From Population to Individual Scale: Data-Driven Exploration of the Connection Between DSSAT and GreenLab Crop Models - Postprint

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Abstract

Research on crop models encompasses the complex processes of crop growth and development, spanning spatial scales from molecules to cells, tissues, organs, individuals, and populations, and temporal scales from seconds to years. Switching the scale of crop models according to different research requirements can enhance their applicability and flexibility. This study specifically addresses the transition from population-scale crop models to individual-scale crop models. Based on existing experimental data from two treatments (irrigated and rain-fed) for four maize varieties and corresponding simulation data from the DSSAT system, this research calibrates the parameters of the functional-structural model GreenLab, uses consistency in computational results as the evaluation metric, explores methods for establishing interfaces between models at different spatial scales, and compares the characteristics of different models. The results demonstrate that the GreenLab model can successfully reproduce both the simulation data from the DSSAT system and actual measured data, and can further invert the allocation of biomass among various organs and perform three-dimensional visualization. Finally, the advantages and application domains of integrating models at different spatial scales are discussed.

Full Text

From Stand to Organ Level—A Trial of Connecting DSSAT and GreenLab Crop Models through Data

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Abstract

Crop modeling encompasses the complex processes of crop growth and development across multiple spatial scales (ranging from molecular to cellular, tissue, organ, individual, and stand levels) and temporal scales (spanning seconds to years). Adapting model scales to specific research requirements enhances model applicability and flexibility. This study addresses the challenge of transitioning from stand-scale to organ-scale crop models. Using existing experimental data from four maize cultivars under two treatments (irrigated and rainfed) and corresponding DSSAT system simulations, we calibrated parameters of the functional-structural GreenLab model. With consistency of computational results as our evaluation metric, we explored methods for establishing interfaces between different spatial-scale models and compared their respective characteristics. Results demonstrate that the GreenLab model can reproduce both DSSAT simulation data and actual measurements, enabling inverse calculation of biomass allocation among various organs and three-dimensional visualization. Finally, we discuss the advantages and application domains of integrating different spatial-scale models.

Keywords: crop model; different model scales; functional-structural plant model; model integration; DSSAT; GreenLab; parameter estimation

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Introduction

Models serve as powerful tools for testing hypotheses, synthesizing knowledge, describing and understanding complex systems, and comparing different scenarios, with applications in decision support systems, greenhouse climate control, forecasting, and production planning [1]. Since the 1960s, advances in information technology and deeper understanding of plant growth mechanisms have fostered interdisciplinary collaboration and propelled the development of crop models. By systematically analyzing and quantitatively describing crop growth and development processes and their dynamic relationships with the environment using computers, these models can predict crop phenological development, morphogenesis, dry matter accumulation and distribution, and yield, thereby providing comprehensive knowledge expression and deeper insights into crop growth processes [2,3].

Crop modeling research addresses complex growth processes across various spatiotemporal scales, with spatial scales ranging from molecular to cellular, tissue, organ, individual, and stand levels, and temporal scales spanning seconds, days,

and years [4]. The choice of model scale depends on the research objectives, processes under investigation, and level of human understanding. Figure 1[Figure 1: see original paper] illustrates the classification of crop models across spatiotemporal scales from gene to ecosystem [5], which helps clearly position the scale of the studied model and ensures discussion within a consistent scale. Integrating different-scale models can combine their respective strengths, thereby enhancing model applicability.

Crop models can be categorized as either descriptive models (statistical, regression, empirical, or black-box models) that directly establish input-output relationships without concerning internal mechanisms, or explanatory models (process-based models) that quantitatively and dynamically describe crop growth, development, and yield formation processes along with their environmental responses [6], typically at the stand level. Common process-based crop models such as CERES [7], TomSim [8], STICS (Simulateur mulTIdisciplinaire pour les Cultures Standard) [9], and APSIM (Agricultural Production Systems sIMulator) [10] simulate photosynthesis and assimilate partitioning processes, primarily using Leaf Area Index (LAI) to predict biomass yield per square meter while considering radiation, temperature, and basic inputs (irrigation and fertilizer). These models generally treat different organ types as aggregated pools, focusing on total fruit weight, leaf weight, etc., making it difficult to describe intra-plant structural changes and their impact on yield.

