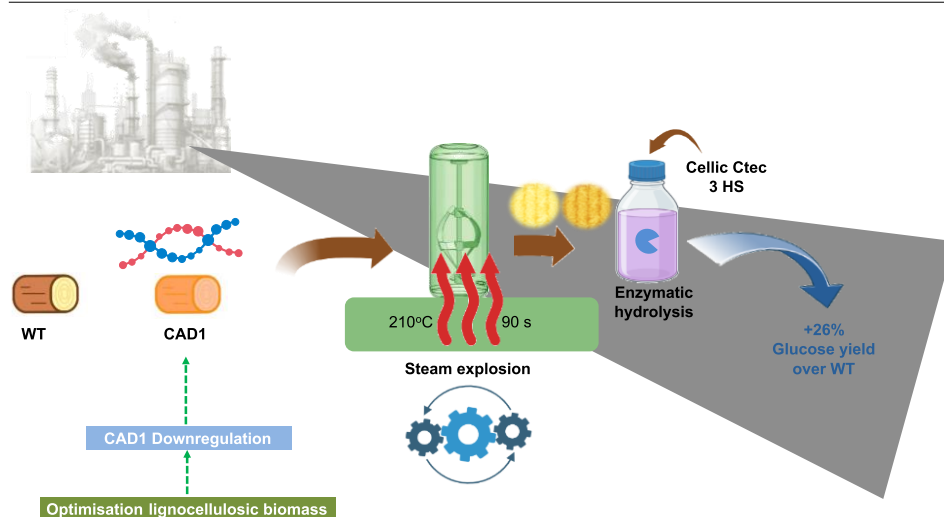
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HIGHLIGHTS

- Wood from three-year-old, field-grown, *CAD1*-downregulated poplar was subjected to STEX.
- *CAD* wood delignified 25% compared to 15% in the control.
- Saccharification yielded 26% more glucose than the control wood.

GRAPHICAL ABSTRACT



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ABSTRACT

Genetic modification of lignocellulosic biomass can enhance its processability by reducing its recalcitrance to pretreatment and enzymatic conversion to chemicals such as biofuels. Downregulation of cinnamyl alcohol dehydrogenase 1 (*CAD1*) in poplar results in the increased incorporation of sinapaldehyde in the lignin polymer. Here, we investigated steam explosion as a pretreatment strategy for the enzymatic hydrolysis of field-grown *CAD1*-downregulated and wild-type (WT) poplar. Steam explosion at 210°C for 90 s resulted in a significantly higher lignin reduction of 25% for *CAD* wood, compared to 15% for WT wood. Under limited conditions at 8.4% solid loading and 8 filter paper units of Cellic Ctec3 HS per gram dry weight, enzymatic hydrolysis resulted in a significantly higher average glucose yield of 76% for *CAD* wood compared to 60% for WT wood. Our data show that steam explosion pretreatment of *CAD1*-modified poplar is a promising strategy to improve enzymatic hydrolysis without the need for additional chemicals.

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Abbreviations, Nomenclatures, and Symbols

AIL	Acid insoluble lignin
ASL	Acid soluble lignin
Bn	Block, referring to the position of the trees in the field trial, with 'n' the number assigned to the block.
CAD 1	Cinnamyl alcohol dehydrogenase 1
CAD 4	Poplar line hpCAD 4
CAD 24	Poplar line hpCAD 24
CAD wood	Cinnamyl alcohol dehydrogenase 1 deficient poplar wood
CoD	Coefficient of dispersion
C3'H	Coumarate 3' hydroxylase
C4H	Cinnamate 4-hydroxylase
F5H	Ferulate 5-hydroxylase
G	Glucose concentration [g/L]
G _m	Maximum glucose concentration, calculated [g/L]
G _{max}	Maximum glucose concentration, model estimation [g/L]
m _{dw}	Mass dry wood [g]
r _{0G}	Initial reaction rate [g/L/h]
r _{0Y}	Relative initial reaction rate [(m/m%)/h]
S ₀	Severity factor [-]
SRC	Short rotation coppice
STEX	Steam explosion
S/G ratio	Syringyl to Guaiacyl ratio
t	time [min]
T	Temperature [°C]
V _{total}	Total Volume [L]
WT	Wild type
Y _G	Glucose yield [m/m%]

1. Introduction

The significant CO₂ emissions and broader environmental impacts associated with fossil-derived fuels and chemicals necessitate reducing their use. Consequently, the production of biofuels from renewable resources has

increased substantially over recent decades. For instance, the global energy production from bioethanol and biodiesel rose from 201 TWh in 2004 to 1425 TWh in 2024 (Ritchie et al., 2025). However, life-cycle assessments have demonstrated that not all biofuels deliver net climate benefits. In particular, first-generation biofuels derived from food crops have been associated with higher net greenhouse gas emissions than the fossil fuels they replace, depending on system boundaries and land-use change assumptions. These crops usually require intensive cultivation and high levels of fertiliser. They also sequester less carbon in the soil than perennial woody systems and compete with food production for land and resources (Ma et al., 2023; Sandford et al., 2024).

In contrast, second-generation lignocellulosic feedstocks, such as short-rotation coppice (SRC) poplar, offer a more sustainable alternative. SRC poplar requires comparatively low management intensity and fertiliser inputs, can be harvested on multi-year rotations without replanting, and can be cultivated on marginal or reclaimed land, including former gravel extraction sites (NNFCC, 2010). These characteristics make SRC poplar a promising feedstock for sustainable biofuel production. Despite their advantages, second-generation biofuels and biochemicals often occupy a smaller market share than their first-generation counterparts. The global market share of, e.g., second-generation cellulosic bioethanol was valued at 885.82 million USD in 2022, while the total bioethanol market was estimated at around 83.4 billion USD (Polaris Market Research, 2023; Statista, 2024). The main reasons for this relatively small market share compared with first-generation products are the technological barriers related to the natural recalcitrance of lignocellulosic materials when they are converted into fermentable sugars. This results in lower product yields and higher production costs (Hemansi et al., 2019).

To significantly improve the market competitiveness of second-generation bioethanol and biochemicals in general, technological innovation is required. A well-supported strategic route is to optimise the starting material, i.e., the lignocellulosic matrix itself, by breeding or genetic engineering (Bryant et al., 2020; Vanhevel et al., 2024). Since lignin in the plant cell wall is the main contributor to the recalcitrance of lignocellulosic biomass towards biomass deconstruction (Fang et al., 2025), research to optimise bioethanol production has largely focused on genetic modification of the lignin biosynthesis pathway. All genes encoding enzymes in the monolignol biosynthetic pathway have been downregulated or overexpressed to alter lignin content or alter its composition in poplar. In addition, poplar has been transformed with heterologous genes to alter lignin structure and enhance saccharification (Sulis et al., 2023; Wang et al., 2025). These studies have shown that reducing lignin content often results

in improvements in cellulose-to-glucose conversion rates upon saccharification.

Altering the lignin syringyl to guaiacyl (S/G) ratio also affects saccharification efficiency, with higher S/G ratios generally leading to better saccharification. However, the magnitude of this effect depends on the lignin amount, as was demonstrated by the analyses of poplar wood samples from a set of undomesticated *Populus trichocarpa* trees with contrasting lignin content and S/G ratios (Studer et al., 2011). Most of these studies were conducted using wood harvested from greenhouse-grown poplars, whereas only a limited number have investigated wood obtained from field-grown trees (De Meester et al., 2022b; Li et al., 2024). Here, the deconstruction and enzymatic hydrolysis of three-year-old field-grown cinnamyl alcohol dehydrogenase1 (*CAD1*)-downregulated poplar wood (CAD wood), genetically modified using an RNAi approach, were examined. This genetically modified wood, which was characterised by an increased incorporation of sinapaldehyde into the lignin polymer, resulted in an increased enzymatic hydrolysis after alkaline pretreatment (Van Acker et al., 2017; De Meester et al., 2022a). This effect has mainly been attributed to the fact that sinapaldehyde incorporation into the lignin leads to a higher proportion of β -ether moieties with conjugated γ -carbonyl functionalities, which are more susceptible to alkaline hydrolysis than the non-conjugated β -ether moieties (Lapierre et al., 1999; Van Acker et al., 2017). However, the increased incorporation of syringaldehyde and sinapaldehyde into the lignin polymer is also expected to (i) reduce the size of the lignin polymer chains, (ii) make lignin more hydrophobic, resulting in fewer non-covalent interactions with hemicellulose, and (iii) reduce the ether or ester bonding between hemicellulose and lignin, potentially reducing recalcitrant lignin-carbohydrate complexes (Mottiar et al., 2016; Van Acker et al., 2017).

Besides optimised substrates, efficient pretreatment of the woody biomass is essential to achieve economically viable monomeric sugar yields in the subsequent saccharification step, where cellulose and hemicellulose are converted into monomeric sugars (Hoang et al., 2023; Gautam et al., 2024). Significant improvements in saccharification yield have been reported for genetically engineered poplar wood following alkali, acid, green liquor, ozone, or hot water pretreatments (Bryant et al., 2020). However, research into the pretreatment and saccharification of CAD genetically engineered poplar wood is limited. The focus has primarily been on its alkaline pretreatment (Van Acker et al., 2017; De Meester et al., 2022) and soda pulping (Segmehl et al., 2018), as well as acidic conditions, such as acidic bleaching (Segmehl et al., 2018) and dilute acid pretreatment (Van Acker et al., 2017; du Pasquier et al., 2025). To the best of our knowledge, the present study is the first to examine steam explosion pretreatment (STEX) of CAD wood. STEX is one of the most energy-efficient and environmentally friendly pretreatment techniques. It requires less energy for particle size reduction compared to grinding or milling, and it usually requires only water (steam) without added chemicals (Shrotri et al., 2017; Hoang et al., 2023). Although the production of compounds that inhibit the subsequent fermentation process is often cited as a disadvantage of STEX, it is one of the most promising lignocellulose pretreatment methods and is already being applied industrially (Oliveira et al., 2013). Research on STEX pretreatment of wood derived from genetically modified trees has thus far been limited to greenhouse-grown poplar trees in which either *FERULATE 5 HYDROXYLASE* (*F5H*) was overexpressed (C4H::F5H trees) to increase the S/G ratio, or *p-COUMARATE 3' HYDROXYLASE* (*C3'H*) was downregulated (RNAi-C3'H trees) to reduce lignin content (Mansfield et al., 2012).

In the present study, the stem biomass of field-grown *CAD1*-deficient poplars (CAD wood) and wild-type (WT) trees was pretreated using STEX. This was followed by enzymatic hydrolysis using a commercially applied enzyme complex, Cellic Ctec 3 HS. The data on the release of monomeric sugars were then compared with the data from the compositional and structural analyses of the wood. Mass balances were set up for the major constituents of lignocellulose. We showed that STEX pretreatment of CAD wood leads to significantly higher delignification than STEX of WT wood. Subsequent enzymatic hydrolysis yielded a significantly higher glucose yield compared to WT wood.

2. Materials and Methods

2.1 Plant material

The plant material comprised chopped whole stems and or branches (with bark) derived from the *hpCAD 4* and *hpCAD 24* poplar lines and their respective WT trees, all harvested in winter. All of these were *Populus tremula* $\times$ *Populus alba* cv. 717-1B4. These genetically modified lines have been described before (Van Acker et al., 2017). Throughout the article, this stem biomass will be referred to as CAD 4, CAD 24 (or simply CAD wood), and WT wood. The trees were grown in a field trial as SRC culture for two consecutive rotations of one and three years, of which the three-year-old wood is used in this study (De Meester et al., 2022a). Three biological replicates of each of the two CAD lines and the WT line, corresponding to three different blocks of trees in the field trial, were analysed. Each biological replicate itself was composed of wood from 40 trees. Each tree contained, on average, 6 stems due to the coppice. The blocks from which the wood was harvested were block 1 (B1), B4, and B5 of the field trial for the WT, B4, B5, and B6 for the CAD 4 line, and B1, B2, and B3 for the CAD 24 line (De Meester et al., 2022a). The field plot is presented in Figure S1.

2.2 Preparation of the poplar stem biomass for steam explosion pretreatment

CAD 4, CAD 24, and WT woody stems were chipped in a wood chipper without prior debarking. The range in length of the resulting stem chips is shown in Figure S2. Fifty grams of the dry chips were placed in Schott bottles, and 1 L of demineralised water was added. The bottles were inverted three times to ensure contact between the wood and the water. The mixtures were kept at room temperature for 16 h. After pre-soaking, the stem chips were separated from the soaking liquid by sieving through a Steel mesh sieve with a pore size of 38 μ m (Endecotts LTD, London, UK).

