

XPlantGL: A Software of Functional-Structural Plant Modelling for Crops

Xiujuan Wang, Bowen Zheng, Beda Innocent Adji, Haoyu Wang, and Jing Hua

Abstract—This paper presents XPlantGL, a Matlab-based software for functional-structural plant model (FSPM) derived from the GreenLab model, designed for addressing the practical limitations of existing FSPM tools (e.g., poor interactivity, limited support for branching/stochastic crop growth, and complex parameter calibration). XPlantGL enables precise simulation of plant architectures and growth dynamics via sink-source relationships, and integrates a generalized least square method (GLSM) for single-stage or multi-stage model parameter estimation from measured data. The software is validated on over ten crops (lettuce, cucumber, tomato, maize, rice, etc.), covering field crops, horticultural crops, and herbaceous plants. As a user-friendly FSPM tool, XPlantGL provides a reliable platform for researchers and educators in plant growth modelling, digital phenotyping, and smart agriculture research. Its core innovations include enhanced interactivity, native support for stochastic/branching crop growth, and streamlined parameter fitting workflows. Future research will focus on environment factor integration and high-fidelity visualization optimization.

Index Terms—Functional-structural plant model (FSPM), GreenLab, parameter calibration, plant growth simulation, plant development, plant architecture modelling

I. INTRODUCTION

WITH the increasing global demand for food security and sustainable agriculture, understanding plant growth and development at both structural and functional levels has become crucial [1, 2]. Functional-structural plant models (FSPMs) have emerged as powerful tools to integrate biological processes with plant architecture [3], enabling precise simulations of plant growth under varying environmental conditions [4, 5].

GreenLab is a dynamic organ-level FSPM, which has been developed through the collaboration between Chinese and French institutes since 1998 [6, 7], proposed by Professor Philippe de Reffye and developed for more than two decades [8–10]. Based on the core assumptions adopted in process-based models (PBMs), GreenLab mainly includes the concept

of a common biomass pool, the dependence of biomass production primarily on leaf area index (LAI), light use efficiency (LUE) or water use efficiency (WUE), and the regulation of biomass distribution by the source-sink relationship [9]. The model combines four key components: a functional model for biomass production and allocation, a developmental model for plant organogenesis simulation (i.e., the initiation and growth of plant organs), a set of geometrical parameters for three-dimensional (3D) plant architecture reconstruction, and a parameter identification module for acquiring model parameters by fitting measured experimental data [8–10]. This integration enables GreenLab to link plant physiological processes, developmental dynamics, and spatial structure, forming a comprehensive framework for plant growth simulation.

The core operation mechanism of GreenLab relies on a series of mathematical equations to quantify the entire plant growth process [9]. Starting from a single seed, the model simulates the photosynthetic process of leaves, which converts light energy into biomass and puts it into the common biomass pool. Subsequently, the accumulated biomass in the pool is allocated to various plant organs (such as stems, leaves, roots, flowers, and fruits) according to the source-sink relationship—specifically, sources refer to organs that produce and export biomass (e.g., mature leaves), while sinks are organs that absorb and utilize biomass (e.g., young leaves, growing stems, and fruits). This process cycles until the plant senesces or matures, thereby completing the dynamic simulation of the entire plant life cycle.

A distinctive advantage of GreenLab is its ability to realize dynamic plant growth and development based on static plant architecture data. Specifically, by analyzing the structural parameters of plants (e.g., organ number, shape, and spatial position) observed at different growth stages, the model can calculate the size and weight of each organ at corresponding stages, and further estimate the key source and sink parameters using the generalized least square method (GLSM) combined with measured experimental data [6, 9]. The model calibration process supports both single-stage and multi-stage fitting strategies: single-stage fitting uses biomass or structural data from a single growth stage to optimize parameters, while multi-stage fitting integrates data from multiple growth stages to improve the accuracy and robustness of parameter estimation. Through this calibration method, GreenLab can effectively reconstruct the temporal dynamics of biomass production and partitioning throughout the plant growth period. Finally, the model can visualize the simulated plant in either two-dimensional (2D) or 3D form, intuitively present-

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ing the structural changes and growth status of the plant at different stages.