Recognizing the importance of crop architecture, Functional-Structural Plant Models (FSPM) have emerged at the individual scale to simulate crop morphological structure, biomass production and allocation, and their intrinsic relationships. FSPM represents modeling and simulation of the complex plant system from individual organs to whole plants [11], experiencing rapid development over the past two decades to become a major research focus in plant modeling. The GreenLab model, a functional-structural crop model, considers the sequential production of similar organs and employs the concepts of common pool and source-sink relationships. It models plant growth at the phytomer scale (organ level) while maintaining compatibility with process-based crop models (stand level). Based on plant automaton theory [12], GreenLab uses recursive algorithms to calculate organ numbers produced at each time step, then allocates biomass from the common pool to different organ categories according to relative sink strength and organ quantity. This process is described through mathematical formulas without requiring individual organ-level biomass allocation simulation, resulting in computational efficiency—a key advantage of GreenLab. Furthermore, GreenLab' s distinctive feature lies in its ability to inversely estimate source-sink parameters affecting biomass production and allocation from measured organ weights, with applications to over a dozen crops including maize [13], wheat [14], rapeseed [15], cucumber [16], and tomato [17] [18]. However, GreenLab simplifies environmental influences into a single environmental factor E, limiting its capacity to adequately simulate impacts of climate, soil, and management practices on crop yield.

Recent years have witnessed rapid development in crop phenotyping equipment, enabling collection of various phenotypic information including plant height, leaf area, grain number, physiology, and photosynthesis. Consequently, analyzing these large phenotypic datasets has become a pressing issue [19]. Integrating different crop models facilitates deeper understanding of crop behavior and maximizes model utility. This study employs the DSSAT system (stand scale) and GreenLab model (organ scale) to investigate the fusion of stand- and individual-scale models, exploring the potential for interaction between models constructed at different spatial scales and using different approaches. This integration enables simultaneous simulation of crop genetic characteristics, management practices, and environmental influences, while also modeling dynamic growth and development processes of individual plant organs. Such detailed understanding allows for comprehensive description of yield components and three-dimensional crop visualization for comparison with phenotypic information. Through this model fusion, we provide a foundation for plant breeding, phenotyping, and crop system optimization.

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2 Materials and Methods

Figure 2[Figure 2: see original paper] Technical roadmap for DSSAT and GreenLab integration

The overall research framework is illustrated in Figure 2[Figure 2: see original paper]. The model integration concept acknowledges that model developers and implementation methods differ and form independent systems; therefore, we chose to connect the models through unified output results rather than attempting to merge model components. First, the DSSAT system was used to simulate daily maize leaf, stem, and cob weights. Based on these data, combined with the experimental data from (1), DSSAT simulated daily data for four maize cultivars, including daily leaf, internode, cob, and total aboveground weights. This study selected DSSAT simulation data from 11 growth stages with leaf numbers of 7, 10, 15, 20, 23, 27, 30, 33, 36, 39, and 40 for GreenLab model simulation calculations.

2.1.1 Experimental Data Selection

The experimental data comprises two parts: (1) Field trial measurements from Soler et al. [20] conducted in 2002 in Piracicaba, Brazil (22.7°W, 47.4°S, 580 m altitude) for four maize cultivars (AG9010, DKB333B, DASCO32, and EXCELER) under two treatments: irrigated (I) and rainfed (R). The data include soil, climate, and management information, along with seven periodic measurements (on March 12, 21, 27, April 7, 18, 28, and May 14) of maize LAI and total aboveground weight, comprising eight comparative experiments. AG9010 is a short-season cultivar (904 Growing Degree-Days (GDD) from planting to silking, base temperature 8°C), DASCO32 and EXCELER are short-season cul-

tivars (995 GDD), and DKB333B is a conventional cultivar (1037 GDD) [21,22]. All trials followed a randomized complete block design with four replications. Each plot measured 20 m in length with 0.8 m row spacing, four rows total, and a planting density of 5 plants/m^2. (2) Based on the data from (1), the DSSAT system simulated daily data for the four maize cultivars, including daily leaf, internode, cob, and total aboveground weights.