2.3 Steam explosion pretreatment

STEX was performed on pre-soaked stem chips from WT, CAD 4, and CAD 24 poplars using the STEX equipment of the BioWAVE research group at the University of Antwerp (ATI Sistemas, A Coruña, Spain). This equipment consists of a 7-L reactor and a steam generator capable of producing steam at pressures of up to 40 bar (Fig. S3). The maximum operating pressure of the reactor is 20 bar. Prior to sample treatment, the reactor is preheated by performing a steam explosion in the empty reactor to ensure that the first sample is treated under conditions identical to those of subsequent samples. For steam explosion pretreatment, the reactor is first opened and loaded with the pre-soaked chips. During the subsequent heating phase, from the preheating temperature to the target temperature, the reactor is heated using both an electric heating mantle and hot steam introduced from the steam generator. The sample is then kept at the desired temperature under high-pressure saturated steam for the selected incubation time, after which the explosion valve (ball valve) opens in less than a second, propelling the biomass into the expansion vessel, which is located directly below the reactor. This expansion vessel is connected to the outside and is under atmospheric pressure. This sudden explosive decompression disrupts the stem biomass chips at the cellular level. All steam explosions were performed at 210°C (19 bar) for 90 s, which is considered a high temperature and a short time (Ziegler-Devin et al., 2021). The short time frame was chosen to evaluate whether CAD and WT wood would react differently, while minimising energy input. To evaluate whether all stem chips were treated uniformly, reactor temperature and pressure were continuously recorded over time, and the resulting data were used to calculate the severity factor, S^0 [–], as defined by Equation 1 (Jacquet et al., 2012):

$$S^0 = \log\left(\exp\left(\frac{(T-100)}{14.75}\right) dt\right) \quad \text{Eq. 1}$$

where t represents time [min], and T is temperature [°C].

The severity factor was calculated using Riemann integration, taking into account every second that the sample was exposed to temperatures above 100°C during both the heating and incubation phases. The calculation formula is shown in Equation 2 (Jacquet et al., 2012):

$$S^0 = \log \sum \frac{14.75(t_{n+1}-t_n)}{(T_{n+1}-T_n)} \left(\exp\left(\frac{T_{n+1}-100}{14.75}\right) - \exp\left(\frac{T_n-100}{14.75}\right) \right) \quad \text{Eq. 2}$$

where $(t_{n+1} - t_n)$ is one second and T_n is the temperature [°C] at t_n . 14.75 is a value calculated using the Arrhenius equation, which corresponds to the doubling of the reaction rate of xylan removal with a 10°C increase in temperature (Bhagia et al., 2016). To evaluate the difference in steam explosion severities, a coefficient of dispersion (CoD) was calculated (Eq. 3):

$$CoD = \frac{\sum_{i=1}^n |x_i - \eta|}{n * \eta} \quad \text{Eq. 3}$$

where x_i is the severity factor of the STEX [–], n is the total number of values, and η is the median severity factor [–].

As a consequence of the STEX pretreatment, the stem chips were disintegrated into fibres, which were subsequently recovered from the expansion vessel together with the STEX hydrolysate. Most of the hydrolysate was removed by sieving through a 38 µm sieve. The wet weight of the remaining wood pulp, which was measured for mass balance analysis, increased 7 to 8.5-fold due to the soaking and the STEX pretreatment. A full process scheme showing the dry and wet weights of each sample after each step in the process is provided in Figures S5a and S5b. Table S1 shows the average wet weight per poplar line after soaking and STEX.

2.4 Washing of wood pulp after STEX

After the sieving step, the wood pulp was washed three times with demineralised water to further remove the hydrolysate remaining in the pores of the solid STEX-pretreated wood fibres. Herein, 100 g of the wet wood pulp, which is about one third to one fourth of the total wet mass recovered, was added to 300 mL of demineralised water and shaken vigorously by hand for 1 min. The mixture was then centrifuged for 10 min at 3077 ×g (4000 rpm) using a SIGMA 3-16KL centrifuge (SIGMA, Osterode am Harz, Germany), and 200 mL of the washing water was decanted. Hereafter, another 200 mL of demineralised water was added, and the pulp was washed two more times in the same way. After the last step, the pulp was separated from the washing water using Büchner filtration over a Whatman number 1 filter paper.

2.5 Enzymatic hydrolysis

The dry weight percentage of the washed wood pulp was determined gravimetrically in triplicate by drying approximately 0.5 g of the wet wood pulp in pre-weighed Eppendorf tubes in an oven (Memmert, Schwabach, Germany) at 105°C overnight. Based on this dry weight percentage, a well-determined mass of the wet, filtered, pretreated wood pulp equivalent to 6.5 g of dry wood pulp was brought into 250 mL Schott bottles. Enzymatic hydrolysis was carried out in a 0.05 M citrate buffer (Avantor, Radnor, USA) at pH 4.8. Then, 7.74 mL of 0.5 M citrate buffer, pH 4.6, was added. Per gram of dry wood pulp, 60 µL of a 10 g/L tetracycline (Merck, Darmstadt, Germany) in 70% ethanol solution was added. Cellic Ctec 3 HS cellulase complex, kindly donated by Novonosis (Bagsvaerd, Denmark), was added in different concentrations depending on the experiment at a volume corresponding to 8, 16, 24, or 32 Filter Paper Units (FPU) per gram of dry wood pulp. The activity of the enzyme stock solution was 216.52 FPU/mL as determined according to the NREL/TP-510-42628 protocol (Adney, 1996).

The volume of the liquid reaction mixture was brought to 77.4 mL by adding demineralised water. If the wood pulp contained more water, less additional water was added to the mixture. This way, a solid-to-liquid

loading of 84 g dry wood pulp per litre of reaction mixture was obtained in all cases. This was the highest solid loading that could be achieved, in which all wood pulp was submerged in the hydrolysis mixture. A flowchart of the applied process conditions is provided in Figure S4.

The hydrolysis reaction mixtures were incubated at 50°C and shaken linearly at 250 rpm using a reciprocal shaker (Ohaus SHRC0719DG, Parsippany, USA). The glucose concentration of each mixture was followed up in time as follows. After allowing the solids to settle for about 1 min, 0.5 mL of the supernatant was sampled into a 1.5 mL centrifuge tube with a screw cap. The samples were then placed in a boiling water bath for 15 min to denature the enzymes and subsequently cooled in an ice bath for 10 min to precipitate the enzymes. The samples were diluted 10 times with Millipore water and filtered through a 0.22 µm PES syringe filter in an HPLC vial.

The maximum glucose concentration G_m [g/L] that can be achieved through the enzymatic hydrolysis of lignocellulosic biomass with a certain cellulose content [m/m%], as determined by compositional analysis, was calculated using Equation 4.

$$G_m = \frac{\text{cellulose content} * m_{dw} * MM_{glucose}}{V_{total} * MM_{cellulose unit}} \quad \text{Eq. 4}$$

where m_{dw} [g] is the mass of dry wood introduced into the hydrolysis mixture, i.e., 6.5 g, $MM_{glucose}$ [g/mol] is the molar mass of glucose, i.e., 180 g/mol, V_{total} [L] denotes the total volume of the reaction mixture, i.e., 0.0774 L, and $MM_{cellulose unit}$ [g/mol] is the molar mass of one cellulose unit, i.e., 162 g/mol.

The glucose yields Y_G [%] were then calculated using Equation 5.

$$Y_G = \frac{G}{G_m} * 100\% \quad \text{Eq. 5}$$

where G [g/L] is the glucose concentration determined by HPLC.

This yield was calculated per initial volume of liquid in the reaction mixture. As cellulose in the wood was partially hydrolysed and dissolved during the process, the total liquid volume increased slightly. However, this increase was considered negligible. The applied process conditions of the STEX pretreatment and enzymatic hydrolysis are summarised in Table 1.

Table 1.
Process conditions used for STEX and hydrolysis of WT and CAD poplar wood.

Parameter	Value
STEX Severity [–]	3.59 ± 0.04
Enzyme loading [FPU/g dry stem biomass added]	8
Solids loading enzymatic hydrolysis [g dry stem biomass/mL total liquid volume]	84
Hydrolysis time [h]	96

2.6 Estimation of hydrolysis parameters

For each hydrolysis reaction mixture, the glucose concentration, G [g/L], determined by HPLC as a function of time, t [h], was fitted using a modified Holtzapple model (Holtzapple et al., 1984) implemented with the *lsqnonlin* function in MATLAB. Although the Holtzapple model is generally used to describe reducing sugar concentrations, glucose was considered the platform molecule in the present study. For completeness, the xylose concentrations and yields obtained during enzymatic hydrolysis are shown in Figure S6. Other reducing sugars are much less abundant in the hydrolysate than glucose and xylose, and were not considered (Donaldson

et al., 2017). The parameters of the modified Holtzapple model, i.e., maximum glucose concentration G_{max} [g/L] (i.e., the final glucose concentration in case of complete conversion of the available cellulose) and the initial reaction rate r_{0G} [g/L/h], were calculated. The simplified model applied is presented in Equation 6.

$$G = (G_{max} * t) / (t + \frac{G_{max}}{r_{0G}}) \quad \text{Eq. 6}$$

Equation 6 was further adapted for application to the calculated enzymatic hydrolysis yields, Y_G (see Eq. 5), by accounting for the variable cellulose content of the pretreated wood samples, as expressed in Equation 7.

$$Y_G = (Y_{Gm} * t) / (t + \frac{Y_{Gm}}{r_{0Y}}) \quad \text{Eq. 7}$$

where the model parameters Y_{Gm} , representing the maximum glucose yield [m/m%], and r_{0Y} , representing the relative initial reaction rate [m/m% /h], were estimated.

Evaluation of model robustness was performed by calculating the standard error of the model parameters (Akkermans et al., 2018). Model validation was based on visual inspection of the residual plots as presented in Figure S7.

2.7 Compositional analysis

The poplar stem biomass composition was determined after grinding the stem chips and freeze-drying them in a lyophilisator (SIGMA, Osterode am Harz, Germany) using the method of Wittner et al. (2023). Briefly, 300 ± 2 mg of ground lyophilised sample was subjected to a two-stage dilute acid hydrolysis with sulfuric acid following the standard NREL/TP-510-42618 protocol (Sluiter et al., 2012). Acid-insoluble lignin (AIL) was determined gravimetrically, while acid-soluble lignin (ASL) was measured spectrophotometrically. Finally, cellulose and hemicellulose percentages were calculated from the concentration of their monomers, glucose and xylose, which were determined by an HPLC system (Agilent, Santa Clara, USA) equipped with a Coregel ORH 801 7.8 × 300 mm column (Altmann Analytik, Munich, Germany) kept at 70°C and a Refractive Index Detector at 55°C. Eight mM sulfuric acid (Avantor, Radnor, USA) was used as the mobile phase at a flow rate of 0.6 mL/min. The injection volume was 20 µL (Broos et al., 2024).

2.8 Glucose and xylose determination

During enzymatic hydrolysis assays, the glucose and xylose concentrations were determined using HPLC, applying the same equipment and methodology as described above.

2.9 Macroscopic image analysis

Three-dimensional stitched images of fibres from the different pretreated wood types and blocks were acquired using a digital microscope (Keyence, Mechelen, Belgium). Each sample was spread in a Petri dish, and nine adjacent locations were selected for imaging. At each location, at least five images were captured at 20× magnification, each focused at a different depth within the sample. The images obtained from each location were subsequently overlaid to generate a single sharp image. Finally, the images from all locations were stitched together to produce a comprehensive high-resolution image capturing the heterogeneity of the STEX-treated samples.

2.10 Separation of fibre aggregates into fractions by size

The STEX-pretreated wood pulp was air-dried. The fibre aggregates were left undisturbed and were sieved for 5 min on a Yellow Line OS 10 orbital shaker at 300 rpm through pore sizes of 5, 2, 0.5, and 0.2 mm. Sieving

is a commonly used and easy method to characterise STEX-treated poplar wood (Shu et al., 2020).

2.11 Microscopic analysis of individual fibres

Fibre sizes were measured according to Romero et al. (2026). One gram of dry, pretreated wood fibre aggregates was transferred into a 100 mL Schott bottle. 20 mL of Franklin solution, consisting of 30% H₂O₂ and 99% glacial acetic acid, was added, and the mixture was incubated in an oven (Memmert, Schwabach, Germany) at 60°C for 48 h. The macerated fibres were then separated from the liquid by sieving. The pulp was washed five times in 50 mL of demineralised water, each time shaken manually for 1 min before being sieved over a 75 µm sieve (Endecotts LTD, London, UK). The fibres were then dispersed in water, and one droplet was mounted onto a glass slide and examined under an Olympus CX43 light microscope (Analis, Namur, Belgium). The length of the fibres was measured in Fiji (ImageJ). Five slides were examined for each biological replicate (technical replicates). On each slide, 5 to 12 intact fibres were searched and measured, totalling 33 to 42 measurements per biological replicate.

2.12 Statistical analyses

Throughout the study, CAD 4 and CAD 24 wood were compared with WT wood using unpaired t-tests based on three biological replicates. The figure captions specify whether technical or biological replicates were considered, as well as the significance level applied. The analyses assumed normal data distribution and comparable variance among the three poplar wood types.