To facilitate its application in different research scenarios and plant types, GreenLab has been implemented in several specialized software versions, each with distinct features and application scopes. GreenScilab, developed based on the Scilab platform, is mainly designed for crop growth simulation, providing basic functions of biomass simulation and parameter analysis [11]. Qingyuan, developed using C++ language, supports both crop and tree simulations, integrating core functions such as growth process simulation and 3D architectural visualization, with high computational efficiency suitable for large-scale simulation [12]. Gloops, a more complex version developed in Matlab, is compatible with both crops and trees, offering comprehensive functions including detailed growth simulation, multi-objective parameter fitting, and sensitivity analysis [13]. MiniGloops/StemGL, also based on Matlab, is a simplified version tailored for single-stemmed plants (e.g., maize and sunflower), focusing on efficient simulation and parameter calibration with lower computational resource requirements [14].

However, existing GreenLab software still has obvious limitations in crop-specific research: most versions lack optimized support for branching crop growth and stochastic developmental processes, and some software requires advanced programming skills due to complex operation processes, which increases the application threshold for plant science researchers. To further enhance the convenience and applicability of the GreenLab model in crop research, we developed XPlantGL, a Matlab-based FSPM software specifically for crop research. On the basis of retaining the core functions of GreenLab in simulation and parameter fitting, XPlantGL adds support for branching plant types and stochastic growth processes, optimizes the graphical use interface (GUI) to simplify the operation process, expands the model's application scope, and standardizes FSPM parameter calibration. It thus provides a user-friendly tool for digital crop phenotyping and smart breeding research, while laying a technical foundation for crop growth digital twins by integrating with high-throughput phenotyping systems. This paper focuses on the design principles, software architecture, and parameter system of XPlantGL, details the specific steps of crop growth simulation and model parameter calibration, and verifies the reliability and effectiveness of the software through case studies of maize, tomato, and rice.

II. SOFTWARE OF XPLANTGL

A. Software Architecture

The XPlantGL software was independently developed in the Matlab environment (specifically Matlab R2018a), which ensures its good compatibility and operability in scientific computing and data visualization, and its intuitive GUI is illustrated in Fig. 1. As a derivative and extended tool based on the GreenLab model, XPlantGL inherits all the core functions of the original GreenLab model and further optimizes its operability and functional comprehensiveness. Specifically, its functions are mainly divided into two interrelated modules: simulation module (XPlantGLS) and calibration module (XPlantGLA), as shown in Fig. 2, which work together to

realize the complete process of plant growth modeling, simulation, and parameter estimation.

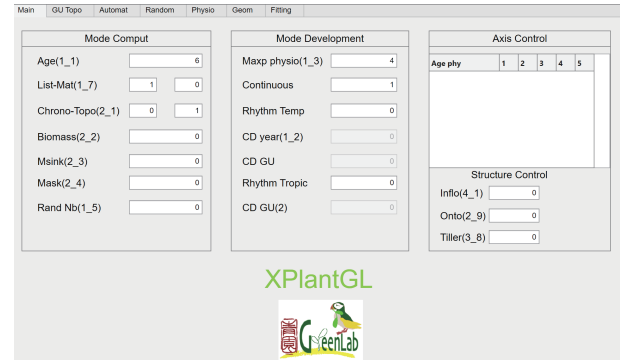


Fig. 1 Interface of XPlantGL.

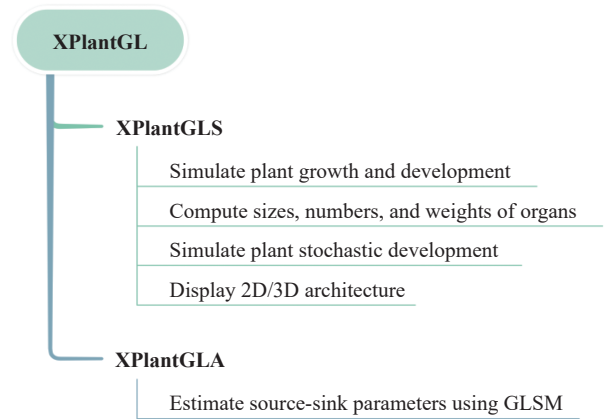


Fig. 2 Architecture of XPlantGL.

