

PLANT BIOTIC INTERACTION

Genetics of herbivory

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Credit: Photograph courtesy of Cristina Sahagun

Plant–insect interaction has been a broadly concerned topic due to its ecological and agronomic importance. While important insights into the specific signalling pathways have been revealed by previous research, the molecular basis underlying the co-evolutionary interactions remained elusive. Sumitha Nallu from the Department of Ecology and Evolution, University of Chicago, and colleagues now greatly expand our understanding of this interaction by studying the *Arabidopsis thaliana*–Cabbage White butterfly system.

The researchers conducted parallel genome-wide association studies (GWAS) to identify genetic variants associated with herbivory. *Arabidopsis* GWAS analysis using 96 natural accessions identified 389 candidate genes associated with herbivory phenotype, 12 of which received good supports containing more associated single-nucleotide polymorphisms or functionally validated by mutant analysis. On the butterfly side, the researchers first assembled a high-quality reference genome for the butterfly and then resequenced unrelated offspring of 96 wild-caught females. GWAS revealed two strongly associated regions in the genome, containing genes such as *Glyoxalase 1* and *Defective proboscis*

extension response 6 (dpr6) involved in host-plant detoxification or the gustatory response to host-plant material.

By monitoring transcriptomic dynamics in the plant and insect over the time course of their interaction, the researchers found that genes identified in GWAS analysis showed highest induction during their interaction, confirming their roles in herbivory. Butterfly egg-laying, rather than larval feeding, caused massive effects on *A. thaliana* transcriptomes by altering the expression of about half the plant genes. Consistently, on the insect side, the butterfly eggs displayed an elevated transcriptomic response to host compared to the larva. However, this elevated response to oviposition was not observed in three additional plant–insect systems, suggesting it is not a general pattern. Comparative transcriptomic analysis among the four systems revealed a set of conserved genes that respond to herbivory.

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