3. Results and Discussion

The stems derived from two field-grown, genetically modified CAD-deficient poplar lines and their WT control were pretreated by STEX and enzymatically hydrolysed. For both CAD-deficient lines and the WT, three biological replicates, each comprising 40 pooled trees collected from different positions in the field, were analysed. The first step in the conversion of wood into fermentable sugars is the pretreatment of the lignocellulosic biomass, consisting of presoaking, STEX, and washing. A presoaking step is applied to improve the uniformity of the heat transfer during the subsequent STEX. The STEX pretreatment aims to increase the porosity, surface area, and permeability of the lignocellulosic biomass to make it more accessible for the subsequent enzymatic conversion. This is achieved by partially depolymerising the hemicellulose fraction, disrupting the lignin-carbohydrate complexes, and removing part of the lignin (Zhang et al., 2021).

3.1 Influence of pretreatment on poplar wood composition and mass balances

The STEX conditions applied were similar for all experiments. The severity factor (Eq. 2) was calculated for all STEX performed (Table S2). The severity factors ranged between 3.56 and 3.63, corresponding to a dispersion coefficient of 0.6%. This coefficient is sufficiently small to consider the applied STEX severities as equal.

Mass balances of the poplar stem chips, the corresponding wood pulps after STEX, and their components, i.e., cellulose, hemicellulose, and lignin, were calculated for the CAD 4, CAD 24, and WT wood by weighing and performing compositional analyses before and after the different pretreatment steps, i.e., after presoaking, STEX, and washing. This allowed estimating the yields and losses over the entire process. The results are shown as averages of the three biological replicates of the WT, CAD 4, and CAD 24 lines in Figure 1. The data for each biological replicate are presented in Figure S8. The average wood composition of the WT, CAD 4, and CAD 24, before and after STEX are presented in Figures S9 and S10. Figure S9 compares the composition of the CAD wood to the WT wood, whereas Figure S10 compares the effect of the STEX pretreatment on the composition of each wood type. The same data presented in Figures S9 and S10, but shown separately for each biological replicate, are provided in Figure S11.

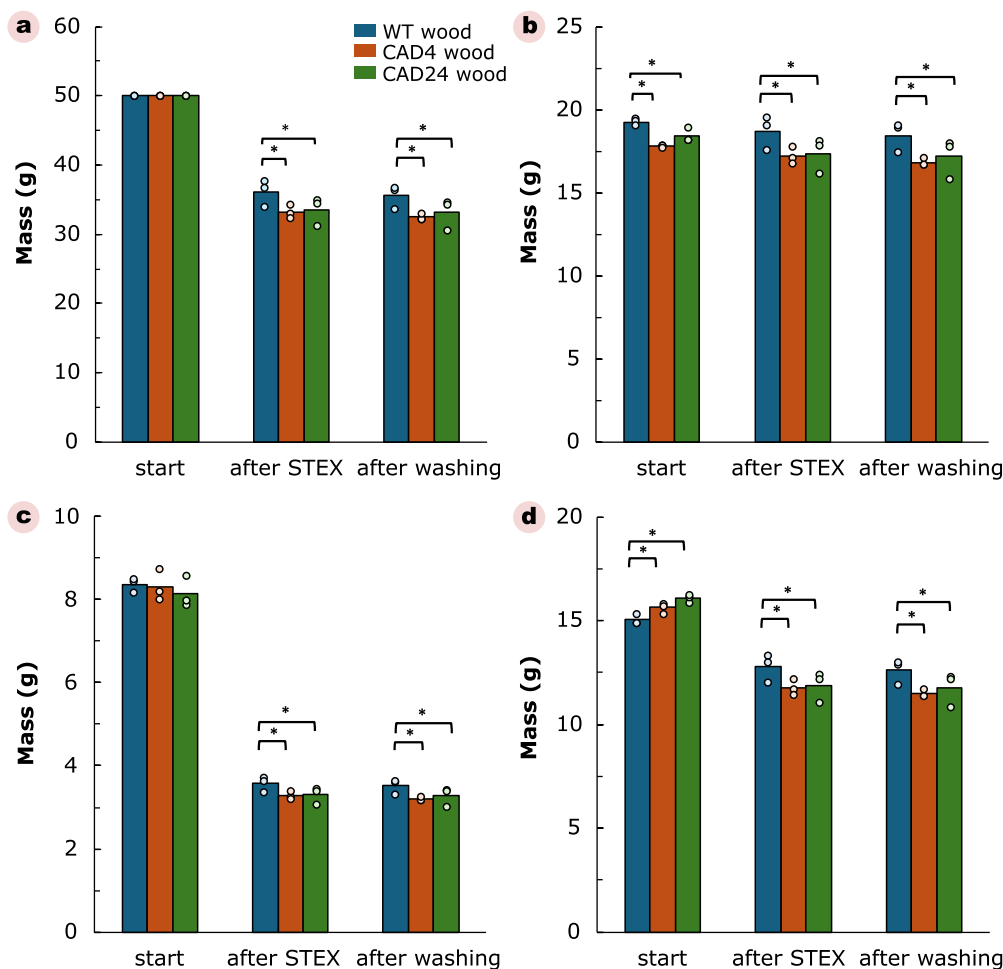


Fig. 1. Mass balances and compositional analysis of (a) dry stem biomass, (b) cellulose, (c) hemicellulose, and (d) lignin. The composition of each biological replicate was determined in triplicate. Dots represent the mean values of the three technical replicates for each of the three biological replicates. Significant differences compared to the WT, as determined by an unpaired t-test, are indicated by * ($\alpha = 0.05$).

After presoaking, the soaking liquid obtained after sieving through a steel mesh was centrifuged at 3500 rpm for 5 min to measure possible mass losses, but no solids could be pelleted. Mass losses were detected after STEEX (Fig. 1a). No further mass losses were found after washing the STEEX pretreated wood pulp (Fig. 1a).

The total lignocellulosic content of each stem biomass sample before STEEX (see Fig. 1a) was calculated as the sum of the measured masses of cellulose, hemicellulose, and lignin, presented in Figures 1b, 1c, and 1d, respectively. The average total lignocellulosic content was $85.40 \pm 2.33\%$ of the dry weight for the WT, $83.54 \pm 4.15\%$ for CAD 4, and $85.32 \pm 4.40\%$ for CAD 24. Data from literature report total lignocellulosic contents of 91% and 92% for WT *Populus alba* and *Populus tremula*, respectively (Rego et al., 2019). The fact that the material analysed here was not debarked may have resulted in a lower total lignocellulosic content and higher lignin content in the starting material (Safdari et al., 2011).

Figure 1a shows that significantly more biomass was lost after STEEX pretreatment of CAD 4 and CAD 24 compared to the WT. Figure 1b depicts that the cellulose (glucan) mass in the starting material was significantly lower in the CAD 4 and CAD 24 wood than in the WT wood (a difference of 7.6% and 4.4%, respectively). After STEEX treatment, there was still significantly less cellulose present in both CAD lines compared to the WT ($p < 0.05$). This is due to a higher loss of stem biomass from the CAD wood,

but also to a lower cellulose content after STEEX in the CAD 4 wood (see Fig. S9).

As shown in Figures 1c and S8, the hemicellulose (xylan) content before and after STEEX indicates that the removal of hemicellulose was large in all samples, and that the loss in hemicellulose was slightly but significantly greater for the CAD lines ($p < 0.05$) than for the WT, even when accounting for the greater loss in biomass in the CAD lines (Figs. S9 and S10). The removal of hemicellulose is one of the key mechanisms by which STEEX pretreatment enhances the accessibility of the lignocellulosic matrix to enzymes during enzymatic hydrolysis. However, this process also reduces the maximum theoretical yield of pentoses that can be generated during hydrolysis.

The most pronounced compositional alteration in the wood types resulting from STEEX is the change in lignin content (see Fig. 1d). Before STEEX, the CAD lines contained significantly more lignin than WT wood, while after STEEX, the CAD lines contained significantly less lignin than WT wood. The reduction in lignin content resulting from STEEX pretreatment was significantly greater for both the CAD 4 line and the CAD 24 line ($p = 0.03$ and $p = 0.02$, respectively) compared to the WT, i.e., a 25% and 26% reduction for CAD 4 and CAD 24, respectively, compared to 15% for the WT. This is partially explained by the larger wood biomass loss in the CAD lines in general, but also by a comparatively higher loss in lignin.

The cellulose and hemicellulose retention rates, as well as the lignin removal rates, are summarised in [Table S3](#). They were calculated using [Equations S1–S3](#), respectively. Of these three, only the lignin removal rate was significantly different from that of the WT for both CAD lines, as determined by an unpaired t-test ($p = 0.04$ and $p = 0.01$ for CAD 4 and CAD 24, respectively). The results indicate that the changes in lignin structure of the CAD wood made lignin more easily removable under the applied STEX pretreatment conditions, i.e., 210°C for 90 s. The applied conditions corresponded to a high temperature, short residence time, and moderate severity ([Ziegler-Devin et al., 2021](#)). These conditions were chosen not to optimise the STEX process for poplar, but rather to clearly reveal the differences in composition and enzymatic hydrolysis between the two wood types after pretreatment.

STEX is an acid-catalysed pretreatment process in which the catalyst originates from the release of organic acids from the biomass itself, a process called autocatalysis ([Deng et al., 2023](#)). The susceptibility of the lignocellulosic matrix of CAD to moderate acid-catalysed pretreatments is supported by a recent article reporting that dilute acid pretreatment results in higher cell wall deformation in CAD wood than in WT wood ([du Pasquier et al., 2025](#)). The authors suggested that this deformation is linked to the presence of more hydrophobic and shorter lignin chains and fewer non-covalent interactions between lignin and carbohydrates. Nevertheless, the authors did not observe significant changes in lignin removal after dilute acid pretreatment, unlike after the STEX pretreatment in the present study (see [Fig. 1d](#)). It is difficult to compare the severity of the two pretreatment methods, as longer times and lower temperatures were applied to the dilute acid pretreatment. The difference could potentially be due to the physical aspect of the explosion phase in the STEX pretreatment. By contrast, previous studies have shown that CAD wood is more susceptible to delignification by alkaline pretreatments than WT wood, primarily due to the increased presence of cinnamaldehydes within its lignin polymer ([Van Acker et al., 2017](#); [De Meester et al., 2022a](#)). Apparently, both the acid and alkaline pretreatments exert distinct effects on CAD wood.

3.2 Enzymatic hydrolysis after STEX pretreatment of the different poplar types

Subsequently, the effect of the genetic modification of the wood on the enzymatic hydrolysis after STEX pretreatment was evaluated. First, a screening experiment using different enzyme loadings (i.e., 8, 16, 24, and 32 FPU/g dry wood) was performed on pretreated stem biomass from block B1 of the WT and block B1 of CAD 24 in order to obtain a suitable enzyme concentration for the comparison. We aimed to convert between 50% and 80% of the cellulose for each wood type to ensure that the differences in hydrolysis efficiency between WT and CAD wood were easily revealed. The glucose yields were calculated using [Equation 5](#) ([Fig. S12](#)). Initial reaction rates were estimated by the model [Equation 6](#) and are shown in [Figure S13](#). Based on these screening results, an enzyme loading of 8 FPU/g dry wood was selected as the most suitable for our analysis. At this loading, the glucose yields were 64% for the WT and 83% for the CAD 24 wood. Following that, the selected enzyme loading was tested on the three poplar wood types. [Figure 2](#) shows the average enzymatic hydrolysis results of this experiment based on three biological repeats.

The average glucose concentrations after 96 h of hydrolysis were 28.96 ± 1.63 g/L for the WT wood, 36.65 ± 1.76 g/L for CAD 4 wood (+26%), and 36.46 ± 0.64 g/L (+26%) for CAD 24 wood. These glucose concentrations were significantly higher for both CAD lines than for the WT wood in the applied conditions, with p-values of 0.0051 and 0.0018 for CAD 4 and CAD 24, respectively, as determined by an unpaired t-test. No significant difference was detected between the two CAD lines ($p = 0.87$). The corresponding glucose yields, as calculated using [Equation 5](#), were $59.96 \pm 3.38\%$ for the WT wood, $75.87 \pm 3.63\%$ for CAD 4 (+27%), and $75.49 \pm 1.33\%$ for CAD 24 (+26%). The model estimated the maximum glucose concentrations, G_{max} , to be 35.76 ± 0.88 , 46.70 ± 1.62 , and 42.87 ± 1.05 g/L, respectively. However, these concentrations were not reached within the experimental timeframe.

Improved glucose yields after the pretreatment of CAD poplar wood in acidic conditions at an average severity were also reported by [du Pasquier et al. \(2025\)](#). Consistent with the results reported here, these authors found

that the improved enzymatic hydrolysis was attributable to differences in lignin structure rather than differences in lignin content between the two wood types. [du Pasquier et al. \(2025\)](#) suggest that the increased incorporation of aldehydes in the lignin of CAD wood leads to shorter and more hydrophobic lignin, resulting in fewer noncovalent lignin-carbohydrate interactions and, hence, fewer recalcitrant lignin-carbohydrate complexes, as also discussed by [Van Acker et al. \(2017\)](#). The lignin in CAD wood likely covers the cellulose to a lesser extent, making it more accessible to the enzymes, particularly after the hemicellulose degradation under moderately acidic conditions. Increasing the severity of the pretreatment would lead to a trade-off between higher hemicellulose degradation, reduced cellulose crystallinity and more advanced destruction of the lignocellulosic matrix on the one hand, and cellulose degradation, higher inhibitor concentrations, and potentially overcooking on the other hand ([Szadkowski et al., 2023](#)).

