The Decision Support System for Agrotechnology Transfer (DSSAT) crop modeling ecosystem: evolution and advances

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1 Introduction

The Decision Support System for Agrotechnology Transfer (DSSAT) ecosystem is a combination suite of software created to facilitate the development and use of integrated crop, soil, weather, and management components and the datasets required for this development and applications. The DSSAT Cropping System Model (CSM) is the standalone executable component of DSSAT that simulates the dynamic performance of different crops and makes use of DSSAT's tools for input, output, analysis, and applications for simulating crop and soil performance for specific climates and management conditions.

In this chapter, we discuss the evolution of the DSSAT-CSM as it has been improved to simulate different crop and soil processes, examples of adding capabilities to simulate additional crops, model adaptation for new crop species, and examples of model applications for genetic improvement in the face of climate change. This chapter reviews the crop C, water, N, and P balance processes in the DSSAT-CSM and the tools and utilities in DSSAT.

2 The origins of the Decision Support System for Agrotechnology Transfer (DSSAT)

DSSAT originated out of the International Benchmark Sites Network for Agrotechnology Transfer (IBSNAT) project funded by the United States Agency for International Development (USAID). In the early 1980s, the USAID made a bold step to support a project based on systems analysis of agricultural production to address food security in developing countries. The IBSNAT project for improving agricultural production was led by Professor Goro Uehara,

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a soil physicist at the University of Hawaii, and co-led by Fred Beinroth, a soil scientist from the University of Puerto Rico. The IBSNAT project was a follow-up to the International Benchmark Soils Project also funded by USAID. Professor Goro Uehara, the leader of the initial soil project, concluded that predicting yields only based on soil type (similarity) was insufficient and that there was a need to consider the weather, plant genetics, crop and soil management aspects in addition to soil information. This led to the combined soil-crop-systems modeling approach in the IBSNAT project with an emphasis on field experimentation and minimum data required to be used in this integrated systems approach. The IBSNAT Project was funded from 1982 through 1992. However, in later years, USAID and other federal agencies were less supportive of funding for basic model development and improvement, although there was some funding for model applications.

At the start of the IBSNAT Project, crop modeling teams from the University of Florida (SOYGRO and PNUTGRO models) and from USDA-ARS in Temple, Texas (CERES-Maize and CERES-Wheat models) were invited to collaborate with scientists from the University of Puerto Rico, the University of Edinburgh (Scotland), the University of Guelph (Canada), and the International Fertilizer Development Center in Muscle Shoals, Alabama (Wilkerson et al., 1983; Ritchie et al., 1985; Boote et al., 1986; Jones and Kiniry, 1986; Jones et al., 1987). The SOYGRO model was developed by Wilkerson et al. (1981, 1983) and the PNUTGRO model by Boote et al. (1986). The CERES-Maize model had been developed by Allen Jones and Jim Kiniry (Jones and Kiniry, 1986) with guidance by Dr. J. T. Ritchie. The CERES-Wheat model had been developed by Ritchie et al. (1985) on a project funded by the US Central Intelligence Agency. Their goals were to develop relatively simple models that could simulate wheat and maize production in the Cold War regions based on satellite mapping of crop area presence and presumably satellite sensing of temperature, solar radiation, and likely rainfall. The CERES-Maize model is simpler in structure than SOYGRO or CROPGRO. It uses a simple radiation use efficiency approach that goes directly to dry matter, whereas CROPGRO considers leaf photosynthesis and growth respiration costs (Penning de Vries et al. 1974). CERES models use approaches for leaf area progression and partitioning to leaf and stem, based on hard-wired algorithms in the source code. The CROPGRO models are more mechanistic for partitioning and leaf area growth and are more generic, with parameters and relationships for processes being placed in external "read-in" files.

Early during the IBSNAT project, the investigators realized that the CERES-Maize, CERES-Wheat, and SOYGRO models had different input file types (structure, variable names, and placements), which required different subroutines for inputting weather, soils, management, and cultivar information. There was a lack of common file structures and a lack of common input "read"

methods across the different crop models. Dr. Jim Jones solved these issues during his 1983 sabbatical at the University of Hawaii, working with Professor Uehara and his team to set up common file formats for weather, soil, and management information. This required standardizing the exact structures of these three types of files (*.WTH, *.SOL, and various management input files), along with creating common read subroutines for both models. This effort was successful and led to the first official release of the DSSAT software Version 2.1 by 1989 (IBSNAT, 1989). DSSAT Version 3.0 (IBSNAT, 1993) was released at the end of the IBSNAT Project. As other models were developed and added to DSSAT, such as CERES-RICE and SUBSTOR-Potato, those models were required to use the same input file structure.