2.1.2 Data Processing

The DSSAT model operates on a daily time step, whereas the GreenLab model simulates based on phytomers, with each new leaf production considered one Growth Cycle (GC), i.e., the phyllochron. Therefore, conversion from days to growth cycles is necessary. Plant development is regulated by transforming calendar time (days) into thermal time (cumulative temperature), which enables definition of the cycle concept.

In the GreenLab model, a meristem produces one phytomer per growth cycle, with leaves receiving energy proportional to the accumulated light radiation during that cycle. Based on daily data and thermal time from DSSAT, corresponding growth cycles in the GreenLab model were calculated. Weights of various organs per plant were computed according to planting density.

2.2 Model Parameter Settings

Process-based crop models calculate biomass produced from light intercepted per unit land area at each daily time step. Plant light absorption can be computed using the Beer-Lambert law:

$$I/I_0 = e^{-kL}$$

where k is the extinction coefficient; I is radiation level at canopy depth L, W/m^2; I_0 is radiation level at the canopy top, W/m^2; and k typically ranges from 0.5 to 0.8 [1]. Light absorption increases with leaf area but leaf shading reduces light interception.

Biomass can be calculated using Equation (2). The formula for biomass production is:

$$Q(t) = a(jtP\phi j = iS_p \bullet \sum Q(ji+1)\max(t,t_a)i = tt_a + 1\mathrm{mx}\phi N\phi\phi = 1a(i)$$

The GreenLab model is based on the biomass common pool concept [23] and source-sink relationship assumptions, utilizing the concepts of crop growth age and physiological age. Growth age refers to the number of growth cycles a plant has experienced, applicable to all organs. Physiological age distinguishes different branch types in plants, with the main stem having physiological age 1 and branches age 2.

In GreenLab, the time step is transformed into growth cycles. During each cycle, meristems produce new phytomers (development), while leaves perform photosynthesis to produce biomass that is allocated to various organs according to their sink strengths (growth). Thus, plant development and growth are simulated on the same temporal scale. This approach allows temporal scaling even after apical development ceases (tassel emergence). The linear relationship between growth cycle number and thermal time is established during the developmental phase and then extrapolated to the growth phase.

Additionally, DSSAT model weight units are g/m^2, requiring conversion to per-plant organ weights based on planting density. This study focuses on leaf, internode, and fruit weights.

2.2.1 Model Growth Parameter Settings Based on a planting density d of 5 plants/m^2, the initial value of S_p was set to $1/d = 2000$ and subsequently adjusted according to fitting results. The r value corresponding to DSSAT' s Radiation Use Efficiency (RUE: 4.2 g/MJ) and GreenLab model empirical values was set to 50. Based on DSSAT simulation data, expansion periods for leaves, internodes, and fruits were set to 15, 25, and 20, respectively, with functional periods all set to 25, along with parameters for calculating sink strength variation functions [13]. The relative sink strength of leaves was set to 1.

2.2.2 Development Parameter Settings For maize, each phytomer contains one leaf and one internode or fruit. According to DSSAT data, final leaf numbers ranged from 19 to 21. DSSAT model data indicated that all four maize cultivars had a single fruit type located at the 16th or 17th internode of the main stem.

2.3 Model Parameter Fitting

Based on Equation (3), with the r value fixed, we fitted environmental parameter E and sink strength parameters P_o (o represents leaf b, internode i, and fruit f), while adjusting S_p values according to simulation results. Empirically, environmental variations have minimal impact on GreenLab sink strength parameters [13]; therefore, we adopted a constant environmental parameter E (averaged) rather than reading environmental sequences for simulation. Additionally, two remobilization parameters k_m and k_k required fitting. Transfer proportions k_{mb} and k_{mi} were estimated from experimental data as 0.8, while transfer rate parameters k_{kb} and k_{ki} were obtained through model fitting.

Since biomass from leaves and internodes transfers to fruits during late maize growth, the remobilization process must be considered, whereby mature organs (leaves and internodes) reallocate partial biomass to fruits according to the following formula:

$$q(t) = q_{\text{maxo}}(1 - k_{mo} \cdot (1 - k_{ko})^t$$

where t is plant growth age (GC); $q_{\mathrm{max}o}$ is maximum organ weight (g); k_{mo} is the proportion of biomass transferred from the organ (%), estimable from measurements; k_{ko} is biomass transfer rate (g/GC), obtained through model inversion; and o denotes organ type (leaf b and internode i in this study).