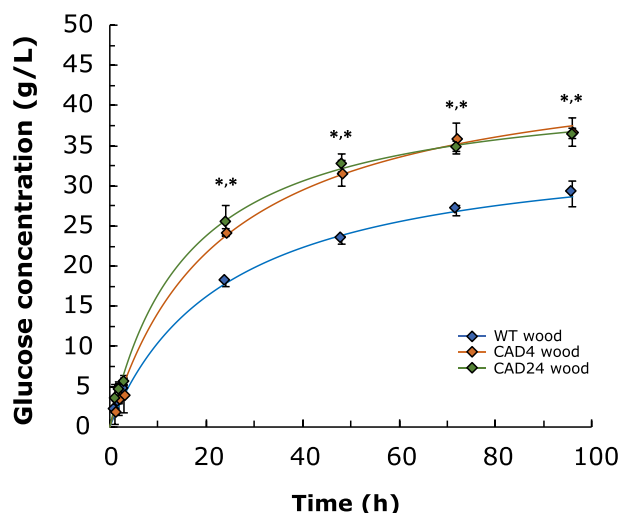


Fig. 2. Glucose production over time during enzymatic hydrolysis of STEX-pretreated WT wood, CAD 4 wood, and CAD 24 wood. — represents the fitted curve by applying the Holtzapfle model ([Eq. 6](#)). STEX conditions were 210°C – 90 s in all cases. The enzymatic hydrolysis was performed at 8.4% solid loading and 8 FPU/g wood Cellic Ctec 3 HS. Error bars represent the standard deviation of the experimental results of three biological replicates. ** indicates that the experimental value of both CAD 4 and CAD 24 is significantly higher compared to the WT wood ($\alpha = 0.05$).

Similar xylose concentrations were obtained for the CAD lines and the WT, despite the significantly higher yields observed for the CAD lines. This indicates enhanced enzymatic digestibility of the hemicellulose fraction in the CAD lines following STEX. This increase is offset by the significantly higher hemicellulose loss in the CAD lines ([Fig. 1c](#)). The initial hydrolysis reaction rates were estimated using the modified Holtzapfle model ([Eq. 6](#)) as shown in [Figure 3](#).

Based on the averages from the three biological replicates, the estimated initial reaction rates were 1.49 ± 0.084 g/L/h, 1.99 ± 0.16 g/L/h (+34%), and 2.68 ± 0.20 g/L/h (+80%) for the WT, CAD 4, and CAD 24 wood, respectively. These unpaired t-test revealed significant differences ($p = 0.0087$ and $p = 0.0007$ for CAD 4 and CAD 24 compared to the WT, respectively), indicating that CAD wood not only achieved a higher glucose concentration in this condition, but also had a higher initial reaction rate.

3.3 Glucose from biomass yields

Next, we calculated the average amount of glucose (based on three biological replicates) that could be produced from 1 kg of the original biomass under the applied conditions by extrapolation and by combining the mass balances ([Figs. 1 and S5a](#)) with the achieved glucose concentrations ([Fig. 2](#)).

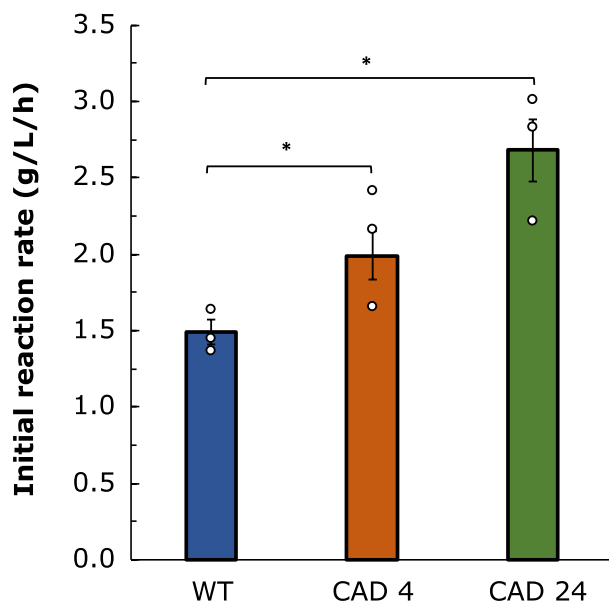


Fig. 3. Initial reaction rates during enzymatic hydrolysis of STEX-pretreated biomass as estimated by the modified Holtzapfel model (Eq. 6) based on the average model data for the wood samples. Dots represent model estimations for the data of each of the three individual biological replicates. Error bars represent the standard errors on the estimated parameter values. * indicates significant differences compared to the WT as determined by unpaired t-test ($\alpha = 0.05$).

This amounted to 245.70 ± 25.77 g for the WT, 283.59 ± 17.88 g (+15%) for CAD 4, and 295.08 ± 13.92 g (+20%) for CAD 24. Wood from both CAD lines produced significantly more glucose compared to the WT, as determined by unpaired t-tests ($p = 0.0023$ and $p = 0.0363$ for CAD 4 and CAD 24, respectively). From an industrial point of view, enhanced enzymatic hydrolysis yields either require a lower STEX severity or a lower enzyme dose to achieve a similar glucose yield. Pretreatment accounts for 11-27% of the total bioethanol production costs, while enzymes account for 16% (Ceaser et al., 2025). However, it must be noted that, despite the higher glucose yield per kg of CAD wood, CAD trees have a total biomass yield penalty amounting to 32% for CAD24 and 40% for CAD40 when grown in the field (De Meester et al., 2022a). The biomass penalty is due to the strong reduction in *CAD1* gene expression in these lines. This implies that the increase in glucose yield per kg of CAD wood does not outcompete the total biomass yield penalty. Given that the CAD trees are smaller than the WT, one possible approach would be to cultivate the engineered trees at a higher planting density to maintain an overall biomass yield per hectare comparable to that of WT trees. However, a more desirable strategy would be to eliminate the yield penalty altogether. The yield penalty can be overcome by creating lines in which *CAD1* is less severely downregulated. Indeed, genetically modified poplar lines with more modest *CAD1* downregulation had no yield penalty when grown in the field, yet they did exhibit significant improvements in kraft pulping, a highly alkaline process, due to their aldehyde-rich lignin (Pilate et al., 2002). Alternatively, the yield penalty can potentially be avoided by targeting the *CAD1* downregulation to the fibres only (Gui et al., 2020) or by creating weak alleles by CRISPR/Cas9, as shown for *CCR2* in poplar (De Meester et al., 2020).

3.4 Chemical and structural differences between WT and CAD wood

The rapid decompression step of the STEX process, achieved by suddenly opening the explosion valve between the reactor and the expansion vessel, tore the stem chips of all three wood types into fibre-like shreds, thereby producing a wet wood pulp. However, it was visually clear that smaller fibre aggregates were present in the CAD lines than in the WT

wood, despite comparable stem chip size before STEX (see Fig. S2) and similar mechanical properties of CAD wood to those of WT before STEX (Özparpucu et al., 2018). These differences in the size of the fibre aggregates were visualised in 3D image stitching pictures of the fibres from the STEX-pretreated wood samples derived from the three different biological replicates of the three poplar wood types (Fig. 4).

These microscopy pictures show that the fibre aggregates of the CAD lines appear smaller and thinner. To confirm this observation, the fibre aggregates were dried and sieved into different fractions without disrupting the aggregates. Additionally, to compare the individual fibres, the STEX-pretreated material of all poplar wood lines and blocks was macerated in Franklin solution, and the separated fibres were examined under a microscope. Their length was determined using ImageJ. The results of the sieving and microscopic analysis are shown in Figures 5a and 5b, respectively.

Figure 5a confirms a difference in fibre aggregate size distribution between the CAD 4 and CAD 24 wood and the WT wood. The data show that the STEX-pretreated CAD lines contained significantly more fibre aggregates in the two smallest size categories than the WT, although slightly more aggregates were also observed in the largest category. However, Figure 5b shows that there is no significant difference in individual fibre size between the treated CAD lines and WT wood when intact fibres are observed. A possible explanation for the increase in smaller fibre aggregates of the CAD wood after STEX is the difference in cell wall structure between the WT wood and the CAD 4 and CAD 24 wood. These differences and, more specifically, the differences in lignin structure, are well documented (Van Acker et al., 2017; De Meester et al., 2022a). The changes in lignin structure of CAD wood caused by the increased incorporation of syringaldehyde and sinapaldehyde, leading to shorter lignin polymer chains with more free phenolic end groups and conjugated carbonyl functions, making the lignin easier to break down under alkaline conditions. Lignin is also more hydrophobic, leading to fewer noncovalent associations between hemicellulose and lignin (Van Acker et al., 2017; Lapiere et al., 2004). Although the effect of STEX pretreatment on the different lignin structures in WT and CAD wood is unknown, the differences in lignin structure could contribute to the smaller fibre aggregates upon STEX. Another notable factor is that CAD wood has been reported to have thinner cell walls compared to WT wood (Nabuqi et al., 2020). In addition, a recent study showed that the wood cell walls collapsed after severe dilute acid pretreatment and that the effect was significantly greater for CAD wood than for WT wood (du Pasquier et al., 2025). This observation suggests that when most hemicellulose is hydrolysed, as is the case in the acid conditions during the incubation phase of the STEX pretreatment, CAD wood cells are less capable of maintaining the cell shape compared to WT wood cells (du Pasquier et al., 2025).

Comparing the enzymatic hydrolysis results obtained for WT poplar wood in this study with published data for poplar wood is not straightforward for several reasons. First, in most cases, wood samples from other poplar species, grown in other environments, were analysed, implying that the starting material was different. Second, the CAD biomass analysed here was chopped biomass from whole stems, including bark and wood. This material was chosen over ground debarked stem samples because chipped whole stems reflect better the type of biomass to be processed in future biorefineries. That said, it is important to note that the hydrolysis yield of wood and bark is different. Van Acker et al. (2014) showed that the saccharification yield of bark samples is only about half that of wood samples from the same poplar genotype as analysed here (*P. tremula* x *P. alba* cv. 717 1B4). They also showed that downregulation of cinnamoyl CoA reductase (CCR) in poplar, which leads to reduced lignin content, enhanced the saccharification yield in wood but not in bark (Van Acker et al., 2014). Differences in biomass type (ground debarked wood vs. chipped whole stem) and growth conditions (greenhouse-grown vs. field-grown) complicate direct comparisons of the magnitude of improvement in saccharification yield across studies and modified lines.

Third, different pretreatment and enzymatic hydrolysis conditions were applied. The STEX conditions employed in the present study involved high temperatures, short times, and average severities (Wu et al., 1999; Jacquet et al., 2015). The enzymatic hydrolysis conditions we used aimed to achieve average glucose concentrations to investigate whether CAD wood is easier

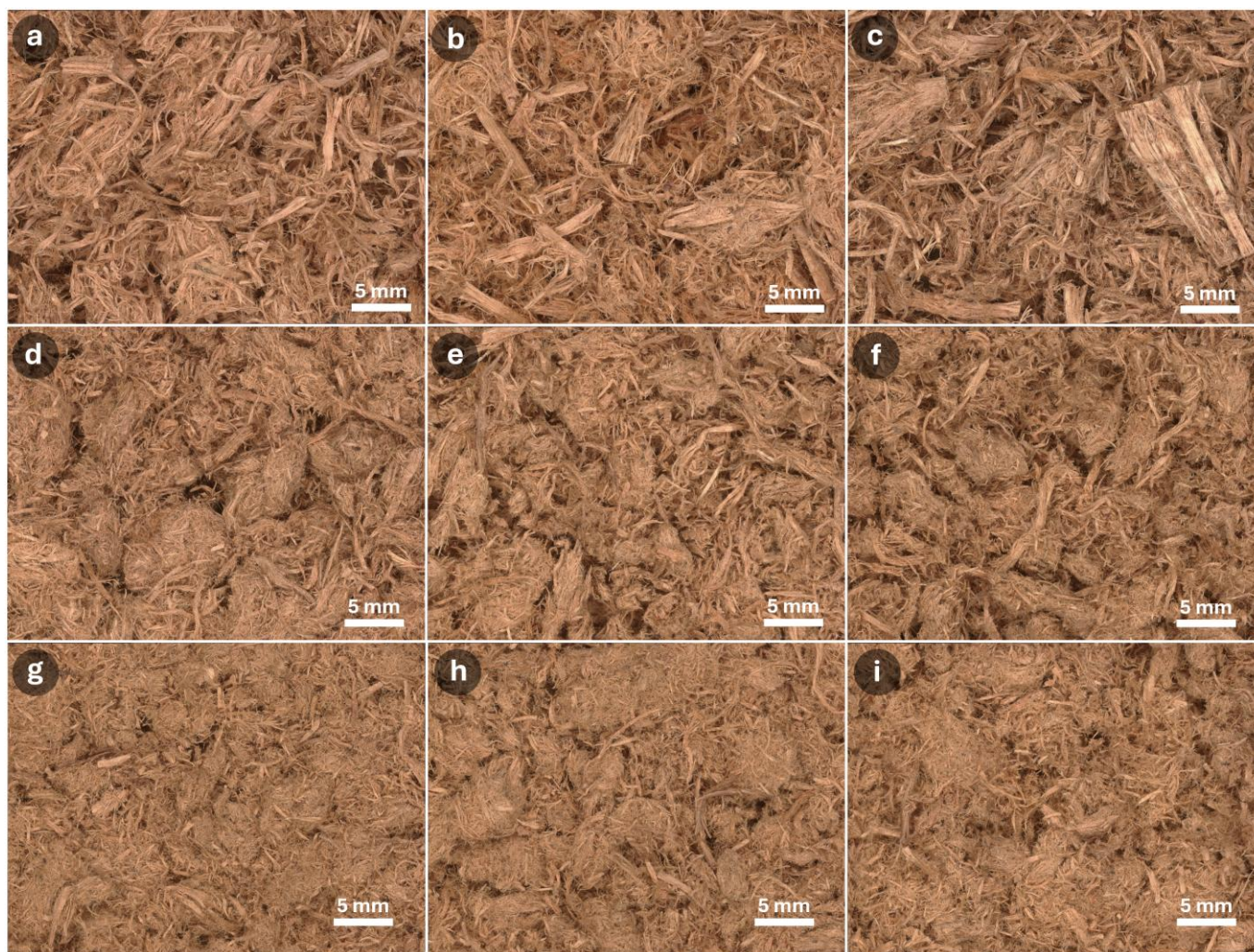


Fig. 4. 3D image stitching of light microscopy pictures at 20 × magnification of STEX-pretreated poplar wood taken using a Keyence VHX-7000 digital microscope. (a) WT B1, (b) WT B4, (c) WT B5, (d) CAD 4 B4, (e) CAD 4 B5, (f) CAD 4 B6, (g) CAD 24 B1, (h) CAD 24 B2, and (i) CAD 24 B3.

