

Revisiting Lignocellulosic Biomass Pretreatment: Water-based Deconstruction Using Heterogeneous Solid Acids

Background/Objective

- Dilute acid pretreatment works, but corrosive acids can't be recovered and create microbe-inhibiting byproducts.
- Test a reusable solid acid, zirconium phosphate (ZrP), as a water-based replacement across feedstocks.

Approach

- Team pretreated sorghum, poplar, and pine with ZrP in water at 120–160 °C, then used enzymes to release sugars.
- Sugar streams fed engineered microbe *R. toruloides* to make bisabolene, a biofuel precursor, with no cleanup step.

Results

- ZrP released up to 94% of glucose from sorghum and 80–90% of xylose across all three feedstocks; poplar glucose rose to ~70%.
- ZrP-derived sugars yielded 800 mg/L bisabolene, beating the 500 mg/L lab-medium control.

Significance/Impacts

- Recoverable, non-corrosive solid acid could cut washing, waste salt, and costly acid-resistant reactors for biofuels.
- Links JBEI deconstruction and conversion: one process feeds sugars and lignin-derived acids to *R. toruloides*



Figure caption: Illustration of the shift from conventional mineral acid pretreatment to a greener, aqueous approach based on solid acid catalysts. Using the image of a balance scale, it emphasizes the substitution of corrosive liquid sulfuric acid with reusable zirconium phosphate in the pretreatment of lignocellulosic biomass. The graphic conveys that heterogeneous solid acids can achieve hydrolysis performance comparable to traditional methods while also allowing easy catalyst recovery and producing sugars that are highly compatible with downstream biological processes.

A Conceptual Framework for Uncertainty-informed system Boundary Expansion in Life Cycle Assessment

Background/Objective

- Life cycle assessment (LCA) boundaries are set by judgment, so missed upstream impacts often go unmeasured.
- Authors set out to build a quantitative, repeatable rule for which processes to include, expand, or omit.

Approach

- Built an algorithm that expands a product's supply chain step by step, flagging hotspots by impact and uncertainty.
- Tested it on 200 synthetic supply-chain trees per setting, varying cut-off threshold, data quality, and impact spread.

Results

- The cut-off threshold was the main driver of model size; lower thresholds built larger systems with less error.
- Uncertainty-aware rules cut error most with poor data; focusing on main supply chains can miss spread-out impacts.

Significance/Impacts

- Makes LCA boundary choices documented and repeatable, improving trust in bioenergy and bioproduct footprints.
- Strengthens JBEI's life-cycle modeling and lays groundwork for AI-assisted LCA automation.