B. Model Parameters

To ensure the accuracy, comprehensiveness, and practicality of the plant growth simulation software, XPlantGL integrated three types of parameters that describe plant structure, function, or morphology. These parameters cooperate with each other to reconstruct the dynamic growth process of plants and simulate their responses to internal developmental rules and external environmental conditions.

a. Topological Parameters

As the core foundation for constructing the structural framework of plants, topological parameters are primarily used to define and quantify the topological structure of plants, which directly determines the overall architectural layout and developmental pattern of the plant individual. Specifically, these parameters include three key aspects: first, the types and quantities of various organs (such as leaves, internodes, fruits, buds, and flowers) contained in each phytomer—phytomers, as the basic modular units of plant growth, their organ composition directly affects the subsequent functional differentiation and resource allocation of the plant; second, the developmental mode of each organ and phytomer, i.e., whether it follows a deterministic development rule (with a fixed developmental sequence and duration, predictable by inherent genetic programs) or a stochastic development rule (affected by random factors such as environmental fluctuations, with certain uncertainty in the developmental process); third, the

maximum number of phytomers that can be formed on each growth axis, including both the main stem (the primary axis supporting the entire plant) and all levels of branches (the secondary axes derived from the main stem), which limits the maximum growth potential and structural complexity of the plant.

b. Functional Parameters

Focusing on the biomass production and distribution processes of plants, functional parameters are used to define the source-sink relationship and related functional characteristics of plants—source organs refer to those that produce and export photosynthates (such as mature leaves), while sink organs refer to those that absorb and utilize photosynthates (such as developing fruits, roots, and young leaves). Development cycle (DC) of each organ type refers to the total time required from the initiation of the organ to its maturity or senescence, and is an important indicator reflecting the growth rhythm of the organ. Organ sink strength (P_o) represents the ability of a sink organ to compete for and absorb photosynthates and directly determines the distribution proportion of resources among different sink organs. Variation coefficients of sink strength (B_a and B_b) describe the dynamic changes of sink strength of each organ during its development (e.g., the sink strength of fruits usually increases rapidly in the early stage of development and stabilizes or decreases in the later stage). Initial seed biomass (Q_0) provides the basic material and energy for seed germination and early seedling growth, and has a significant impact on the survival rate and growth potential of seedlings. Functional duration (T_f) refers to the period from their full expansion to senescence, during which they can carry out photosynthesis, and expansion time (T_x) of each organ refers to the period from leaf primordium formation to full expansion. Projection surface area (S_p) of organs (especially leaves) is closely related to the light interception efficiency of plants and further affects the photosynthetic rate. Resource use efficiency (r), including light use efficiency, water use efficiency, and nutrient use efficiency, reflects the ability of plants to convert external resources into their own biomass.

c. Geometric Parameters

Responsible for describing the spatial morphological characteristics of plant organs and the overall plant structure, geometric parameters are used to define the specific geometric attributes of the plant structure, enabling the model to visually simulate the three-dimensional shape of the plant. These parameters mainly include: the thickness of leaves (which affects the light transmission rate of leaves and the accumulation of photosynthetic products), the spatial angles of various organs (such as the inclination angle of leaves, the divergence angle between internodes, and the branching angle of branches, which determine the spatial distribution of organs and the light interception pattern of the entire plant), and the size parameters of each organ (such as leaf length, leaf width, internode length, internode diameter, fruit diameter, etc.). The specific values and combinations of these geometric parameters directly determine the 3D morphology of the plant.

C. Simulation Module (XPlantGLS)

XPlantGLS simulates the entire growth and development process of plants based on input parameters, including development parameters (e.g., growth cycle (GC) and node differ-

entiation rate), functional parameters (e.g., photosynthetic efficiency and source-sink variation), and morphological parameters (e.g., initial organ size and angle). During simulation, XPlantGLS can dynamically compute and record the dynamic changes of plant organs, such as the quantity (number of leaves, branches, and fruits) and weight of each organ at different growth stages. In addition, considering the randomness of plant growth in natural environments, this module also supports simulating the stochastic development process of plants, which can more realistically reflect the actual growth status of plants. The simulation results can be presented in both 2D and 3D architectural forms, allowing users to intuitively observe the spatial structure and growth process of plants.

For the simulation with XPlantGLS, a parameter file is needed, and also a mask file may be used to set the positions of fruits and branches when simulating stochastic plants. The role of a mask file is to simplify the simulation by transforming the stochastic development into deterministic development of a plant. By setting the topological, functional, and geometric parameters in the parameter file, the XPlantGLS can simulate the development and growth of plants as defined. The software is equipped with an interface for users to set plant age, select whether to generate a target file or a mask file, specify the organ types to be displayed, and set the number of plants to be drawn, etc.