to hydrolyse than WT wood upon STEX (Pažitný et al., 2020; Antczak et al., 2022). A single study by Mansfield et al. (2012) reports on the effects of STEX on the enzymatic hydrolysis yield of genetically modified poplar wood, in which either *F5H* was overexpressed (C4H::F5H) or *C3'H* was downregulated (C3'H-RNAi). These poplars had a significant shift in monolignol composition; lignin of the C4H::F5H lines had an increased frequency of S-units, but similar total lignin amounts, whereas the C3'H-RNAi-suppressed poplar lines contained more H-units at the expense of G-units, as well as less total lignin. The authors reported that the reduction in total lignin content in the C3'H-RNAi-suppressed poplar contributed more substantially to the increased enzymatic hydrolysis yield than either the higher S/G ratio in the C4H::F5H lines or the greater abundance of H-units in the C3'H-RNAi-suppressed poplar lines. Enzymatic hydrolysis yields in the applied conditions were 76% for the WT and 85.2% for the C4H::F5H transgenic line. However, solid loadings were very low at 2%, making it difficult to compare the data with our results. Despite the differences in lignin structure in the C4H::F5H and also lignin amount in the C3'H-RNAi-suppressed lines reported by Mansfield et al. (2012), lignin was not more efficiently removed during STEX in these poplar lines. Conversely, our research findings revealed that significantly more lignin was removed in the CAD lines than in the WT. However, the relative lignin contents of the CAD wood were similar to those of the WT after STEX. Despite similar total

lignin amounts, the enzymatic hydrolysis was improved.

A key difference in lignin structure between the CAD lines, C4H::F5H lines, C3'H-RNAi lines, and most other lignin-modified lines is that higher amounts of syringaldehyde and sinapaldehyde are incorporated into the lignin polymer. The incorporation of sinapaldehydes in the lignin polymer is expected to result in a more hydrophobic lignin because when sinapaldehyde incorporates into the lignin polymer, aromatisation by elimination of the proton on the C8 position outcompetes nucleophilic addition by water. The more hydrophobic lignin will have fewer non-covalent interactions with hemicelluloses. Likewise, nucleophilic attack by other nucleophiles such as alcohol or carboxylic acid groups from hemicellulose will also be hampered, reducing the creation of benzyl ether or benzyl ester bonds that putatively contribute to recalcitrant lignin-carbohydrate complexes (Mottiar et al., 2016; Van Acker et al., 2017). Such a reduction in lignin-carbohydrate complexes may be the cause of the easier lignin removal during the STEX pretreatment. Likewise, it may increase access to the hydrolysing enzymes.

The conditions applied by Mansfield et al. (2012) were very different from those applied here for both the pretreatment step (addition of SO₂, different severity, and different temperature and time altogether) and the enzymatic hydrolysis step (different solid loading, different enzyme loading, and a different enzyme complex). Nevertheless, both our data and

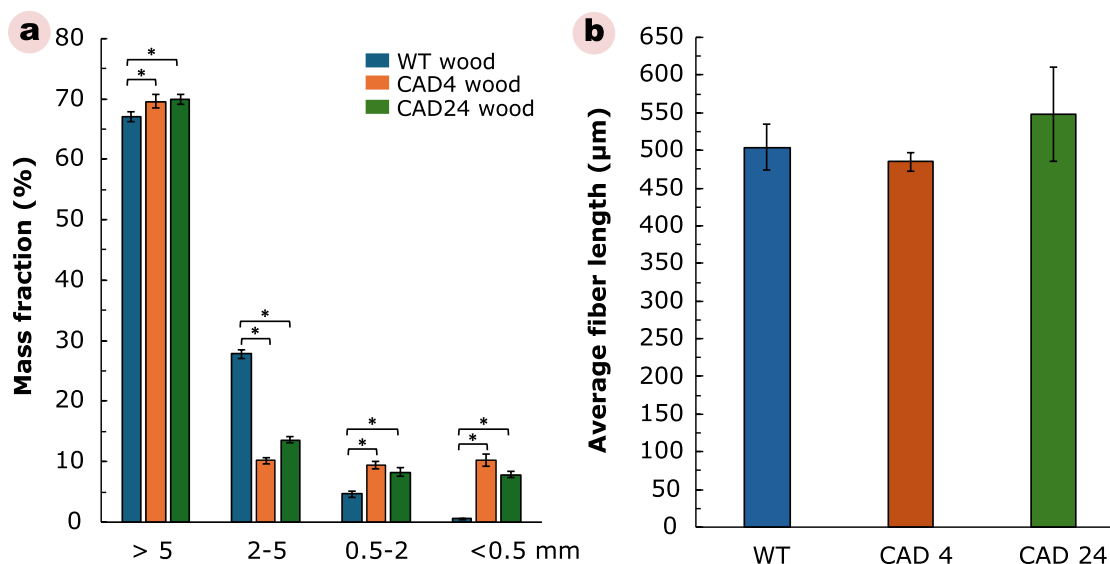


Fig. 5. (a) fibre aggregate size after STEEX pretreatment of WT wood, CAD 4, and CAD 24 as determined by sieving through different pore sizes. Error bars represent the standard deviation of three biological replicates. **(b)** individual fibre size as determined microscopically: WT wood, CAD 4, and CAD 24. Error bars represent the standard deviation on three biological repeats. Each biological replicate (block) was determined on 5 different microscopic slides, by measuring 5 to 12 fibres (technical replicates) * indicate significant differences compared to the WT as determined by unpaired t-test ($\alpha = 0.05$).

those of Mansfield et al. (2012) show that lignin can be engineered to improve enzymatic hydrolysis after STEEX pretreatment. Our data further motivate the interest in so-called designer lignins, in which foreign lignin monomers are introduced specifically to improve the deconstruction of lignocellulosic biomass (Mottiar et al., 2016).

4. Conclusions and Outlook

Wood from three-year-old, field-grown *CAD*-deficient poplar showed 25% delignification upon STEEX compared to 15% for the WT wood, resulting in significantly more small fibre aggregates, and also yielded significantly higher glucose yield upon enzymatic hydrolysis: 76% compared to 60%, respectively. The improved enzymatic hydrolysis results were not caused by different lignin contents after STEEX, but likely by the different lignin composition and the associated thinner wood cell walls. Using wood from *CAD*-deficient trees may reduce processing cost in a biorefinery approach and may contribute to the needed transition from a fossil-based to a bio-based economy. It is important to note that the poplar hybrid used for transformation, *Populus tremula* x *P. alba* cv. 717-1B4 is not a commercial hybrid, but a poplar clone that is easily genetically transformed by *Agrobacterium tumefaciens*. For commercial deployment, elite tree genotypes will need to be transformed, whether from the *Populus* genus or from another wood-producing genus like *Eucalyptus*. When a similar genetic engineering strategy is used as illustrated in this paper, i.e., based on RNA interference, the deployment strategy of the transgenic trees will need to comply with the current regulations concerning the introduction of genetically modified plants into the environment. However, the EU is currently advancing legislation that would exempt certain gene-edited plants lacking foreign DNA from many of the regulatory requirements applied to conventional genetically modified plants, potentially facilitating the commercialisation of CRISPR-edited lines.

Editing strategies that avoid the stable introduction of foreign DNA exist for a variety of species, including poplar (Hoengenaert et al., 2025). As the world faces challenges with climate change and geopolitical instability, alternatives to fossil resources to produce fuels and products are needed. Genetic modification and gene-editing are promising approaches to tailor plants to human needs and are considered similarly safe as conventional breeding strategies (Boerjan and Strauss, 2024). For biofuels, poplar is considered a promising feedstock given its favourable global warming

potential compared to fossil resources. The largest contributor to greenhouse gas emissions is the biomass conversion due to the use of chemicals (Morales-Vera et al., 2022). Our lignin engineering approach precisely addresses this hurdle.

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Author Contributions

Jordi Geerts: conceptualisation, design of experiments, methodology, investigation, data collection, visualisation, writing: original draft and review and editing, **Tim Croes:** data collection, review and editing **Paulien Geertje Corlijn Leemans:** visualisation, review and editing, **Aurore Richel:** Funding acquisition, project administration, review and editing, **Arnaud Besserer:** resources, review and editing, **Nicolas Brosse:** methodology, resources, supervision, review and editing, **Barbara De Meester:** Conceptualisation, design of experiments, methodology, data collection, review and editing **Wout Boerjan and Iris Cornet:** conceptualisation, design of experiments, methodology, investigation, preparation, writing – review and editing, supervision, funding acquisition, resources.

Conflict of Interest

The authors declare that they have no conflicts of interest to disclose.

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Supplementary Information

Table S1.
Mass of the wood at the start of the experiment (dry), after soaking (wet), and after STEX (wet). Values represent the averages and standard deviations of three biological replicates. Underlined values indicate a significant difference compared to the wild type at $\alpha = 0.05$ as determined by an unpaired T-test.

Parameter	WT	CAD 4	CAD 24
Mass start (g)	50.00 ± 0.00	50.00 ± 0.00	50.00 ± 0.00
Mass after soaking (g)	119.99 ± 4.53	126.44 ± 7.13	<u>132.39 ± 1.64</u>
Mass after STEX (g)	354.42 ± 30.15	<u>424.60 ± 12.38</u>	<u>428.23 ± 14.67</u>

Table S2.
Severity factor (S^0) [-] per steam explosion* applied as calculated using Equation 2.

Sample	Severity factor (S^0)
WT wood, B1 (Fig. S9)	3.59
WT wood, B1	3.59
WT wood, B4	3.63
WT wood, B5	3.62
CAD 4 wood, B4	3.62
CAD 4 wood, B5	3.56
CAD 4 wood, B6	3.56
CAD 24 wood, B1 (Fig. S9)	3.57
CAD 24 wood, B1	3.56
CAD 24 wood, B2	3.59
CAD 24 wood, B3	3.58

* The temperature-over-time profile for each steam explosion is available upon request.

Table S3.
Cellulose and hemicellulose retention rate and lignin removal rate during STEX of the different poplar wood types, as calculated by Equations 1-3, respectively. Values represent the averages and standard deviations of three biological replicates. The compositional analysis was performed in threefold for each biological repeat (three technical repeats). Underlined values indicate a significant difference compared to the wild type at $\alpha = 0.05$ as determined by an unpaired T-test.