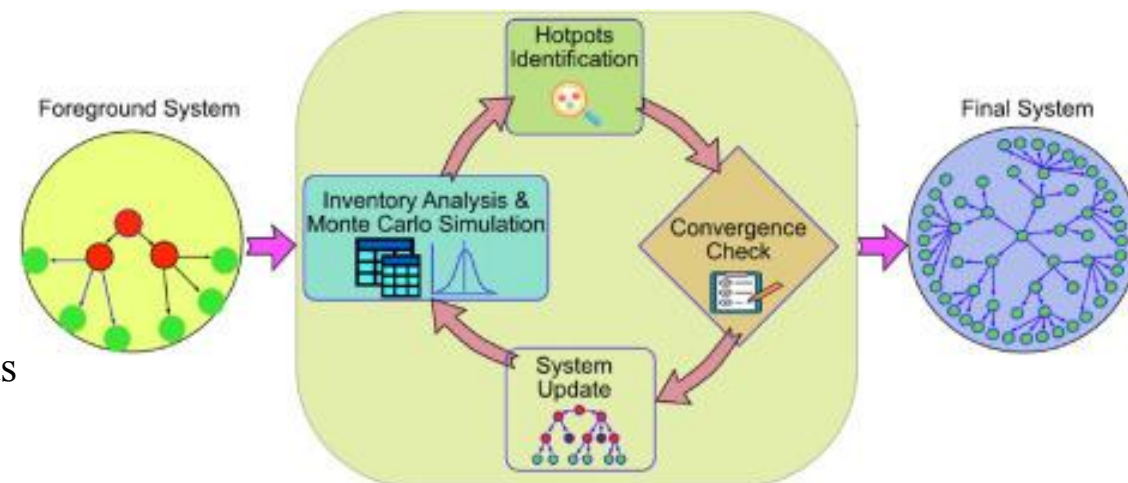


Figure caption: The framework begins with an initial foreground product system containing primary supply chain processes. Each iteration propagates input and emission intensity uncertainties through the active system via inventory analysis and Monte Carlo simulation, then identifies hotspots by comparing each process's mean contribution share and upper-tail distribution risk against cut-off thresholds. A convergence check assesses system completeness against stopping criteria. If the criteria are unmet, hotspots are disaggregated into upstream child processes, non-critical flows are aggregated or omitted, and the loop repeats. The final result is a converged, multi-tiered process network that balances model complexity, data quality, and truncation error.

Ambient Alkaline Pretreatment Enables Isoprenol Fermentation from Lignocellulosic Biomass for Sustainable Aviation Fuel Production

Background/Objective

- Isoprenol supply is the main bottleneck in making DMCO, a jet fuel blendstock that can replace aromatic additives.
- Team tested whether low-energy, room-temperature pretreatment yields sugars *E. coli* can ferment directly to isoprenol.

Approach

- Treated corn stover, rice straw, and hemp hurd with dilute sodium hydroxide at 25 °C; enzymes then released sugars.
- Fed the unpurified sugar stream, without detoxification, to engineered *E. coli*; compared with pure-sugar controls.

Results

- Pretreatment kept >93% of glucan, made no detectable furan inhibitors, and freed 79–93% of glucan as sugar.
- *E. coli* made up to 0.38 g/L isoprenol (rice straw), matching the yield of pure sugar controls (28 mg/g sugar).

Significance/Impacts

- Shows a low-energy, fewer-step route from crop residues to a jet fuel precursor, avoiding high heat and detox steps.
- Tests JBEI's engineered isoprenol strain (AK30) on real biomass sugars, a step toward plant-based jet fuel.

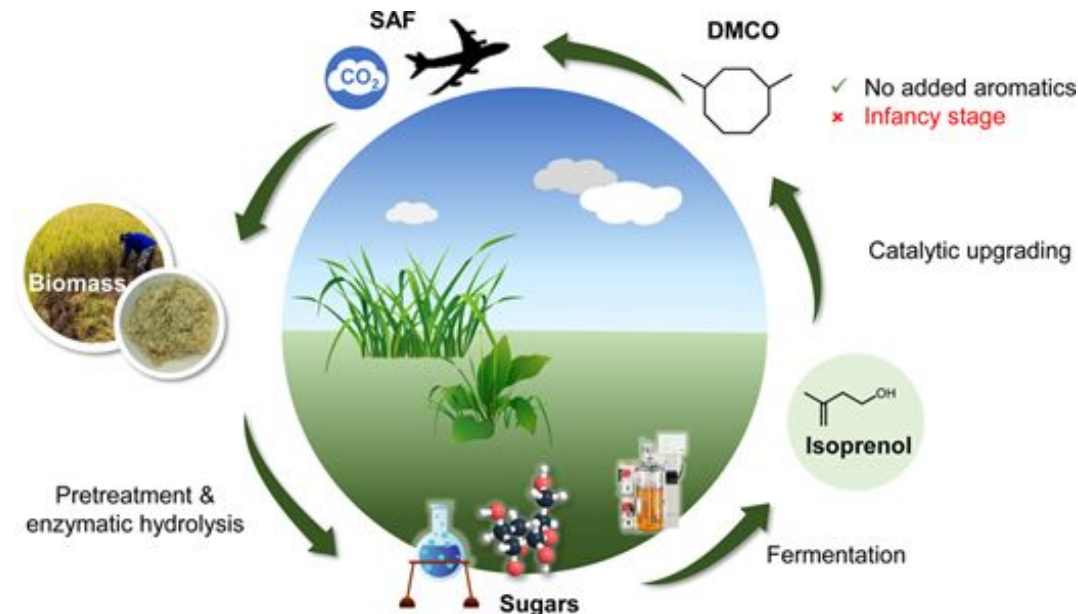


Figure caption: Closed-loop bioconversion of lignocellulosic biomass to Sustainable Aviation Fuel (SAF). Ambient alkaline pretreatment and enzymatic hydrolysis release fermentable sugars without generating furan inhibitors. Engineered *E. coli* ferments the unpurified hydrolysate directly into isoprenol, which is catalytically upgraded to 1,4-dimethylcyclooctane (DMCO), an aromatic-free SAF blendstock. CO₂ released during combustion is recaptured by regrowing biomass, closing the carbon loop.

