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Evolutionary arms race: the role of xylan modifications in plant–pathogen interactions

Background/Objective

The paper is a commentary on a recent publication:
Yu et al. (2024) Evolution of glucuronoxylan side chain variability in vascular plants and the compensatory adaptations of cell wall–degrading hydrolases, New Phytologist, doi.org/10.1111/nph.19957

Results

- Yu et al. identified an arabinosyltransferase, XAPT1, that adds arabinose to xylan in some species. In eucalyptus and related species, the gene has undergone duplication, and one copy, XLPT1, has been neofunctionalized to add galactose instead of arabinose.
- Many plant pathogens use GH30 hydrolases that can cleave xylan when it is not modified by XAPT1 or XLPT1. However, several bacteria living on plants with these modifications have indepedently evolved their GH30 enzymes to be able to degrade xylan.

Significance/Impacts

This is a clear example of an evolutionary arms race between plants and pathogens, involving the detailed cell wall structure and the microbial enzymes that can degrade them

Mortimer, J.C. and Scheller, H.V. New Phytol. doi: 10.1111/nph.20071

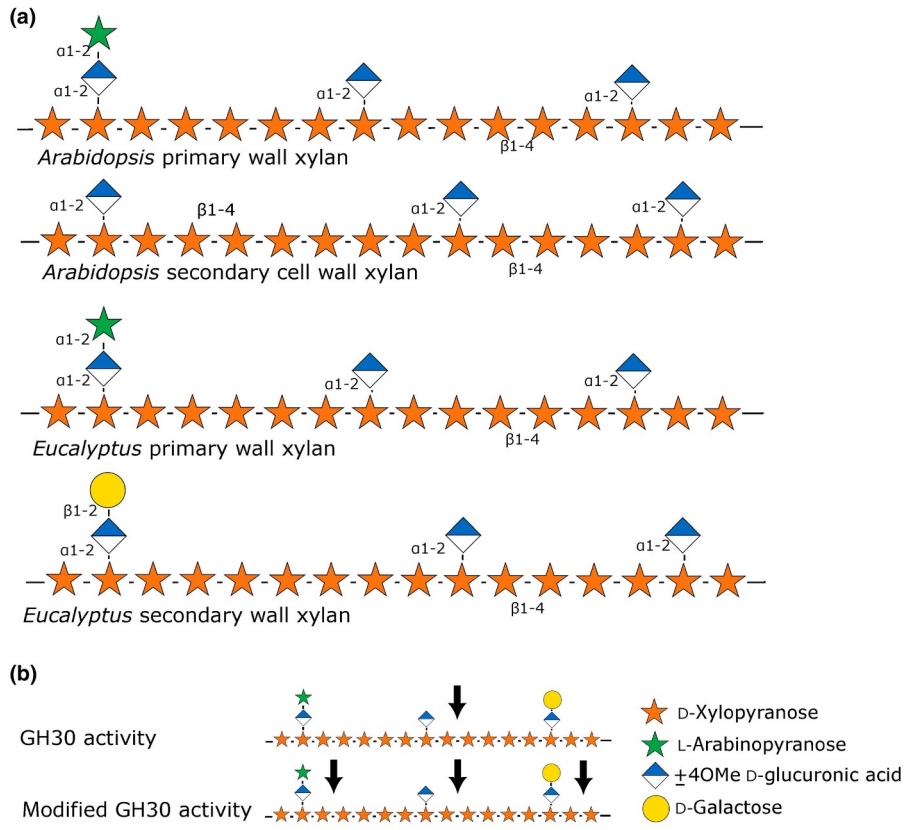

Figure. The impact of XAPT and XLPT on xylan. (a) Example structures of xylan in Arabidopsis and Eucalyptus showing the product of XAPT and XLPT described in Yu et al. (2024). XAPT adds arabinopyranose to some of the glucuronic acid substitutions of xylan and is present in many plants. XLPT adds galactose instead of arabinopyranose and is restricted to Myrtaceae. (b) The impact of the disaccharide substitution on GH30 xylanase activity, and the improved activity seen in some GH30s from pathogenic organisms. Acetylation of the xylosyl backbone is not shown here.