By running the XPlantGLS, the dynamic development and growth processes can be simulated, such as the weight of each organ can be computed for each DC. Moreover, the leaf area index, the number of phytomers, and the demand and biomass production can be computed for each DC, as well as the total weights of each organ type. The sink strength variation of each organ type can also be computed based on the Beta law. The simulation process of XPlantGLS is supported by two core files: the parameter file is the core input, which contains the three types of parameters mentioned above to define the plant growth and development rules; setting parameters according to the actual biological characteristics of the target plant can ensure that the simulation results are consistent with the real physiological laws of plants. The mask file is mainly used for stochastic plant simulation, which predefines the fixed positions of key organs to avoid cumulative errors caused by random variations in organ initiation and placement, thus streamlining the simulation process while maintaining the authenticity of the overall plant structure. During simulation, the system automatically calculates and records a series of key physiological and morphological indicators for each DC, realizing comprehensive monitoring of plant growth status.

D. Calibration Module (XPlantGLA)

XPlantGLA estimates the key source-sink parameters of the GreenLab model, which are crucial for improving the accuracy and reliability of the plant growth model. By inputting the measured plant growth data (e.g., organ weight, quantity, and growth period data) into XPlantGLA, the module can use optimization algorithms to fit the model parameters, so that the simulation results of the model can be highly consistent with the actual measured data. This parameter calibration process effectively solves the problem of inaccurate model parameters caused by differences in plant varieties, growth

environments, and other factors, and further improves the applicability and prediction ability of XPlantGL.

For the calibration (fitting) with XPlantGLA, two essential input files are required: a parameter file and a target file containing the measured experimental data. The parameter file provides the initial set of parameters of the model, which will be iteratively adjusted during the fitting process; the target file takes the actual measured data of the target plant (such as organ weights at specific developmental stages) as the reference standard for evaluating the fitting effect. For plants with stochastic growth characteristics, an additional mask file is also needed to convert the stochastic developmental pattern into a deterministic one, eliminating the interference of random factors on the calibration results.

XPlantGLA is equipped with a dedicated visual interface to standardize the calibration process and improve its operability, where users can set three core parameters: iteration time, random number seed, and fitting repetition number. The iteration time determines the number of parameter adjustment rounds to minimize the deviation between simulated data and measured data; the random number seed ensures the reproducibility of the fitting results, especially when dealing with stochastic-related settings; and the repetition number is used to reduce the impact of random errors by repeating the fitting process multiple times and taking the optimal result.

After completing the parameter configuration via the interface and launching the XPlantGLA calibration process, the model employs the generalized least square method to estimate the key source-sink parameters of the model. The GLSM is selected for its advantage in handling data with heteroscedasticity (unequal variance) and correlation, which is common in plant growth measured data, thus improving the accuracy of parameter estimation. Furthermore, based on the measured data (either single-stage or multi-stage data collected at different developmental periods), the model can compute and output the weight of each individual organ (e.g., each leaf, fruit, or internode) and the total weight of each organ type (e.g., total leaf weight and total fruit weight) for each DC during the calibration process. This allows users to compare the simulated organ weights with the measured data in detail, facilitating the evaluation of the model's performance at the organ level. In addition, the model can calculate and visually display the dynamic evolution of two critical physiological indicators throughout the plant's growth period: the total biomass demand (the total nutrient requirement for plant growth and development) and the actual biomass production (the total organic matter accumulated through photosynthesis). These dynamic curves not only help verify the rationality of the calibrated parameters but also provide insights into the source-sink balance and nutrient allocation characteristics of the plant during its growth cycle.

III. RESULTS

XPlantGL has been successfully applied to simulate and estimate source-sink parameters for dozens of plant varieties, covering three major categories: field crops, horticultural crops, and herbaceous plants (including stochastic plants). These validations demonstrate the model's wide adaptability and reliability in capturing the growth and developmental characteristics of different plant types. Detailed descriptions of the validation results for each category are presented below.

A. Simulations with XPlantGL

By configuring the specific parameters for the simulation process, XPlantGL can accurately model plant growth and development in accordance with the predefined parameter settings. It calculates the number of organs and the biomass of each organ throughout all growth cycles, while also calculating the overall biomass production and precisely allocating the distribution of resources among the various organs in each cycle. Ultimately, XPlantGL is able to visually represent the resulting plant structures, either in 2D or 3D formats, as displayed in Fig. 3.