Video-rate Label-free Molecular Mapping in Living Plant Tissue with a Deployable Optical Encoder

Background/Objective

- Hyperspectral scans temporally mix rapidly evolving in vivo contrast.
- Enable video-rate, label-free molecular mapping in living plant tissues.

Approach

- LDPE encoder in 22-mm miniscope; direct biomolecule decoding.
- Paired Training Data: 6,248 encoded–hyperspectral pairs; lignin and chlorophyll maps.

Results

- Direct inference reduced MAE 0.0105 vs. 0.0269 reconstruction baseline.
- Uncertainty Tracks Error: Predicted uncertainty scale correlated with MAE ($r^2 = 0.849$).

Significance/Impacts

- Shifts hyperspectral goal from datacube recovery to molecular inference.
- Enables non-destructive phenotyping by detecting reduced lignin-associated autofluorescence in engineered poplar lines.

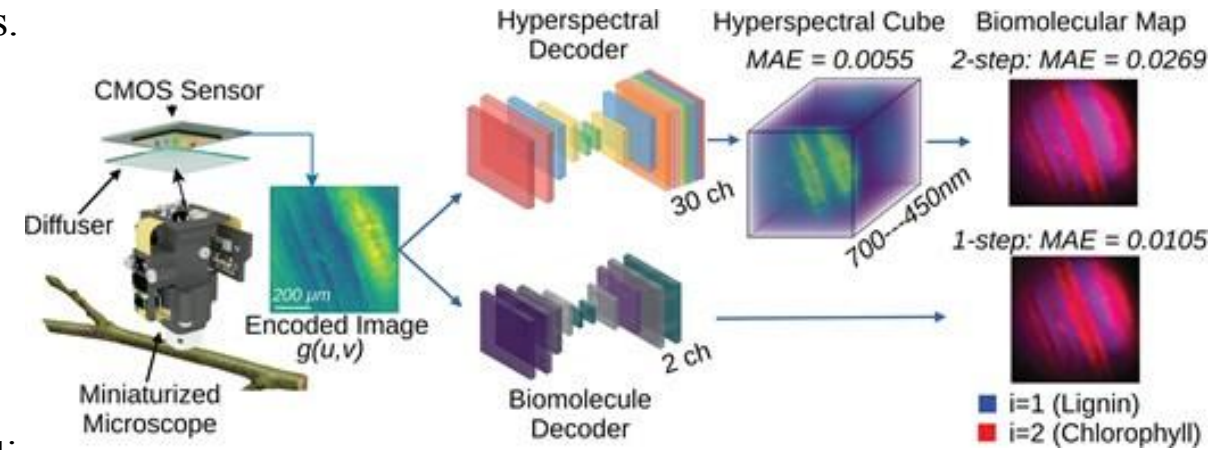


Figure caption: Deployable passive spectral encoding for label-free molecular imaging in living tissue. Excitation at 385 nm generates poplar autofluorescence, captured in a single snapshot without scanning or filter switching. Abundance maps can be derived via a conventional two-step pipeline (hyperspectral reconstruction followed by unmixing) or a direct one-step biomolecule decoder. Direct one-step inference achieves lower molecular-mapping error, successfully separating lignin- and chlorophyll-associated contrast.

Synthetic Biology Unlocks Programmable Control of Complex Plant Glycan Metabolism

Background/Objective

- Always-on gene changes to plant cell wall and sugar-building pathways often stunt growth because these are essential.
- Authors reviewed how synthetic biology tools can control when, where, and under what conditions these genes switch on.