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Neurospora intermedia from a traditional fermented food enables waste-to-food conversion

Background/Objective

- Fungal fermentation of food and agricultural by-products holds promise for improving food sustainability and security.
- The molecular basis of fungal waste-to-food upcycling remains poorly understood.

Approach

We used a multi-omics approach to characterize oncom, a fermented food traditionally produced from soymilk by-products in Java, Indonesia.

Results

- Metagenomic sequencing of samples from small-scale producers in Western Java indicated that the fungus *Neurospora intermedia* dominates oncom.
- 'Omics analysis revealed that oncom-derived *N. intermedia* utilizes pectin and cellulose degradation during fermentation and belongs to a genetically distinct subpopulation associated with human-generated by-products.

Significance/Impacts

These results showcase the traditional significance and future potential of fungal fermentation for creating delicious and nutritious foods from readily available by-products.

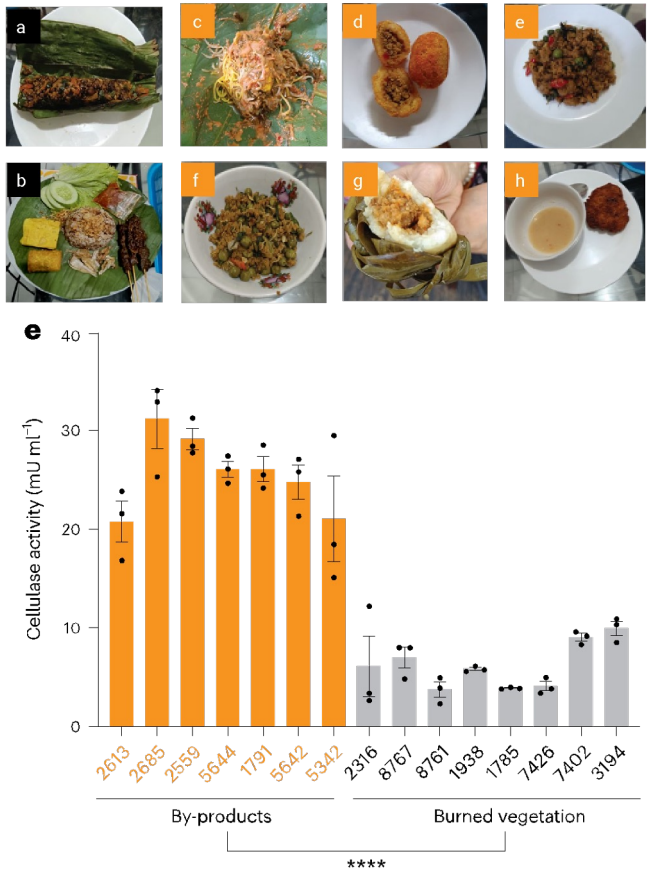

Figure. (Top) Typical preparations of oncom in West Java, Indonesia. **(bottom)** N. intermedia strains used for oncom belong to a genetically distinct subpopulation associated with by-products of human activity. Secreted cellulase activity between burn-associated and by-product-associated strains during growth on okara.

Maini Rekdal, V., et. al. Nat Microbiol. https://doi.org/10.1038/s41564-024-01799-3

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Characterization of lignin degrading enzyme PmdC, which catalyzes a key step in the synthesis of polymer precursor 2-pyrone-4,6-dicarboxylic acid (PDC)

Background/Objective

- Pyrone-2,4-dicarboxylic acid is a valuable polymer precursor that can be derived from the microbial degradation of lignin.
- We wanted to better understand the biological synthesis of this molecule to help enable improved precursor production.