Parameter	WT	CAD 4	CAD 24
Cellulose retention rate (%)	97.07 ± 3.77	96.68 ± 6.97	94.19 ± 3.88
Hemicellulose retention rate (%)	42.64 ± 2.45	39.55 ± 3.10	40.65 ± 1.78
Lignin removal rate (%)	14.98 ± 2.87	<u>24.63 ± 4.80</u>	<u>26.10 ± 3.17</u>

Equations:

$$Cellulose\ retention\ rate\ (\%) = \frac{m_{cellulose\ after\ STEX}\ (g)}{m_{cellulose\ before\ STEX}\ (g)} \times 100\%$$

Eq. S1

$$Hemicellulose\ retention\ rate\ (\%) = \frac{m_{hemicellulose\ after\ STEX}\ (g)}{m_{hemicellulose\ before\ STEX}\ (g)} \times 100\%$$

Eq. S2

$$Lignin\ removal\ rate\ (\%) = \frac{m_{lignin\ before\ STEX}\ (g) - m_{lignin\ after\ STEX}\ (g)}{m_{lignin\ before\ STEX}\ (g)} \times 100\%$$

Eq. S3

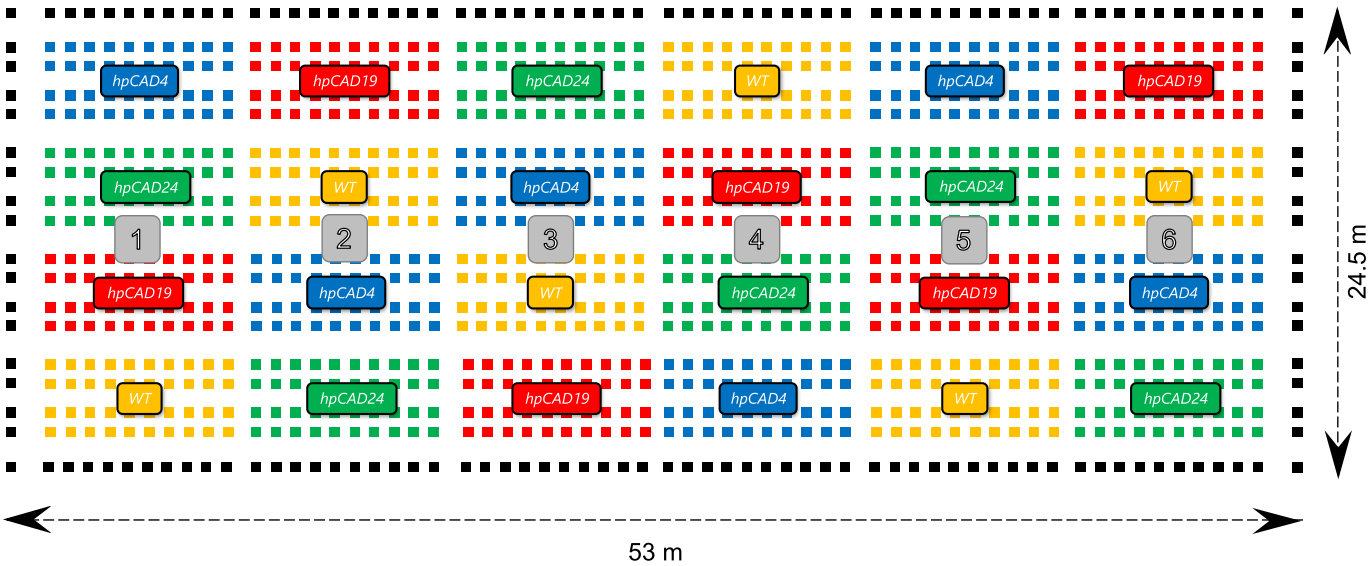


Fig. S1. Plan of the field trial consisting of six randomized blocks, each block containing 40 clonal replicates per line (WT, yellow; *hpCAD4*, blue; *hpCAD19*, red; *hpCAD24*, green). A border line of WT trees is indicated in black and republished from New Phytologist.

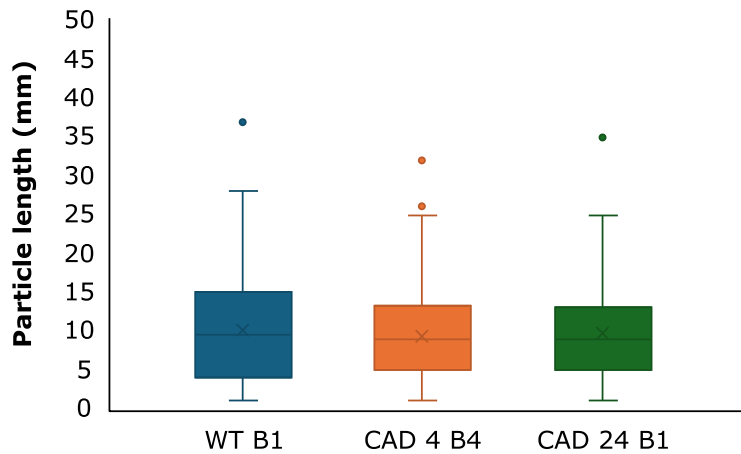


Fig. S2. Distribution of the stem biomass chip length. The length of all stem biomass chips longer than or equal to 1 mm in 10 g of the shown materials was measured (n = 186 for WT, n = 210 for CAD 4 B4, and n = 174 for CAD 24 B1).

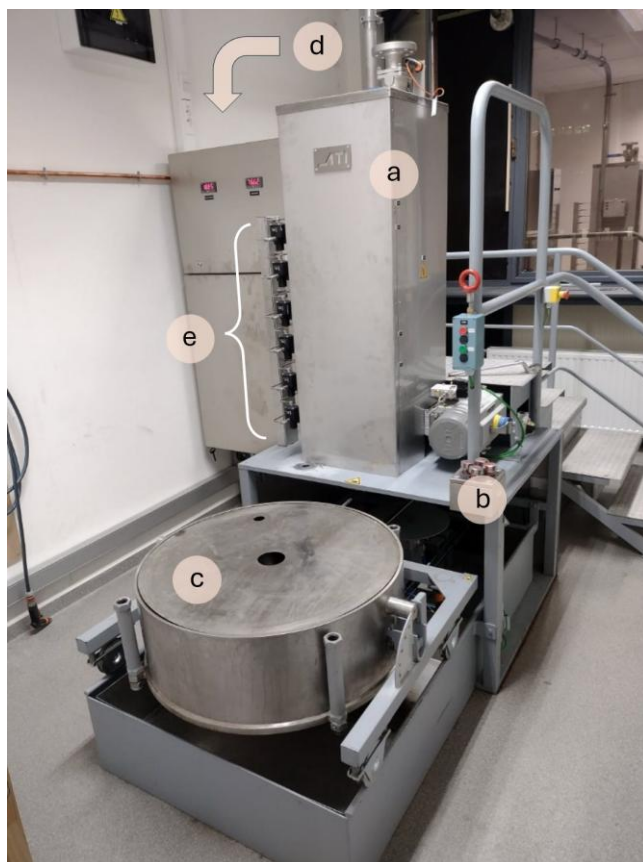


Fig. S3. Steam explosion equipment applied in this article: (a) Vertical reactor, covered by insulation, an electrical heating mantle, and the steam introduction equipment; (b) Explosion valve; (c) Retractable expansion vessel; (d) Steam generator (at the back, not visible), and (e) Steam introduction equipment.

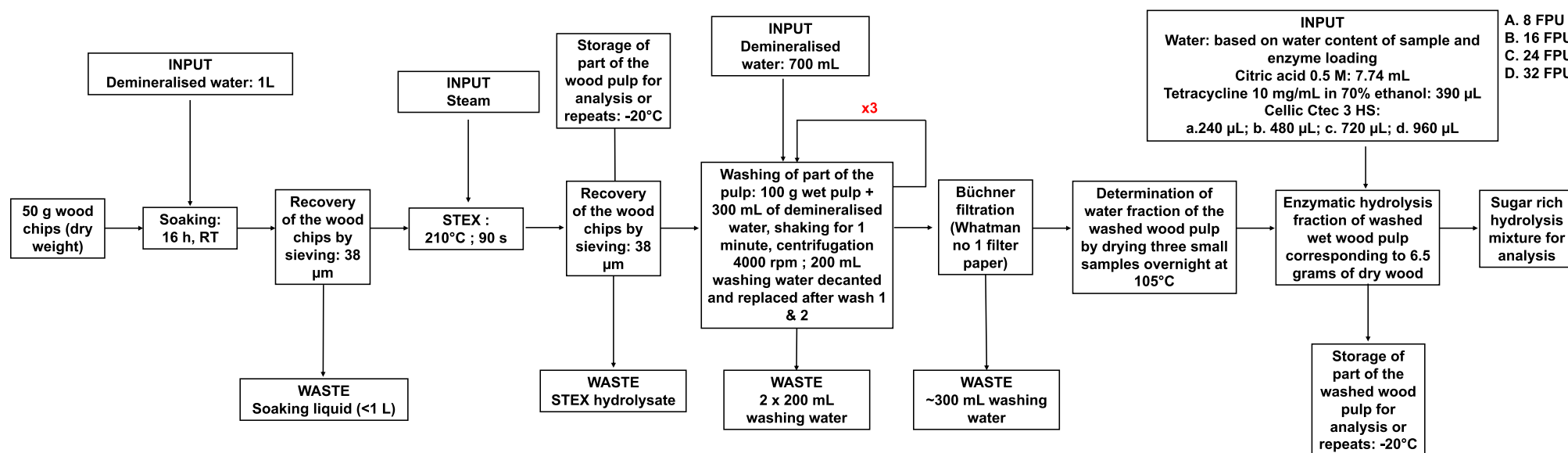


Fig. S4. Flowchart of the applied process conditions in the soaking – STEX – washing – enzymatic hydrolysis process.

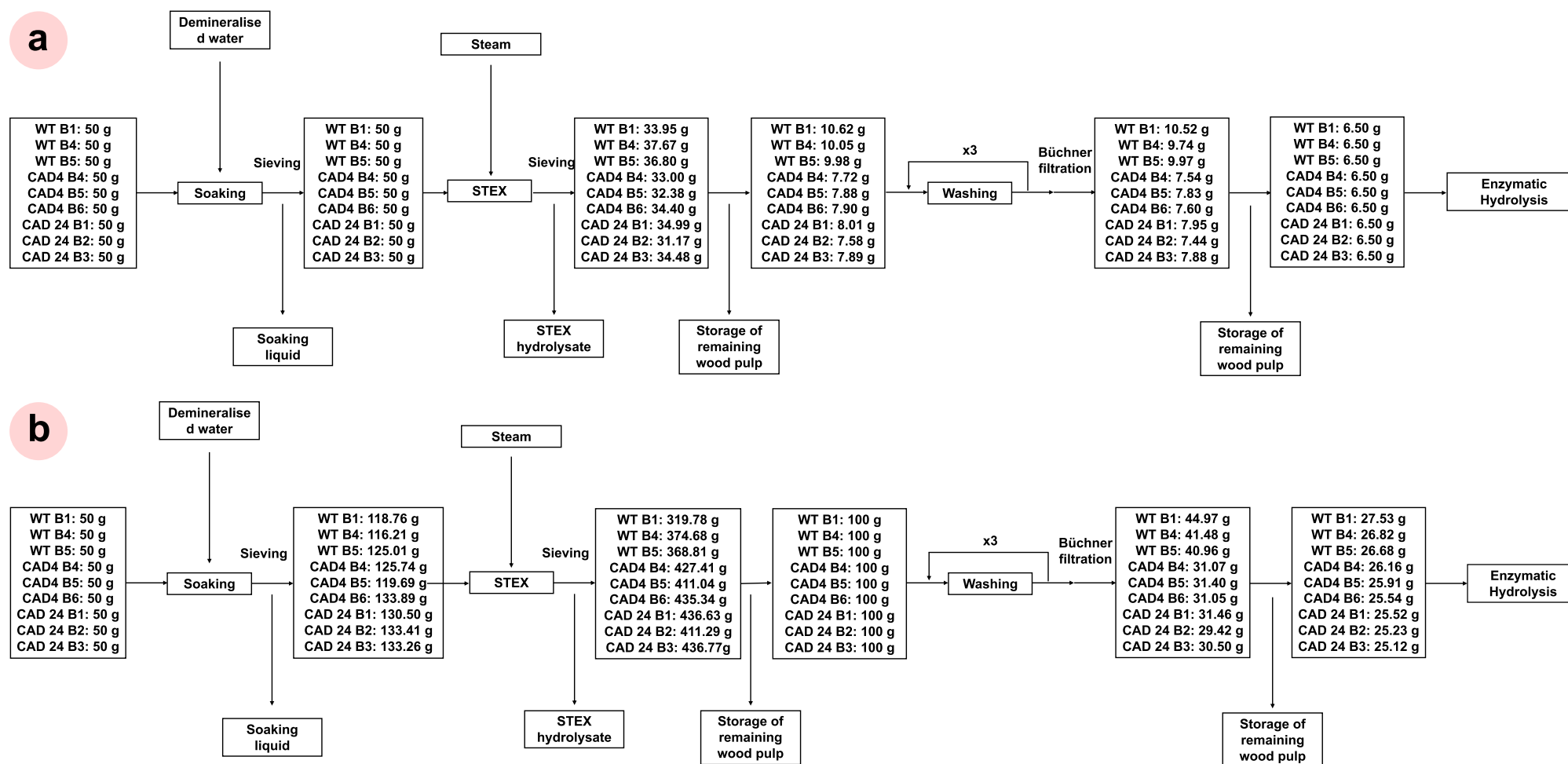


Fig. S5. Simplified process flowchart indicating the mass of each sample separately after every process step. (a) dry weight and (b) wet weight.