Review Focus

- A range of new gene technologies both from plant biology and more broadly have widened the potential for fine control of these complex pathways.
- Surveyed five layers of control: DNA switches, gene silencing, protein blockers, cell signals, and CRISPR editing.
- Examined uses in biofuel crops, plant-made medicines, human milk sugars, plant signaling, and herbicide tolerance.

Significance/Impacts

- Engineering cell walls without hurting growth or yield is key to making plant-based biofuels economically viable.
- JBEI-supported review offers a roadmap of tools to design bioenergy crop cell walls that release more sugar.

Garcia-Daga, S., et.al. Curr Opin Plant Biol. doi: 10.1016/j.pbi.2026.102978 (JBEI #1338)

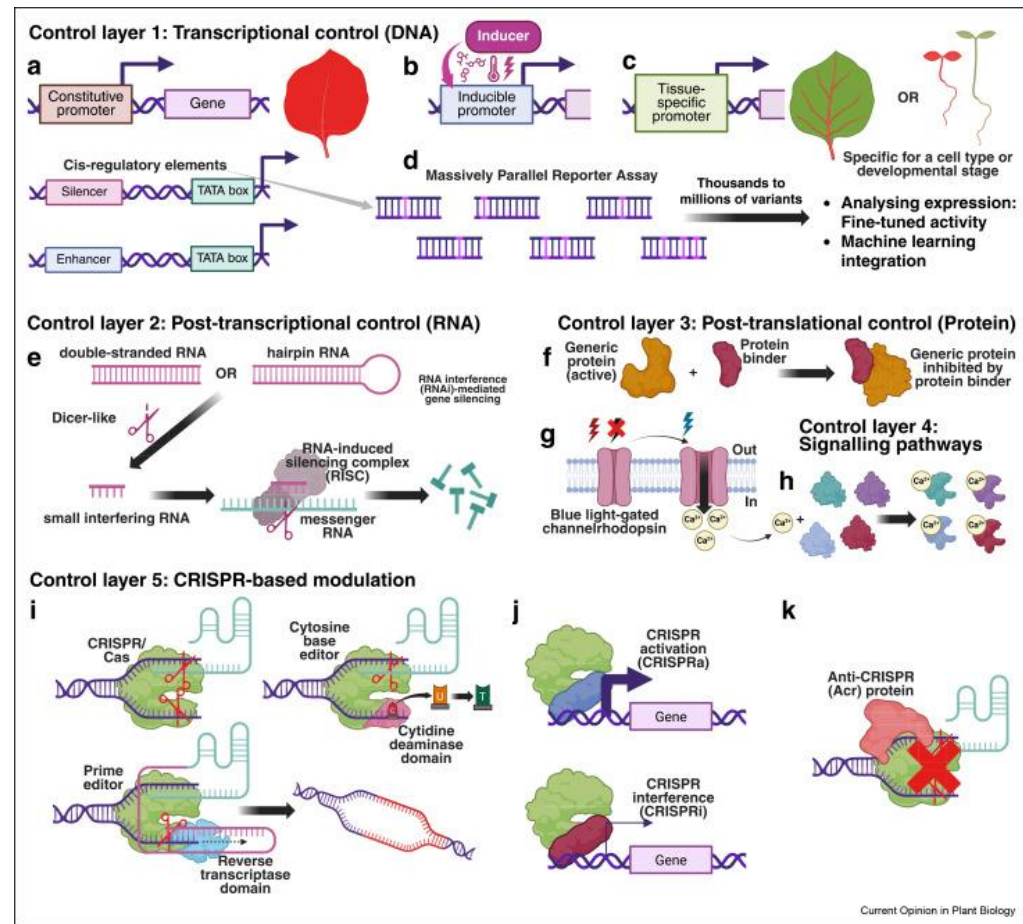


Figure caption: Multi-layered synthetic biology toolkit for plant metabolism. (a) Constitutive, (b) inducible, and (c) tissue-specific promoters. (d) MPRA & machine learning sequence screening. (e) RNAi gene silencing. (f) Protein binder modulation. (g, h) Light-gated and Ca²⁺-transporting channelrhodopsins. (i) CRISPR–Cas knockouts and editing. (j) CRISPRa/CRISPRi expression control. (k) Anti-CRISPR (Acr) inhibition. (l) Cas13 RNA knockdown

Enabled Publications

The Rice Cellulose Synthase-like D4 Gene (OsCSLD4) is Required for Resistance to *Xanthomonas* pv. *oryzae*

Background/Objective

- Plant cell walls, built mainly from cellulose, act as a physical barrier that helps block disease-causing microbes.
- Authors searched for rice genes needed to resist the leaf blight bacterium *Xoo* and asked what role OsCSLD4 plays.

