

Cynipid wasps systematically reprogram host metabolism and restructure cell walls in developing galls

Background/Objective

Many insects are able to engineer plants to produce novel structures called galls, which function to shelter and feed their larva. In doing so, these insects rewire both metabolism and cell walls of plants. Understanding this process may provide unique insights into how scientists may be able to hijack similar processes.

Approach

Here, we characterize the molecular alterations underlying gall development using a combination of metabolomic, histological, and biochemical techniques to elucidate how leaf cells are reprogrammed to form galls.

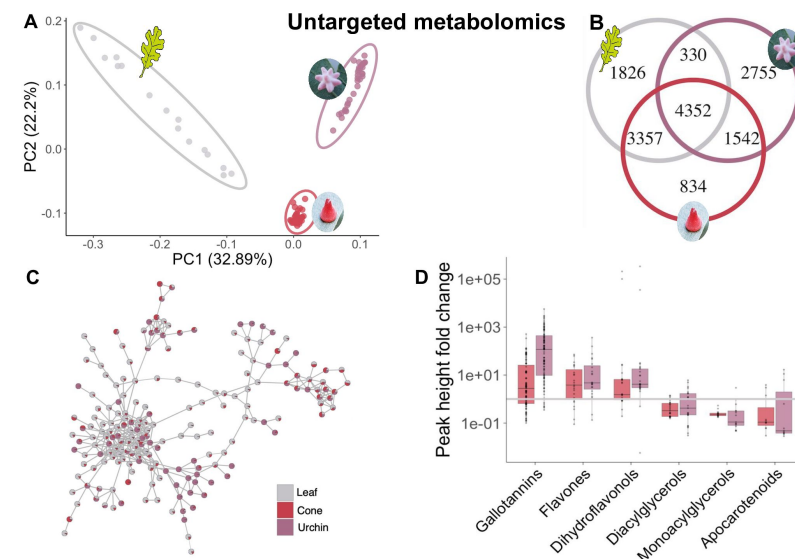
Results

Our results highlight how cynipid wasps can radically change the metabolite profile and restructure the cell wall to enable the formation of galls.

Significance/Impacts

These new insights into the mechanism of gall induction and the extent to which plants can be entirely reprogrammed to form novel structures and organs.

Markel K., et al (2024) Plant physiology. doi: 10.1093/plphys/kiae001



JBEI Enabled Papers

Unveiling a classical mutant in the context of the GH3 β -glucosidase family in *Neurospora crassa*

Background/Objective Genetic screens are often used to elucidate fundamental metabolic pathways. In the filamentous fungus, *Neurospora crassa*, the *gluc-1* mutant strain was isolated long ago and characterized by its low level of β -glucosidase activity.

Approach Based on genomic resequencing, we identified the causative *gluc-1* mutation to be in the β -glucosidase gene *gh3-3* (*bgl6*, NCU08755). In this work, growth patterns, enzymatic activities and sugar utilization rates were analyzed in several mutant and overexpression strains related to *gluc-1* and *gh3-3*.

Results We confirm that GH3-3 is the major extracellular β -glucosidase in *N. crassa* and demonstrate that the two cellodextrin transporters, CDT-1 and CDT-2, are essential for growth on cellobiose when the three main *N. crassa* β -glucosidases are absent.

Significance/Impacts: Our results expand our understanding of cellulose utilization, connecting the roles of hydrolases and sugar transporters.