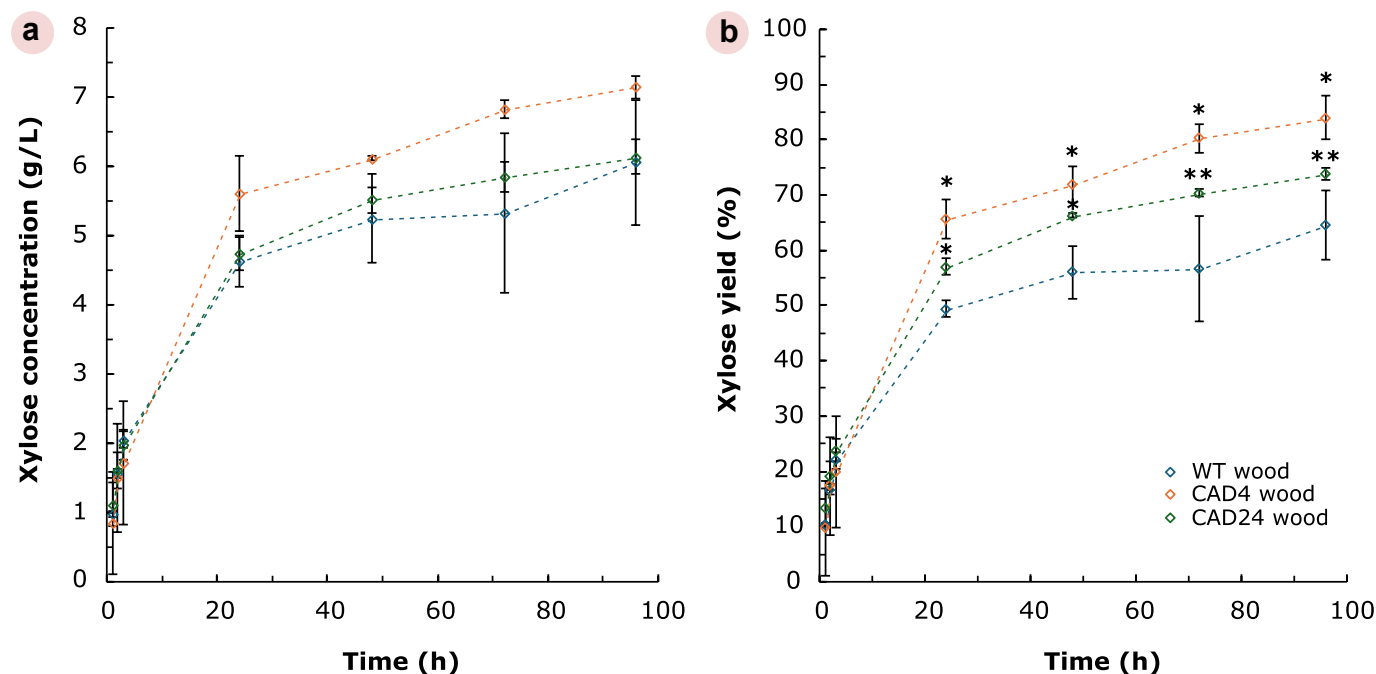


Fig. S6. Supplementary figure to Figure 2. (a) xylose concentration and (b) xylose yield during enzymatic hydrolysis of WT wood, CAD 4 wood, and CAD 24 wood. Error bars represent the standard deviation on three biological replicates. * represents a significant difference compared to the WT at $\alpha = 0.05$. ** represents a significant difference at $\alpha = 0.10$ as determined by an unpaired t-test. Celltec 3 HS was applied as the cellulase complex. The enzymatic hydrolysis was performed at 8.4% solid loading. The enzyme loading was 8 FPU/g (cellulase activity).

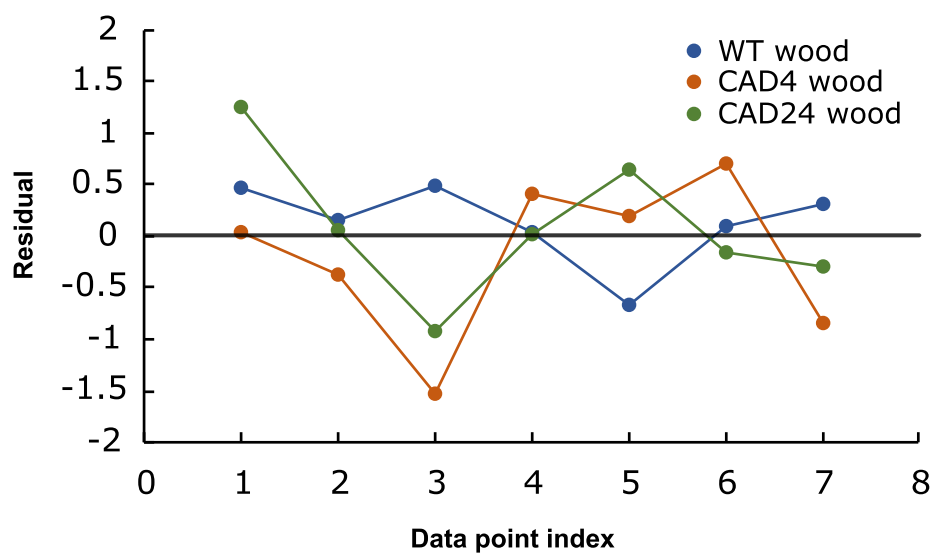


Fig. S7. Residual plot presenting the difference between experimental data and model data for the modified Holtzapple model as applied in Figures 2 and 3 in the main text. WT, CAD 4, and CAD 24. Data points represent the difference between the model values and experimental values (averages of three biological replicates) at 1, 2, 3, 24, 48, 72, and 96 h of hydrolysis, respectively.

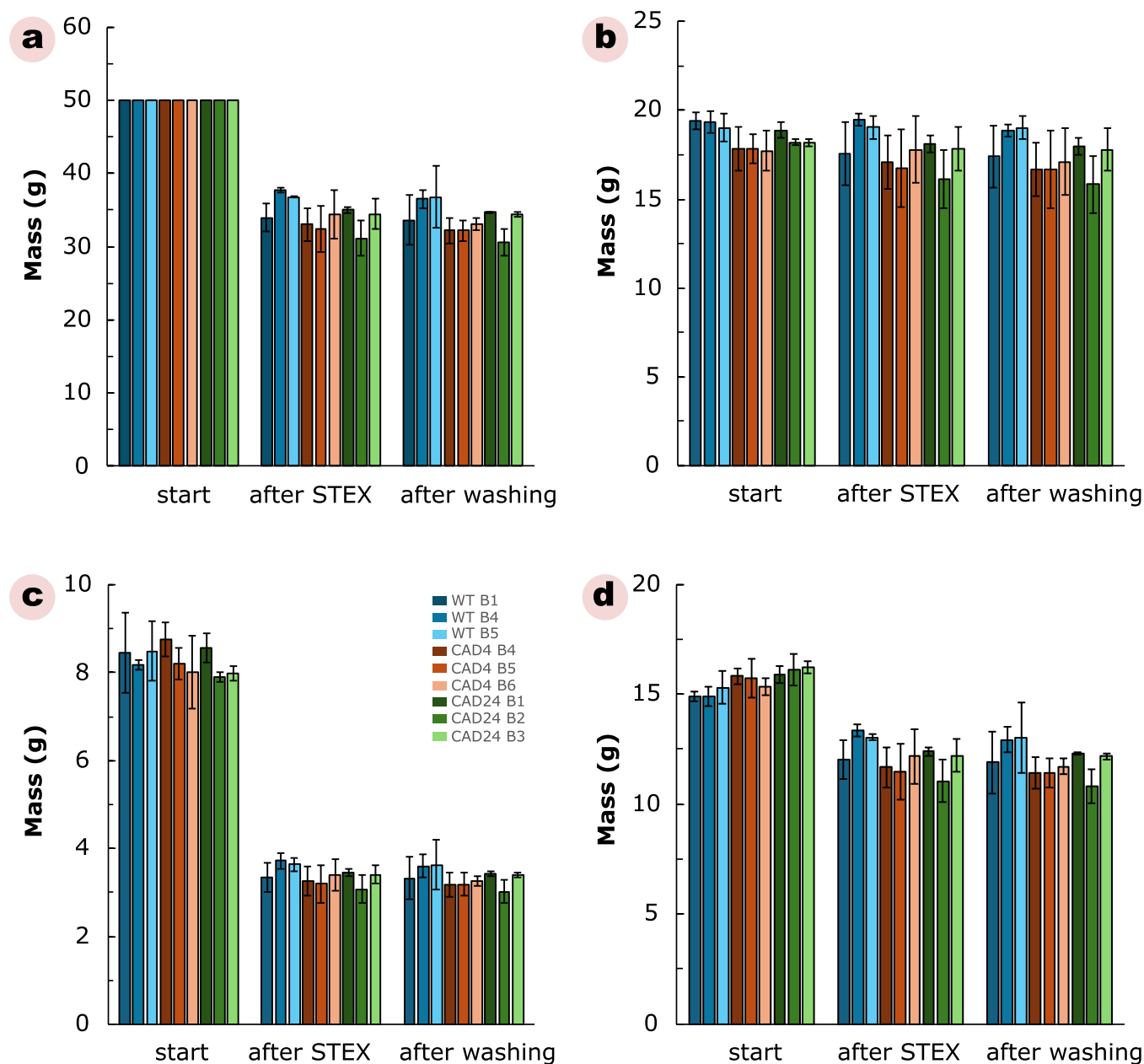


Fig. S8. Mass balances and composition analysis of (a) dry stem biomass, (b) cellulose, (c) hemicellulose, and (d) lignin. Error bars represent the standard deviation on three technical replicates. These are the same data as in Figure 1, but here the values of the individual biological replicates, corresponding to the different blocks in the field, are presented.

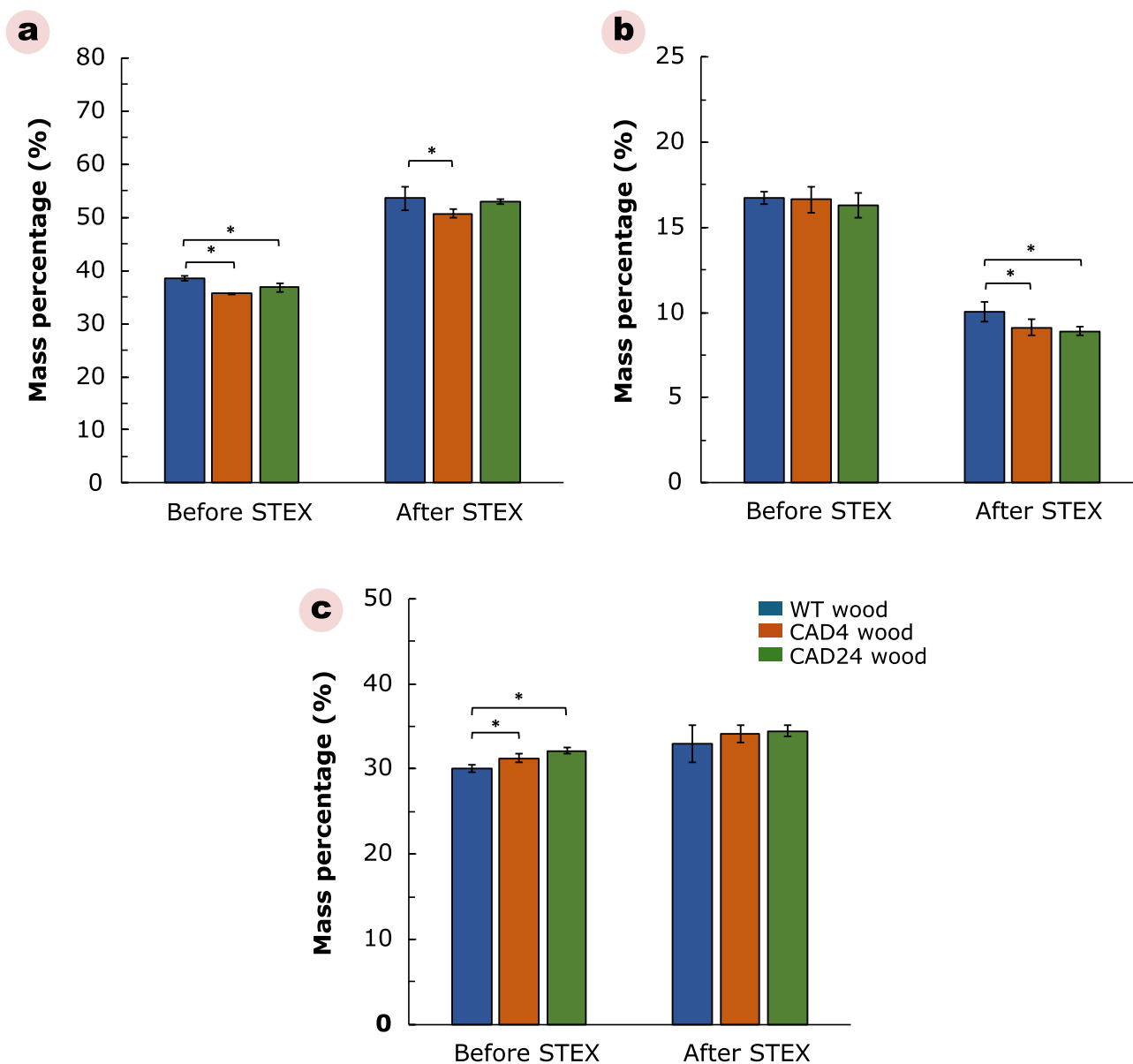


Fig. S9. Comparison of the composition of the stem biomasses before and after STEX. (a) cellulose, (b) hemicellulose, and (c) lignin. Error bars represent the standard deviation of the averaged data of three biological replicates. * indicates a significant difference as determined by unpaired T-test ($\alpha = 0.05$). These are the same data as in Figure S10, but here the CAD stem biomasses are compared to the WT stem biomass.

