Breaking the Interpretation Bottleneck: Toward Scalable and Meaningful Plant Phenotyping

Abstract

As phenotyping technologies continue to advance, the challenge in plant phenomics has shifted from data acquisition to interpretation—specifically, how to maximize the value of complex, high-resolution datasets. High-throughput phenotyping (HTP) provides detailed temporal and factorial data, but also reveals substantial individual-level variation, necessitating robust analytical frameworks. This study utilizes HTP data from the IPK PhenoSphere to examine how plant-plant interactions influence the relationship between shoot and root traits. The experimental design incorporated nitrogen availability, genotype variation, and levels of shoot competition, with 127 phenotypic traits quantified. Statistical modeling approaches are employed to analyze temporal dynamics and interaction effects, highlighting their potential applications in plant physiology research and breeding programs.

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RESEARCH AREAS AND EXPERTISE

- General area: Plant Phenomics, Biostatistics and Genomic Analysis
- Specific area: HTP data modeling and visualization, Genomic–phenomic integration, 3D crop modeling

Cheng-Bin Li is an Assistant Researcher at the Taiwan Agricultural Research Institute, Ministry of Agriculture. He received both his B.Sc. and M.Sc. degrees from the Department of Agronomy at National Chung Hsing University, where he specialized in biostatistics during his graduate studies. His research focuses on statistical modeling of agricultural big data, covering topics such as genomic studies of genetic resources, spatial competition models, and high-throughput phenotyping (HTP) data analysis. As both a phenotyping facility user and a data scientist, he developed an R package named *FlowPhen*, designed to streamline the analysis of HTP data. *FlowPhen* serves as a user-friendly visualization and analytics platform, enabling rapid data interpretation and real-time exploration of spatial variation structures in field trials. Cheng-Bin possesses extensive hands-on expertise in HTP data analysis. In recent years, he has also been exploring the integration of genetic resources with phenomic applications. His current work includes the development of microscopic phenotyping tools and deep learning models, aiming to bridge the gap between phenotyping technologies and their application in breeding and field management. In the field of plant physiology, he is applying 3D reconstruction techniques to build digital crop models for analyzing plant architecture and estimating radiation use efficiency.