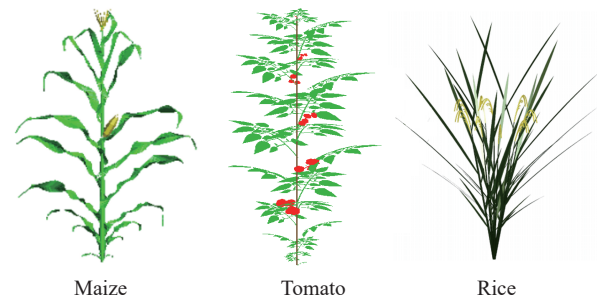


Fig. 3 Plant architectures simulated with XPlantGL.

B. Validation for Field Crops

Maize, a typical single-stemmed field crop, was selected for validation, and the experimental calibration data included measured data from the stage of 28 growth cycles. Based on these data, XPlantGL successfully estimated 11 source-sink parameters that govern maize growth and biomass allocation (Table 1). In addition to parameter estimation, the model computed a series of critical growth information throughout the entire GCs, including the dynamic changes in biomass demand and actual biomass production, the sink strength of each organ type and its variation, the progressive evolution of individual organ weights, and the total weight of each organ type at each GC (Fig. 4). These results reflect the model's ability to accurately reproduce maize's growth dynamics.

C. Validation for Horticultural Crops

Tomato, a typical branched horticultural crop, was used for the second validation, and the experimental dataset included measured data from 3 distinct growth stages (9, 17, and 28 GCs). XPlantGL estimated 12 functional source-sink parameters for tomato based on the multi-stage measured data (Table 2). Consistent with the maize validation, the software computed and output key growth parameters throughout the tomato's growth cycle, including the dynamic changes in biomass demand and production, the sink strength of each organ and its variation over time, the sequential evolution of individual organ weights, and the total weight of each organ type at each growth stage (Fig. 5). These results confirm that XPlantGL can effectively simulate the growth process of branched horticultural crops with complex architectural characteristics, and the parameter estimation results are reliable.

D. Validation for Herbaceous Plants

Rice, a herbaceous plant with inflorescences that exhibits 2 distinct physiological ages, was selected for the third valida-

Table 1 The computed source-sink parameters of model on maize.

Type	Description	Parameter	Value
Source	Light extinction coefficient	r	23.5
	Projection surface area	S_p	2181.7
	Seed biomass	Q_0	0.99
Sink strength	Petiole	P_p	0.95
	Internode	P_i	1.5
	Female	P_f	367.7
	Male	P_m	10.4
	Blade	B_{a1}	2.59
Variation of sink strength	Petiole	B_{p1}	3.64
	Internode	B_{i1}	3.61
	Female	B_{f1}	2.9

Table 2 The computed source-sink parameters of model on tomato.

Type	Description	Parameter	Value
Source	Light extinction coefficient	r	23.1
	Projection surface area	S_p	6694.1
Sink strength	Petiole	P_p	1.56
	Internode	P_i	1.28
	Female	P_f	48.15
	Blade	B_{a1}	2.81
		B_{a2}	1.89
Variation of sink strength	Petiole	B_{p1}	6.42
		B_{p2}	4.67
	Internode	B_{i1}	14.1
		B_{i2}	9.22
	Female	B_{f1}	2.67

tion. The experimental data included measured data from 8 growth stages (7, 10, 12, 15, 18, 21, 25, and 29 GCs), and XPlantGL successfully estimated 15 functional source-sink parameters (Table 3). As with the previous two cases, the software computed key growth parameters throughout rice's growth cycle, including the dynamic changes in biomass demand and production, the sink strength of each organ and its temporal variation, the evolution of individual organ weights on the main stem and tillers, and the total weight of each organ type at each growth stage (Fig. 6). This validation further demonstrates that XPlantGL has good versatility in handling herbaceous plants with complex physiological and structural characteristics, and can accurately simulate the tillering and inflorescence development processes of rice.

IV. DISCUSSION

As a generic FSPM, GreenLab has been successfully applied to more than 20 plant species, showing broad applica-

bility in capturing the growth dynamics of diverse plant types [9]. A key advantage of the GreenLab model is its ability to calibrate core parameters using easily obtainable experimental measurements, which reduces the technical barrier for its application. Additionally, XPlantGL, as a crop-specific derivative of GreenLab, inherits this advantage and further generates a standardized generic target file format, which standardizes the organization of plant measurement data. This standardization simplifies the data collection and processing process, facilitating more efficient model calibration and validation [15], and is consistent with the research conclusion that standardized data management (especially for phenomics and enviromics data) can streamline data integration and improve the efficiency of crop model calibration and validation [16].