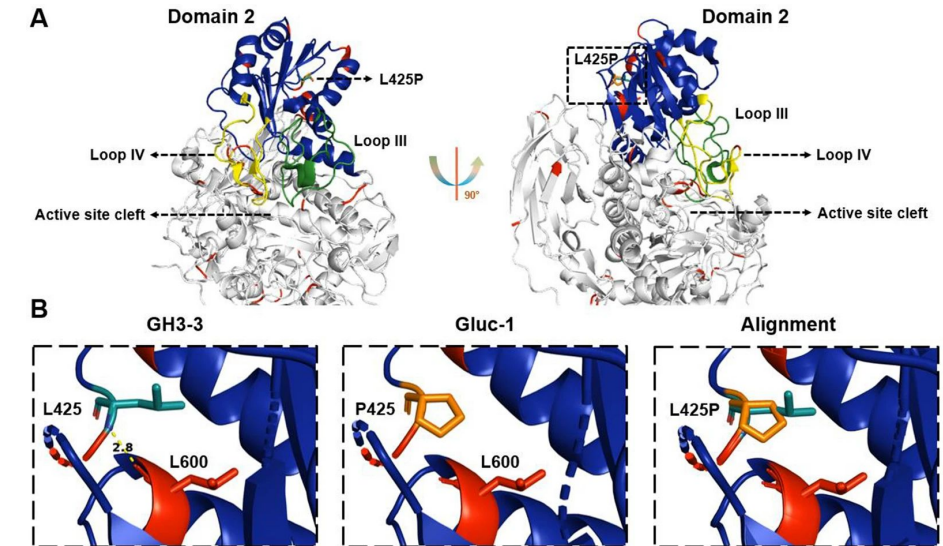


Figure 1: Overview comparison of domain 2 between the GH3-3 crystal structure and the Gluc-1 model. **A.** Domain 2 in GH3-3 and Gluc-1 alignment. Red color indicates mismatched positions between the two structures. The L425P point mutation is highlighted in orange (black box). **B.** Mutated position in the alignment between GH3-3 and Gluc-1. The structure in the L425P region in the structural alignment between GH3-3 and Gluc-1 was compared. The hydrogen bond between L425 and L600 in GH3-3 is colored in yellow within 2.8 Å

Expanding the structural diversity of terpenes by synthetic biology approaches

Background/Objective

- Terpenoids remain one of the largest groups of natural products, and they are structurally and functionally diverse.
- Terpenoids display chemical and structural diversities and important biological activities.

Approach

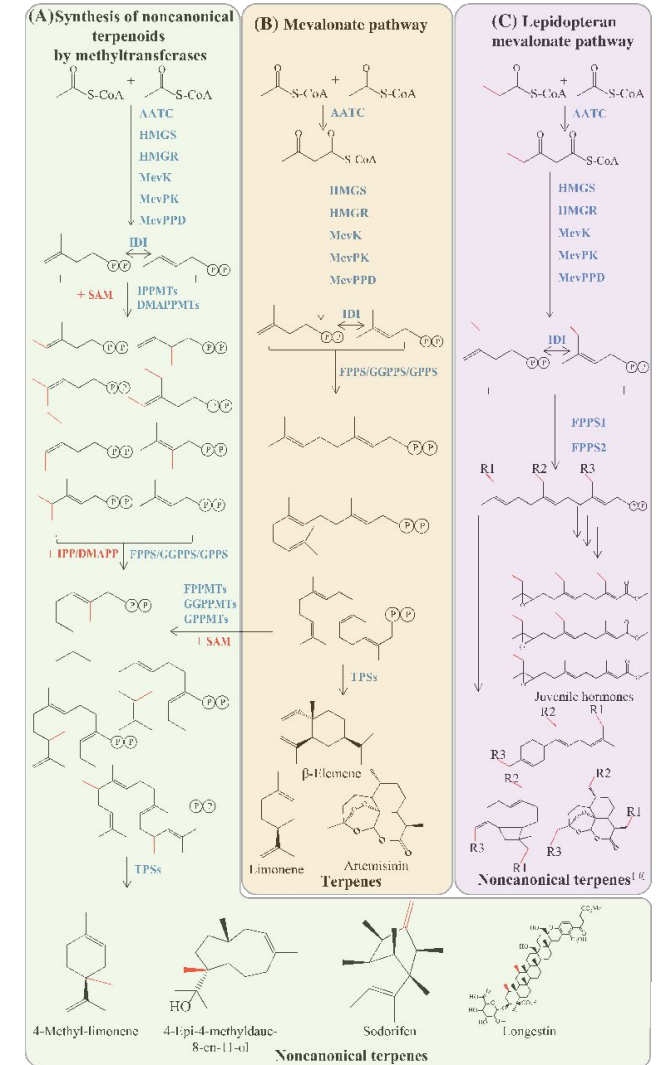
- Despite their extreme variability, the range of these structures is limited by the scope of natural products that canonically derive from interconvertible five-carbon isoprene units.
- New approaches have recently been developed to expand their structural diversity.

Results

- The combinatorial biosynthesis of noncanonical building blocks via the co-expression of the canonical mevalonate pathway and C-methyltransferases, or by using the lepidopteran mevalonate pathway.
- Unnatural terpenoids can be created from farnesyl diphosphate analogs by chemobiological synthesis and terpene cyclopropanation by artificial metalloenzymes.

Significance/Impacts

- Natural and unnatural terpenoids are excellent resources as fuels, commodity and specialty chemicals, and pharmaceuticals.



Complete biosynthesis of the potent vaccine adjuvant QS-21

Background/Objective

- QS-21 is a potent vaccine adjuvant currently sourced by extraction from the Chilean soapbark tree.
- Discover the biosynthetic pathway for QS-21 in the *Quillaja saponaria*

Approach

- A pool of 68 candidate genes together with the genes required to make the glycosylated triterpene QA- TriX-FRXX were infiltrated to the leaves of *Nicotiana benthamiana*
- Extracts of the leaves were sampled for QS-21

Results

- We determined the biogenic origin of the acyl chain, characterized the series of enzymes required for its synthesis and addition and reconstituted the entire 20-step pathway in tobacco.

Significance/Impacts

- This advance opens up unprecedented opportunities for bioengineering of vaccine adjuvants.