Approach

We solved the crystal structure of a key enzyme in the pathway that makes this compound.

Results

The structure of the enzyme identified the residues responsible for binding an important cofactor and substrate. Using structural homology, molecular docking, and quantum chemistry calculations we predicted substrate binding and identified key catalytic residues.

Significance/Impacts

To make biofuels cost effective we need to make full use of lignin from plants. One viable route is the conversion of lignin to valuable products, such as polymers.

Rodrigues, A. V., et al. Journal of Biological Chemistry. doi: 10.1016/j.jbc.2024.107736

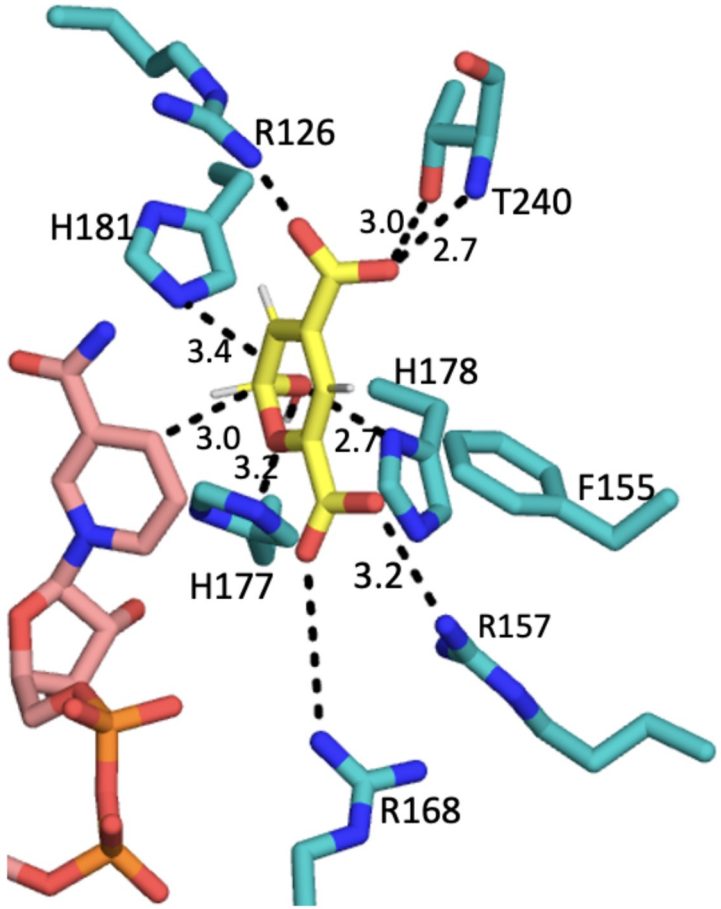

Figure: Key active site residues around the computationally docked substrate 4-carboxy-2-hydroxymuconate-6-semialdehyde (CHMS).

ENABLED PUBLICATIONS

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A Simple and Effective Strategy for the Development of Robust Promoter-Centric Gene Expression Tools

Background/Objective

Streptomyces are well-known prolific producers of natural products and exceptional surrogate hosts for production of high-value chemical compounds and enzymes, but we need robust gene expression tools.

Approach

We introduced an additional −35-like motif upstream of the original −35 region of the promoter, coupled with the integration of a palindromic cis-element into the 5′-UTR region.

Results

- The fully activated oxytetracycline-inducible gene expression system containing an engineered kasOp* promoter (OK) exhibited nearly 10-fold greater activity than the well-established high-strength promoter kasOp* under the tested conditions.
- These tools augmented production of transglutaminase and daptomycin.

Significance/Impacts

This approach has generated a collection of robust constitutive and inducible gene expression tools tailored for Streptomyces.