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3 Results and Analysis

3.1 Experimental Results

3.1.1 Plant Height and Final Yield per Unit Area Plant height and final yield per unit area at harvest for the four maize cultivars under both treatments are presented in Table 1. Irrigated treatments showed higher plant height and final yield than rainfed treatments. Cultivar EXCELER achieved the highest yields under both treatments, followed by DASCO32, with AG9010 showing the lowest yields. Results indicate that irrigation significantly increased yield for all four cultivars, with EXCELER being the optimal cultivar.

Table 1 Plant heights and final yield of the two treatments for the four maize cultivars

3.1.2 Organ Weights Weights of various organs (leaves, internodes, fruits) at harvest for the four maize cultivars under both treatments are shown in Figure 3[Figure 3: see original paper]. All organ weights were higher in irrigated treatments compared to rainfed treatments. However, DSSAT-simulated yields were highest for DKB333B, deviating substantially from measured results. DASCO32 and EXCELER showed similar yields, while AG9010 had the lowest yield, consistent with experimental results in Table 1.

Figure 3[Figure 3: see original paper] Weights of organs (leaves, internode, fruits) and total weight for the four maize cultivars and two treatments

Note: AG, EXC, DAS, DKB represent the four maize cultivars; R = rainfed, I = irrigated

Figure 4[Figure 4: see original paper] Growth cycle and number of leaves with thermal time for the four maize cultivars and irrigation treatments

3.2.1 Temporal Scale Conversion Between the Two Models

Changes in leaf number and theoretical growth cycle number with thermal time were consistent across irrigated and rainfed treatments for the four maize cultivars (Figure 4[Figure 4: see original paper]). Therefore, only the irrigated treatment results are presented. No significant differences in leaf number existed among cultivars (19–21), and the three short-season cultivars AG9010, DASCO32, and EXCELER required similar growth cycle numbers. Only the conventional cultivar DKB333B showed slightly longer growth cycles, but the difference was not significant ($F = 0.097$, $P > 0.5$, $df = 3$).

Phyllochron can be calculated from temperature and leaf number. For maize, thermal time exhibits a linear relationship with the number of developed phytomers, enabling calculation of growth cycles expressed in thermal time and corresponding phytomer numbers per cycle.

After leaf number ceases to increase, maize reaches maturity. Although no new phytomers are produced during this phase, growth continues. Theoretical growth cycle numbers can be determined from the binary linear relationship (slope) between thermal time and leaf number from germination to tassel emergence. Time is discretized to calculate theoretical growth cycle numbers during the growth phase based on the linear relationship established during development (Figure 4[Figure 4: see original paper]).

3.3 Comparison of Simulation Results and Measurements Between the Two Models

Since field experiments only measured LAI and total aboveground weight, we compared simulated LAI and total aboveground weight from both models with experimental data to validate model accuracy.

3.3.1 LAI Comparison Figure 5[Figure 5: see original paper] compares measured LAI values with DSSAT and GreenLab simulations at different stages. The GreenLab model showed better agreement with measured LAI values, while DSSAT simulations for cultivars AG9010 and DKB333B were overestimated during later stages. Results demonstrate that GreenLab can better simulate LAI values when based on DSSAT simulation data.

Note: Cmp, Sim, and Obs represent GreenLab simulations, DSSAT simulations, and observed measurements, respectively; I and R denote irrigated and rainfed treatments. Figure 5[Figure 5: see original paper] LAI values for the four maize cultivars under two treatments

3.3.2 Total Aboveground Weight Comparison Figure 6[Figure 6: see original paper] compares measured total aboveground weight with DSSAT and GreenLab simulations at different stages. Both models showed good consistency with experimental measurements for both irrigated and rainfed treatments, demonstrating that the two models can effectively simulate these values with consistent outputs.

Note: Cmp, Sim, and Obs represent GreenLab simulations, DSSAT simulations, and observed measurements, respectively; I and R denote irrigated and rainfed treatments. Figure 6[Figure 6: see original paper] Total aboveground weight for the four maize cultivars under two treatments

3.4 Organ Weight Simulation

GreenLab simulations of organ weights at different growth stages for the four maize cultivars under both treatments showed excellent results, with all simu-

lation R^2 values reaching 0.99 (Figure 7[Figure 7: see original paper]). Results demonstrate consistency between GreenLab and DSSAT simulations.