Approach

- Screened 21,000 mutated rice plants carrying the XA21 immune receptor and used genome sequencing to find the gene.
- Restored the normal gene in a mutant and tested disease, bacterial growth, and immune signals in several rice lines.

Results

- OsCSLD4 mutants had ~12 cm lesions vs ~2 cm in the resistant parent and 20–30-fold more bacteria at 12 days. (108)
- Mutants had 2–4-fold longer lesions with XA26 and weaker baseline resistance, yet early immune signals stayed intact.

Significance/Impacts

- JBEI Feedstocks Division work tied a cell wall gene to rice disease resistance, separate from immune signaling.
- Showed that turning on early immune signals is not enough to stop infection; a sturdy cell wall is also needed.

Shi, L., et.al. PeerJ. doi: 10.7717/peerj.21562 (JBEI #143)

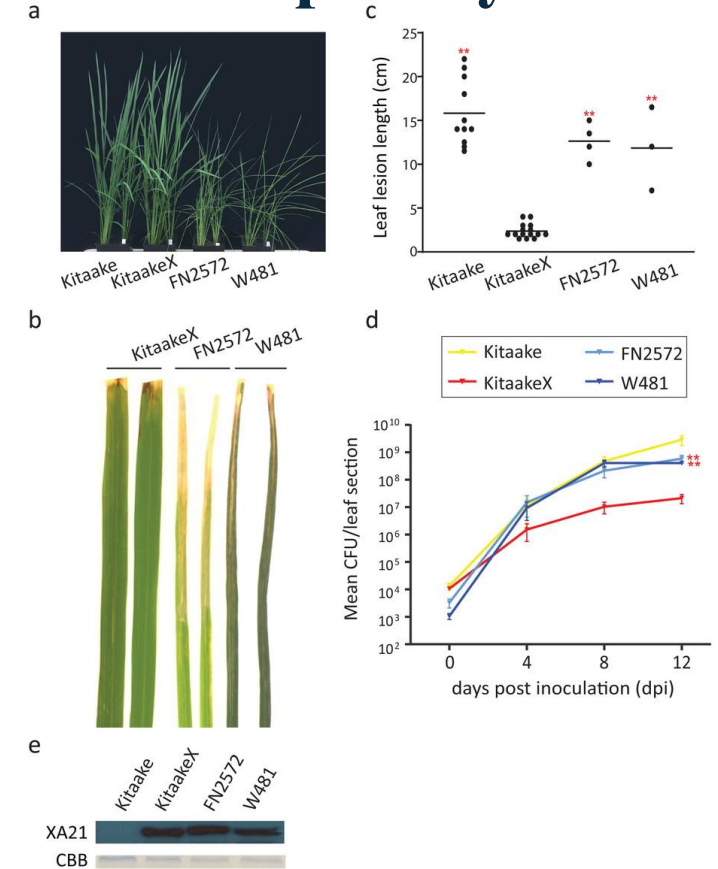


Figure caption: The Xa21-mediated resistance to *Xoo* is compromised in rice mutants FN2572 and W481. (A) Morphology of 5-week-old rice plants. (B) Leaves 14 days post-inoculation (dpi) with *Xoo*. (C) Lesion lengths at 14 dpi (n = 3–15 leaves). (D) *Xoo* growth curves measured at 0, 4, 8, and 12 dpi (mean ± SD, n = 4). Red asterisks in (C, D) indicate P < 0.01 vs. resistant control KitaakeX (Dunnett's test; Kitaake = susceptible control). (E) Western blot of protein extracts probed for XA21 (anti-Myc), with Coomassie Brilliant Blue (CBB) loading reference.