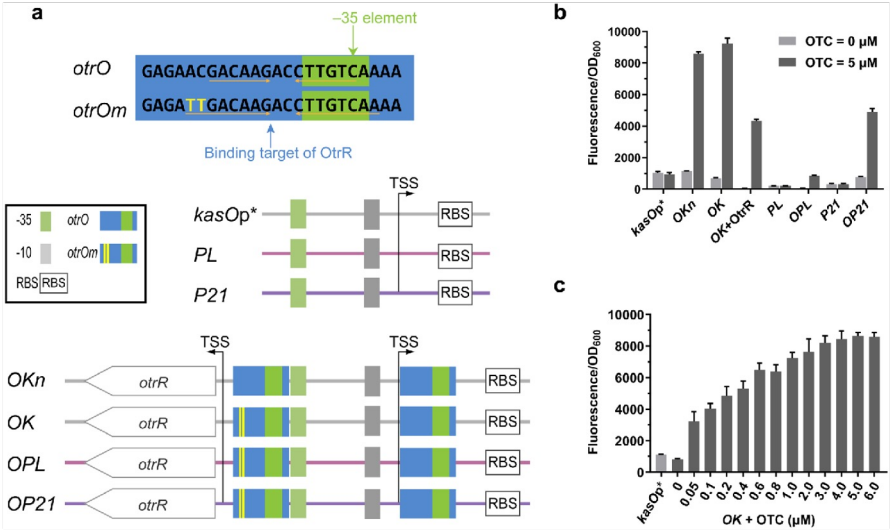

Figure. Development of inducible gene expression systems. (a) Schematic representation of the construction of inducible gene expression systems. (b) Performance evaluation of inducible expression systems. (c) Dose−effect analysis of the inducible expression system OK under different concentrations of OTC.

Yang, T., et. al. ACS synthetic biology. doi: 10.1021/acssynbio.4c00092

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Triumphs and Challenges of Natural Product Discovery in the Postgenomic Era

Background/Objective

Natural products (NPs) are significant roles in medicine and food.

Approach

We first provide a brief historical overview of natural products, their classification and biosynthetic origins, and the microbiological and genetic methods and technologies used for their discovery.

Results

- Comprehensive public databases have listed between 325,508 and 420,270 NP molecules.
- The number of BGCs linked to molecules has significantly increased to over 2,700.
- More than 1.2 million bacterial and more than 12,000 fungal genomes are deposited in GenBank.
- Only 3% of NP–BGC links have been experimentally established.

Significance/Impacts

Systematic heterologous expression and strain-independent discovery, promise to deliver more molecules in vials than ever before.