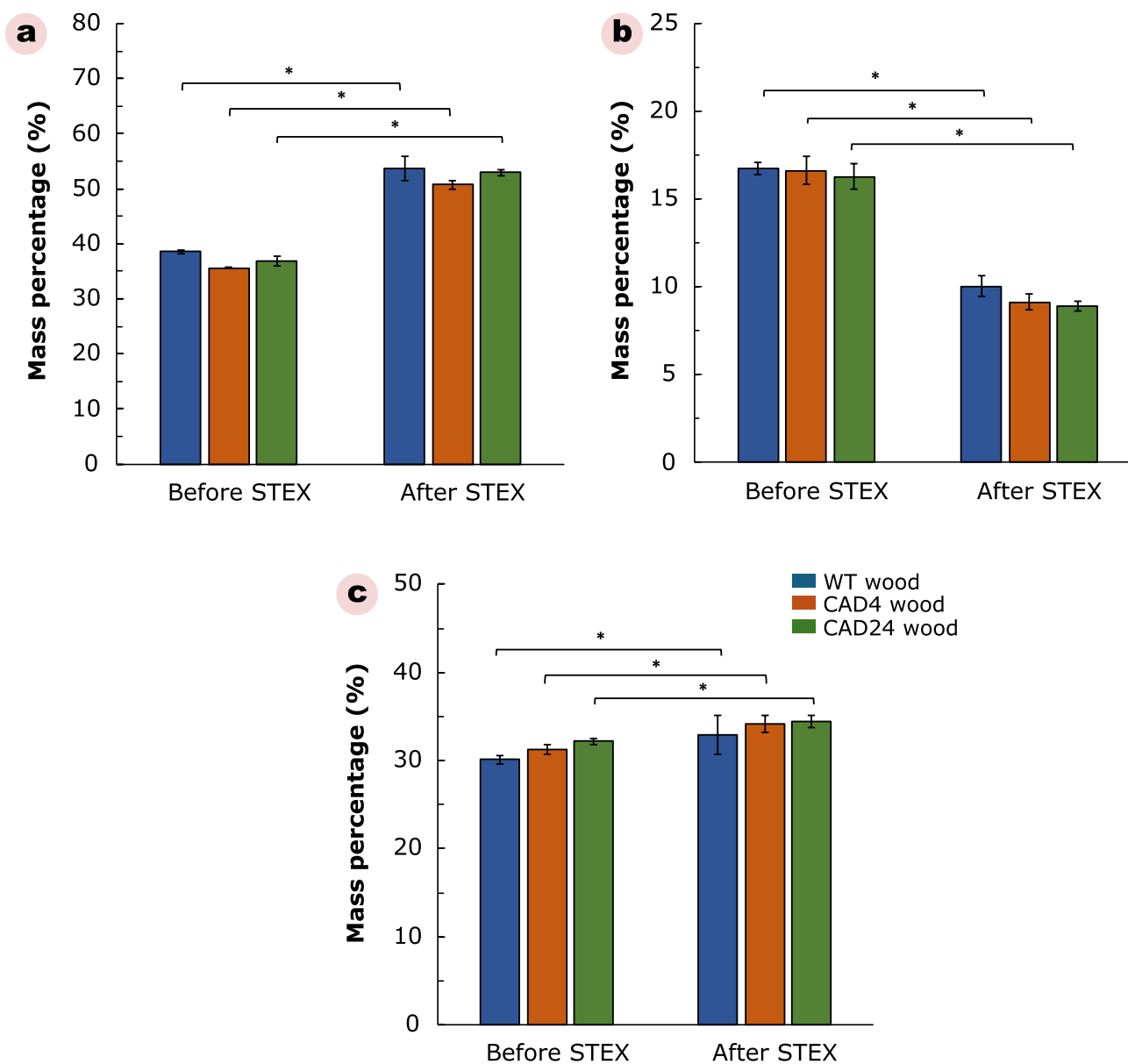


Fig. S10. Comparison of the composition of the stem biomasses before and after STEX. (a) cellulose, (b) hemicellulose, and (c) lignin. Error bars represent the standard deviation of the averaged data of three biological replicates. * indicates a significant difference as determined by unpaired T-test ($\alpha = 0.05$). These are the same data as in Figure S9, but here the effect of STEX pretreatment is compared for the corresponding stem biomasses.

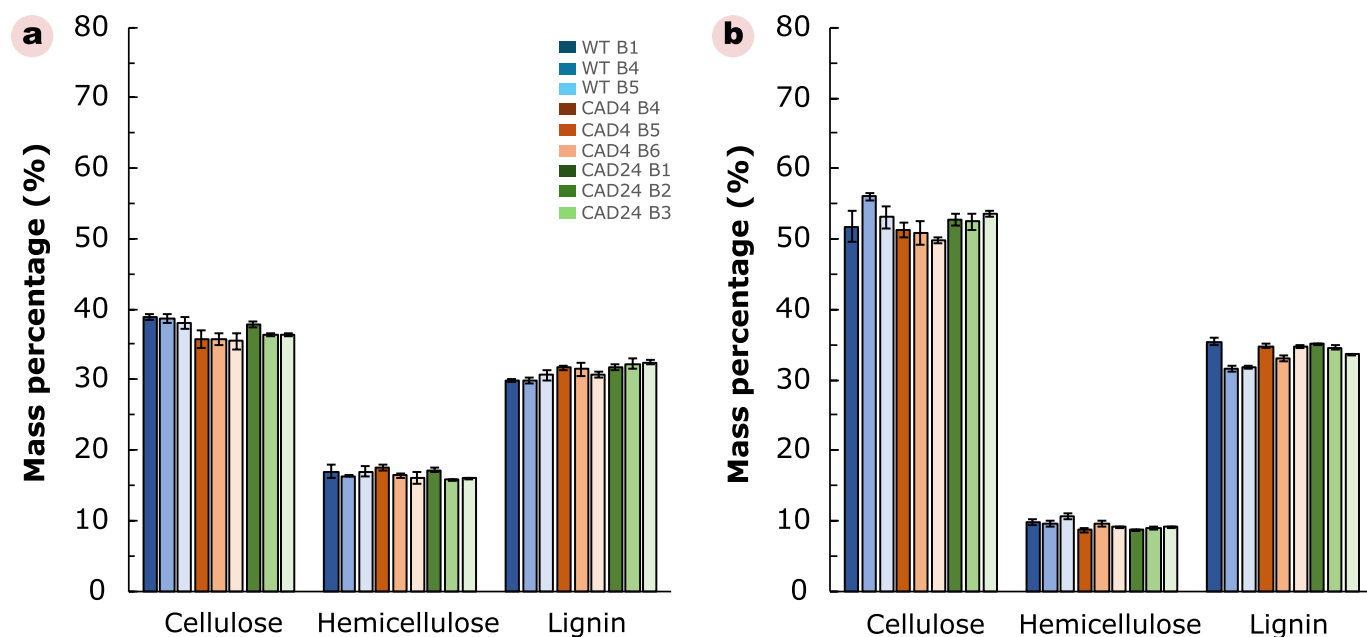


Fig. S11. Comparison of the composition of stem biomasses for each biological replicate. **(a)** Before STEX, and **(b)** after STEX. Error bars represent the standard deviation on three technical replicates. These are the same data as in [Figures S8 and S9](#), but here the values of the individual biological replicates, corresponding to the different blocks in the field, are presented.

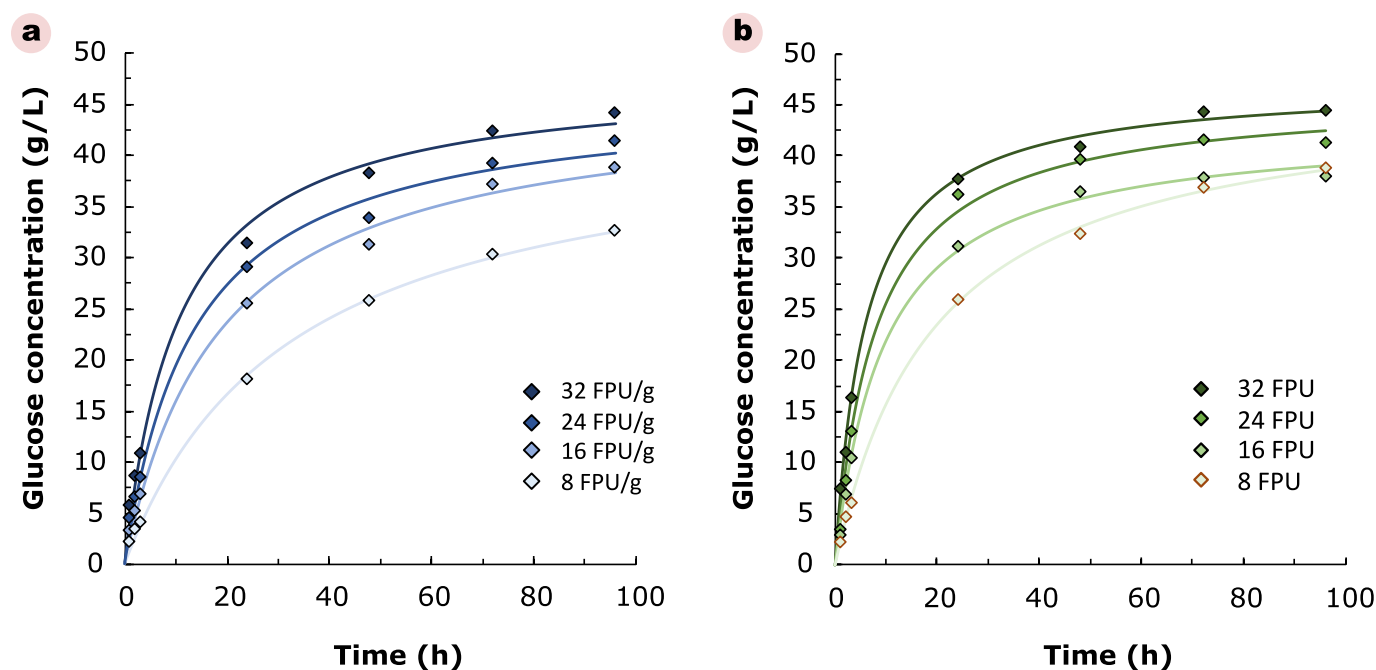


Figure S12. Enzymatic hydrolysis of poplar wood; screening experiment. Glucose production over time during EH of STEX treated **(a)** WT wood, B1; and **(b)** CAD-line 24, B1. The fitted curve obtained by applying the Holtzapfle model, as described in [Equation 5](#), is presented. STEX conditions were 210°C – 90 s in all cases. Cellic Ctec 3 HS was applied as the cellulase complex. The enzymatic hydrolysis was performed at 8.4% solid loading.

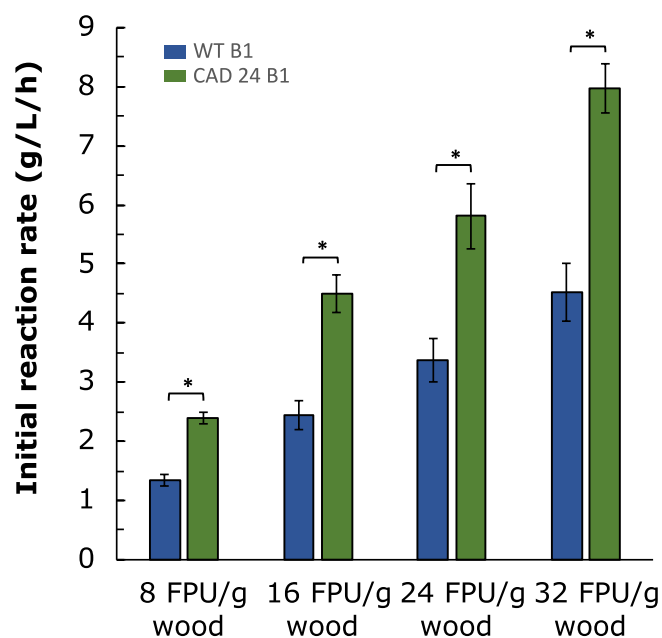


Fig. S13. Initial reaction rates during enzymatic hydrolysis of STEX-treated poplar wood in function of applied enzyme concentration as estimated by the modified Holtzapple model (Eq. 5): WT wood, B1; CAD-line 24, B1. Error bars represent the standard errors on the estimated parameter values. * indicate significant differences compared to the WT as determined by unpaired t-test ($\alpha = 0.05$).