Conversion of minimally processed *Sargassum* to lipids with the yeast *Rhodospiridium toruloides*

Background/Objective

- Seaweed like *Sargassum* grows fast without freshwater or cropland, but it is salty and costly to prepare.
- Team tested whether unwashed, minimally processed *Sargassum* can feed an oil-making yeast, *R. toruloides*.

Approach

- Broke down Gulf of Mexico *Sargassum* with acid, base, or hot water, then enzymes that digest cellulose and alginate.
- Grew the yeast on the resulting sugar mixtures, then measured growth, sugar use, lipid content, and fatty acid types.

Results

- Base pretreatment plus enzymes gave the best growth (to an OD of ~3).
- Yeast stored ~8% of its dry weight as lipid (0.08 mg/mg), mostly C16–C18 fatty acids like those in vegetable oils.

Significance/Impacts

- Suggests seaweed can feed oil-making yeast without freshwater washing, a simpler route to biodiesel and SAF precursors.
- Gives JBEI's *R. toruloides* work a new marine feedstock and a baseline for future strain and process tuning.

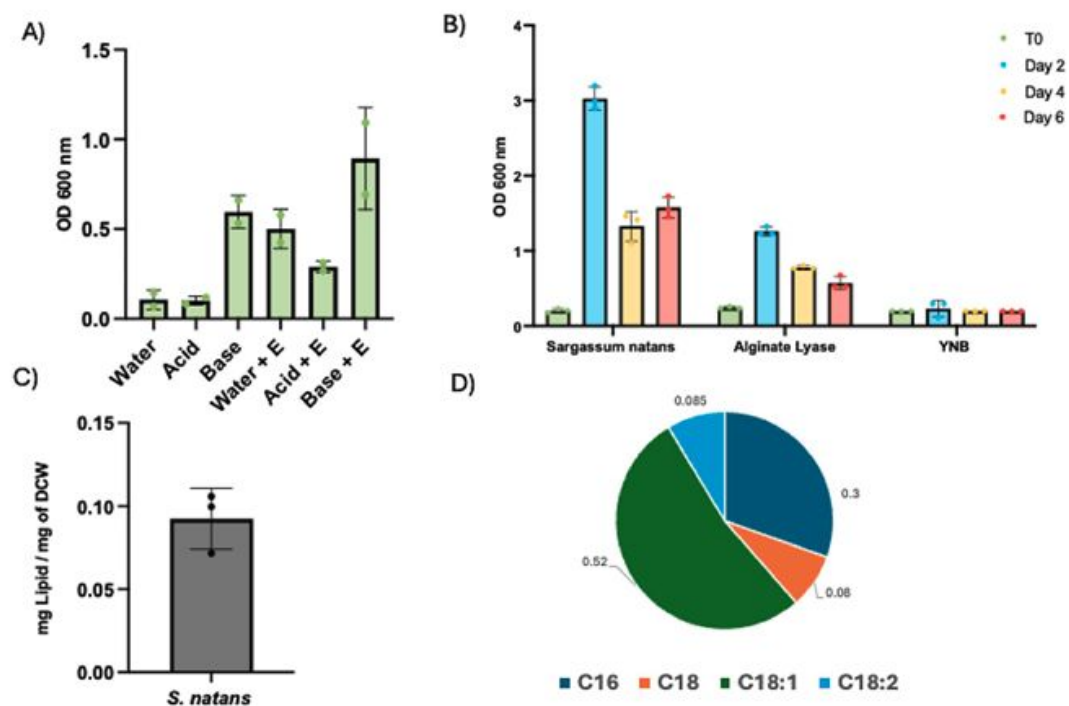


Figure caption: Growth and lipid production of *R. toruloides* on *Sargassum* hydrolysates. (A) Growth on day 3 after water, acid, or base pretreatment, with (+E) or without enzymes. (B) Growth over 6 days on base-pretreated *Sargassum* hydrolysate, digested alginate, and a nutrient-only (YNB) control. (C) Total lipid content (mg lipid/mg dry cell weight). (D) Fatty acid profile, shown as relative proportions of C16, C18, C18:1, and C18:2.