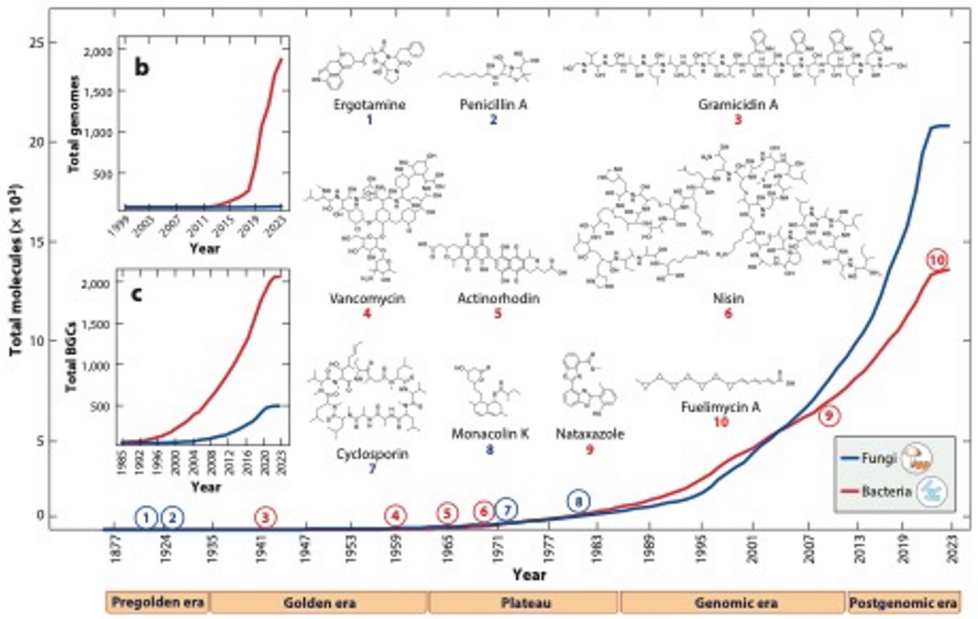

Figure. Historic milestones in NP discovery. (a) The main plot depicts the cumulative number of molecules discovered over the last 145 years. (b) The total number of BGCs and genomes retrieved between 1977 and 2023. (c) The number of genomes and BGCs deposited in the GenBank and MIBiG databases in the last 38 years. The red line corresponds to bacterial data and the blue line to fungal data.

Cano-Prieto, C., et. al. Annual review of biochemistry. doi: 10.1146/annurev-biochem-032620-104731

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Evolution and origins of rubisco

Background/Objective

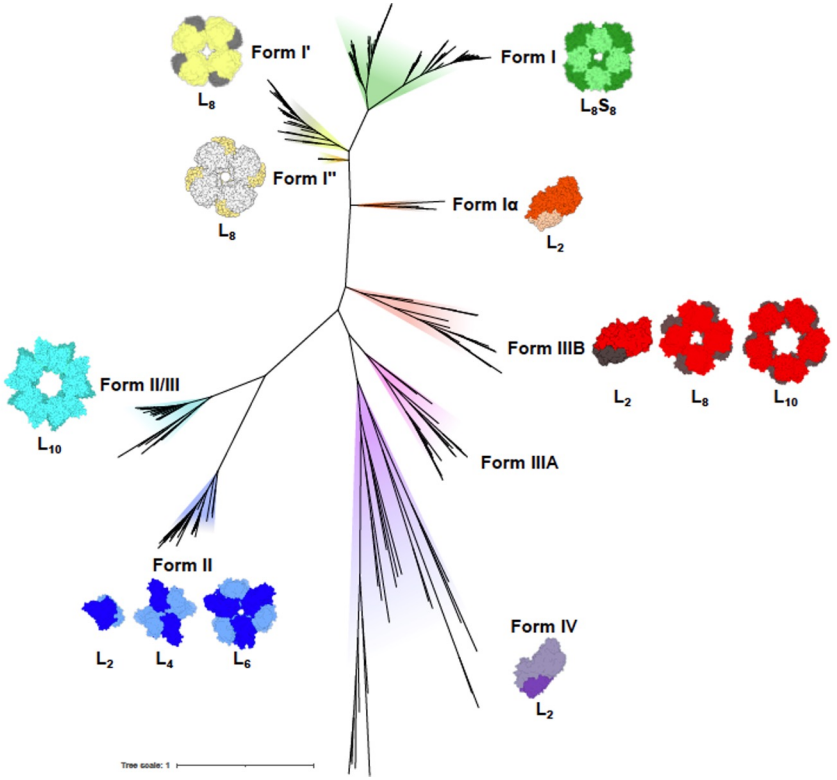
Rubisco catalyses the conversion of inorganic CO2 into organic sugars that underpin almost all of the biosphere, including our entire food chain. Due to its central role in the global carbon cycle, rubisco has been the subject of intense research for over 50 years.

Approach

This is a review on recent advances in understanding the origins of rubisco which have implications on understanding the biophysical challenges in engineering rubisco.

Significance/Impacts

Such evolutionary studies have led both to a better understanding of the origins of more complex rubisco forms and the broader relationship between rubisco's structure and function.



Taylor-Kearney, L. J., et, al. Current biology. doi: 10.1016/j.cub.2024.06.024