The validation results of maize, tomato, and rice show that XPlantGL can effectively simulate the growth and development processes of different types of crops, and accurately esti-

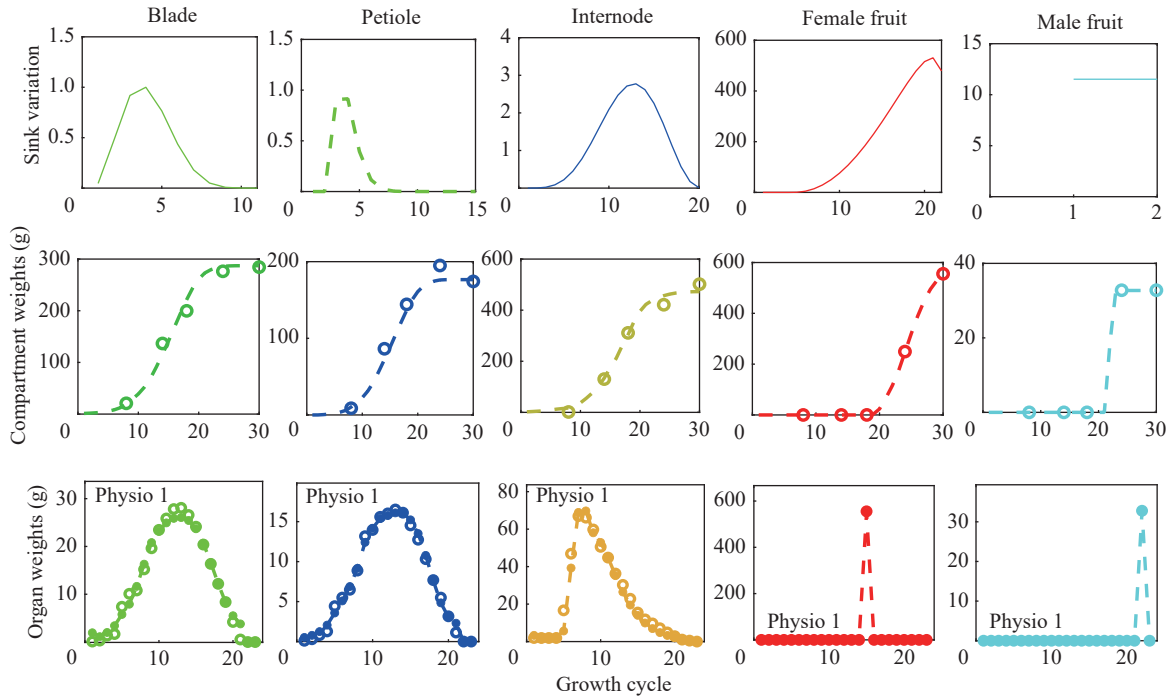


Fig. 4 Validation results of XPlantGL for field plants (maize), including sink strength variation of each organ type, the evolution of individual organ weights, and the total weight of each organ type at each growth cycle. Physio 1 represents main stem.