Note: I and R denote irrigated and rainfed treatments; Cmp and Sim represent GreenLab and DSSAT simulated values, respectively. Figure 7[Figure 7: see original paper] Comparison of GreenLab and DSSAT simulated leaves, internodes, and fruits at different developmental stages for the four maize cultivars under two treatments

3.4.1 Organ Weight Simulation at Different Growth Stages Since field experiments only measured LAI and total aboveground weight, we compared simulated LAI and total aboveground weight from both models with experimental data to validate model accuracy.

3.4.2 Variation of Organ Weight with Position and Growth Stage As an organ-scale model, GreenLab can simulate variations in organ weight with position (Figure 8Figure 8: see original paper) and growth stage (Figure 8(b)). Leaf and internode weights initially increased then decreased with both phytomer position and growth stage.

(a) Leaves and internodes at different phytomer positions and (b) weights of leaves, internodes, fruits, and total aboveground biomass at different growth stages. Figure 8[Figure 8: see original paper] Simulated variation of maize organ weights with phytomer rank and growth stage

3.4.4 Three-Dimensional Structure Simulation of Maize Plants The GreenLab model can simulate three-dimensional maize structures based on measured plant height data. Figure 10[Figure 10: see original paper] presents 3D plant structures at harvest stage for the four maize cultivars under both treatments. Irrigated plants showed greater height than rainfed plants, consistent with experimental measurements (Table 1) [20].

Note: I and R denote irrigated and rainfed treatments. Figure 10[Figure 10: see original paper] Simulated 3D structures of four maize cultivars under two treatments using the GreenLab model

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4 Discussion

4.1 Feasibility of Connecting Different-Scale Models

The GreenLab functional-structural model exhibits good compatibility with process-based models. Lemaire et al. [24] used GreenLab to calculate projection area S_p values based on various organ weights, with results consistent with experimental data. Feng et al. [25] employed GreenLab with differential statistical methods to study yield conversion from individual maize plants to stands, with calculations matching stand-level measurements. These studies demonstrate

that GreenLab can simulate dynamic growth and development of individual organs using only organ weight data. Therefore, as an organ-scale functional-structural model, GreenLab is fully compatible with process-based crop models, bridging the gap between agronomic crop models and botanical architecture models.

This study utilized measured data and simulated daily leaf, internode, and fruit weight data from DSSAT to successfully simulate LAI and total above-ground weight with GreenLab, consistent with experimental results. Furthermore, GreenLab-calculated total weights of various organs (leaves, internodes, fruits) at different stages aligned with DSSAT simulation data, confirming good compatibility between DSSAT and GreenLab. This work preliminarily explores approaches for connecting traditional crop models with functional-structural models [26]. While not necessarily improving process-based model simulations, organ-scale models can provide deeper insights into plant architecture [27]. DSSAT provides aggregated organ information, whereas GreenLab, through organ sequence identification, enables simulation of individual organ growth processes (Figure 8(a)) and dynamic cycle-by-cycle changes in organ sequences (Figure 8(b)). Moreover, the constructed GreenLab model can support further computational experiments to optimize source-sink parameters and investigate structural effects on yield at the individual scale [16].

4.2 Application Domains of Multi-Scale Model Integration

A key research theme in virtual agriculture is the visual representation of how management practices such as fertilization and irrigation affect individual crop growth. Building upon this study' s stand-to-individual scale approach, models can rapidly simulate crop morphological changes under different management scenarios without adjusting individual organ sizes manually.

Individual-scale plant models often contain organ-scale submodels that can integrate with micro-scale genetic models [28] or photosynthesis models [29,30] to conveniently incorporate effects of per-unit-area photosynthetic rates on individual growth, thereby fully utilizing crop phenotyping information. They can also combine with stand-scale process models (such as DSSAT or APSIM), as demonstrated in this study. Individual-scale models can serve as bridges for multi-scale research, enabling broader modeling investigations [31,32]. Application domains include crop growth simulation and yield prediction under climate change scenarios, as well as breeding research.

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Note: Figure translations are in progress. See original paper for figures.