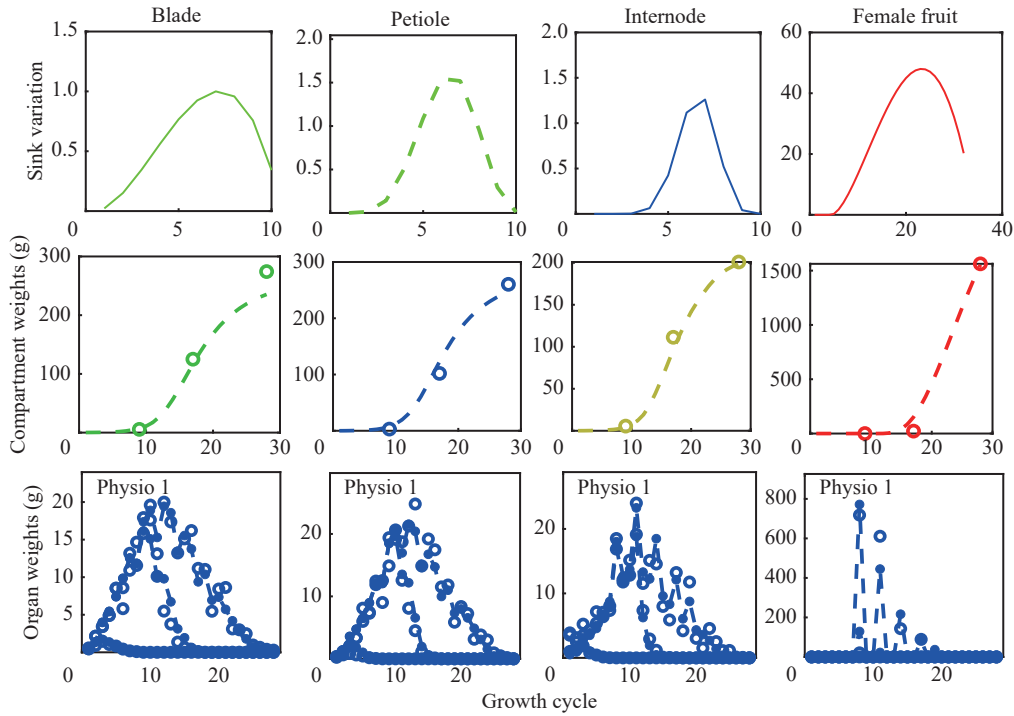


Fig. 5 Validation results of XPlantGL for horticultural plants (tomato), including sink strength variation of each organ type, the evolution of individual organ weights, and the total weight of each organ type at each growth cycle. Physio 1 represents main stem.

Table 3 The computed source-sink parameters of model on rice.			
Type	Description	Parameter	Value
Source	Light extinction coefficient	r	49.3
	Projection surface area	S_p	593.8
Sink strength	Petiole (stem)	P_{p1}	1.13
	Internode (stem)	P_{i1}	0.52
	Female (stem)	P_{f1}	48.15
	Blade (tiller)	P_{b2}	0.76
	Petiole (tiller)	P_{p2}	0.77
	Internode (tiller)	P_{i2}	0.37
	Female (tiller)	P_{f2}	2.22
Variation of sink strength	Blade	B_{a1}	10.2
	Petiole	B_{p1}	7.31
	Internode	B_{i1}	0.4
	Female	B_{f1}	2.79
Remobilization	Blade	K_{rb}	0.18
	Petiole	K_{rp}	0.19

mate key source-sink parameters based on measured data. With the rapid advancement of plant phenotyping technologies [17], a large amount of high-precision plant growth information (e.g., organ morphology, physiological status, and temporal dynamics) can be acquired [18, 19], which provides abundant data support for further validation and optimization of XPlantGL, and helps to expand the application scope of the software to more crop species, thus further improving its reliability and applicability.

XPlantGL currently focuses on the intrinsic growth mechanisms of plants based on the source-sink relationship and

structural parameters, and does not consider the impact of environmental factors (light intensity, temperature, CO₂ concentration, and water and nutrient availability) on photosynthesis and plant growth. To expand the functional scope of the software, the GreenLab model can be integrated with light-photosynthesis models [20, 21], which can make XPlantGL simulate the effects of environmental factors, making the results more realistic and predictive, and make up for the current deficiency of the software in environmental factor modeling. Furthermore, combining the GreenLab model with machine learning algorithms holds great potential for predicting crop yields [22]. Integrating environmental data, genomic and phenotyping information with model simulation results can help XPlantGL realize yield prediction under different environmental and management conditions, and provide technical support for smart breeding [23, 24] and cultivar evaluation under the context of climate change, aligning with the modern plant breeding framework that emphasizes the integration of genomics, phenomics, and enviromics data to optimize crop improvement [16, 25], providing valuable insights for agricultural sustainability and food security.

Compared with other mainstream FSPM software such as OpenAlea and GroIMP, XPlantGL has obvious crop-specific advantages: OpenAlea and GroIMP are general plant modeling software compatible with crops and trees, with bulky architectures and redundant functions for crop-specific research, and their complex operation processes require high programming skills of users; XPlantGL is a light-weight Matlab-based software tailored for crop research, with an optimized GUI that realizes visual operation, and natively supports branching and stochastic crop growth processes, which is more suitable for the research needs of crop science. At the same time, we also recognize that OpenAlea and GroIMP have more advanced 3D visualization effects and

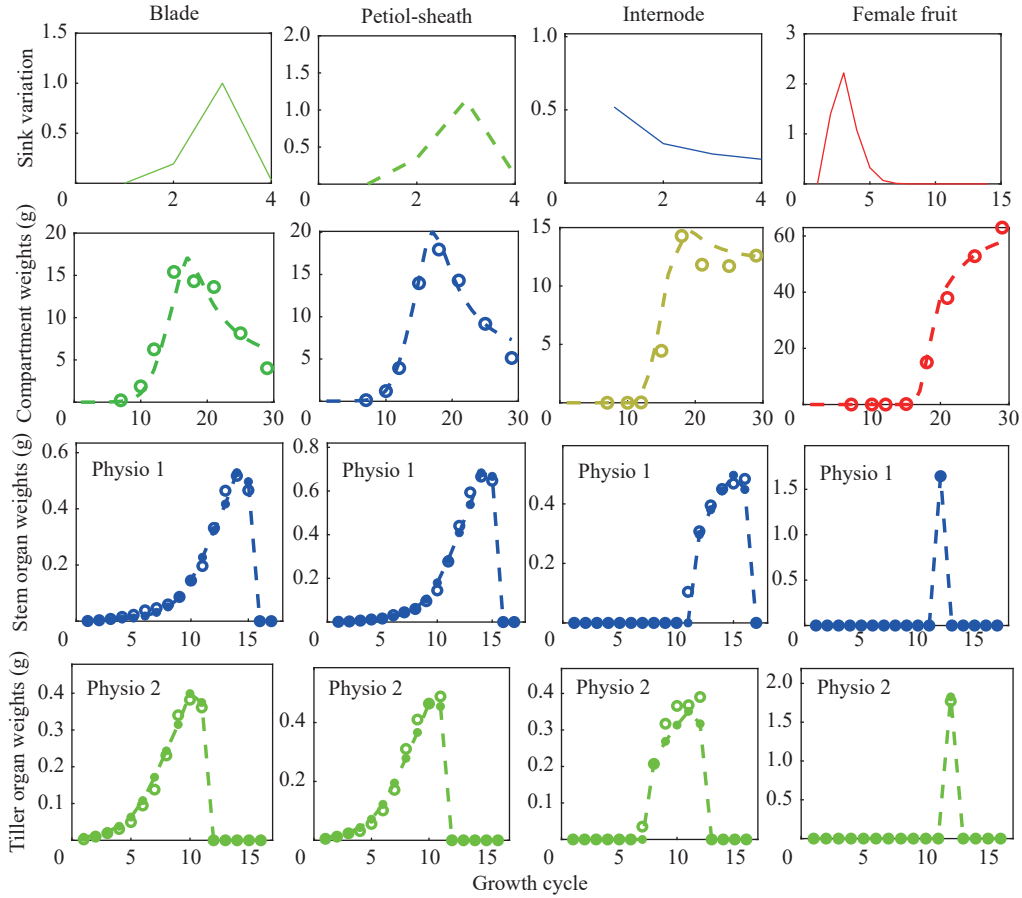


Fig. 6 Validation results of XPlantGL for herbaceous plants (rice). Sink strength variation of each organ type, the evolution of organ compartment weights on the main stem and tillers, showing remobilization, and the total weight of each organ type at each growth cycle. Physio 1 represents main stem. Physio 2 represents tillers.

richer functional modules for plant-tree integrated modeling, which are the directions for the subsequent optimization and improvement of XPlantGL.

V. CONCLUSIONS

XPlantGL, as a Matlab-based software implementation of the GreenLab model for crop research, effectively makes up for the limitations of existing GreenLab derivative software in crop simulation. It retains the core functions of GreenLab in biomass production, allocation simulation, and parameter calibration, and adds native support for branching and stochastic crop growth processes, optimizes the GUI to simplify the operation process, and integrates GLSM to realize efficient single-stage and multi-stage parameter fitting. The validation results of maize (single-stemmed field crop), tomato (branched horticultural crop), and rice (herbaceous plant) show that XPlantGL can accurately simulate the growth dynamics of different types of crops and reliably estimate the key source-sink parameters, which confirms the high accuracy, versatility, and practicality of the software.

As a user-friendly FSPM tool, XPlantGL provides a convenient and reliable research platform for plant growth modeling, and lays a solid technical foundation for digital crop phenotyping, smart breeding, and intelligent agricultural management. In the future, we will combine the software with machine learning algorithms to integrate genomics, phenomics, and enviromics data, and build a crop yield

prediction model to provide more comprehensive technical support for smart agriculture and precision breeding. In addition, we will continue to expand the crop library of XPlantGL, update and maintain the open-source repository regularly, and build a user community to promote the popularization and application of the software in agricultural science research and teaching.

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