A strong emphasis of the IBSNAT project and current DSSAT modelers is the collection and preservation of data on soil water, soil N, final yield, and crop growth analyses collected during experiments. It became clear that such data were needed to develop, improve, and document model performance. Jim Jones participated in a 1984 meeting at the ICRISAT Center in India, where the modelers recognized the need for a common Minimum Data Set (MDS) for all inputs to crop models (ICRISAT, 1984). This led to the creation of the MDS system in IBSNAT and DSSAT that standardized the inputs required for the crop models as well as the file formats used. In addition, strong emphasis was placed on developing protocols for collecting the minimum data set (MDS). This standardization of protocols and standardized inputs led to the development of data utility programs for processing weather, soil, management input data, and experimental observation files, as well as tools for the application and display of output data for the models, forming the basis for the Decision Support System for Agrotechnology Transfer (DSSAT) software. Manuals were created to document the best procedures for data collection, what type of data, suggested frequencies of data collection, and documentation of models and tools in DSSAT (Hunt et al., 1994; Tsuji et al., 1994; Hunt et al., 2001; Hoogenboom et al., 2010; White et al., 2013). These manuals and documents remain available in the latest DSSAT shell: DSSAT Version 3, Volumes 1, 2, 3, and 4 (Tsuji et al., 1994) and DSSAT Version 4.5, Volumes 1, 2, 3, and 4 (Hoogenboom et al., 2010). For further details of IBSNAT activities and outcomes, see IBSNAT (1993), IBSNAT (1994),Uehara and Tsuji (1998), and Jones et al. (2016).

During the IBSNAT project (1980s), we explored available software for entering and storing such data. In this case, dBase2 software was initially used, which turned out to be an unfortunate choice because the company went out of business and no longer provided any support. After learning this lesson, we concluded that the best way to save long-term data was as ASCII files (the default for the past 40 years). While it may be fashionable and convenient to use various other methods of data entry and storage, those methods must be

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able to convert to, and from, ASCII files which are what the CSM model reads and outputs.

3 Advances in model development in the 1990s

Beginning about 1990, we encountered the drawbacks of having three different crop legume models (different source codes for soybean, peanut, and dry bean) that were somewhat different for the crop C and N balance aspects but barely different for soil water balance or soil N balance. We already had a crop parameter file for each of the three species, where that crop parameter file had a similar structure but different values for parameters for given crop species. But when we needed to repair or improve code in the soil water balance, for example, we found it necessary to make the same improvements in the three sets of code. Therefore, we decided to create one common source code for the three crops to avoid those issues. After reviewing the three models (SOYGRO, PNUTGRO, and BEANGRO) (Hoogenboom et al., 1990a, 1990b, 1992, 1994), we developed source code to create a single generic model that would simulate all three crops (Hoogenboom et al., 1991, 1992). This required us to remove any remaining crop-specific hard-coded parameters and relationships from the crop C and N balance subroutines and to put those parameters into an external species file (formerly called the "crop parameter file"). Gerrit Hoogenboom accomplished this complex task. The first trial version was named LeGro in 1993 (Hoogenboom et al. 1999), which later became CROPGRO. Also, during this period of code improvement, we added new code to the legume module in CROPGRO to simulate explicit nodule growth and N-fixation (Hoogenboom et al., 1990a, 1991). Boote et al. (2009) provide details on simulating nodule growth and N-fixation.

3.1 Introduction of leaf-level hedgerow photosynthesis and rubisco kinetics response to CO_2 into CROPGRO

During his career at the University of Florida, Ken Boote researched leaf and canopy photosynthesis and the modeling of those processes (Boote et al., 1983a, Boote et al., 1984; Boote and Loomis, 1991; Boote and Pickering, 1994). We developed a mechanistic model of leaf-to-canopy assimilation coupled with hedgerow light interception, where the leaf-level photosynthesis simulates on an hourly basis for sunlit and shaded leaves (Boote and Pickering, 1994; Pickering et al., 1995; Boote et al., 1998). This model captures the behavior of rubisco kinetics of Farquhar and von Caemmerer (1982) and mechanistically simulates photosynthesis response to CO_2, O_2, temperature, solar radiation, leaf area index, specific leaf area, and leaf N concentration. The simulated response to CO_2 is thus an emergent outcome of the rubisco-kinetics, rather than resulting from an externally prescribed CO_2 response

curve as often used in other models. The simulated leaf-level and canopy-level photosynthesis were tested against observed data and shown to be accurate by Alagarswamy et al. (2006). Since then, this hourly leaf-level photosynthesis method has been the default for all the CROPGRO model crops, in place of the older, but still available, daily canopy photosynthesis option. The CERES-based models in DSSAT are based on radiation use efficiency (RUE), and they use an externally prescribed CO_2 response modifier based on observed CO_2 response data.

The need to account for the CO_2 responsiveness of the models was recognized in the 1990s (Rosenzweig et al., 1995) and led to model evaluations against available CO_2-response data along with CO_2 impact assessment (Curry et al., 1995). In the late 1990s, we created DSSAT code and parameters that set CO_2 level for the actual years of the observed crop experiments based on the Mauna Loa Observatory CO_2 record, first established by Keeling et al. (1976). The need to do this became obvious as the CO_2 increased over decades from 315 ppm in 1959 to 427 ppm in 2024, which has increased simulated soybean yield by 19% (CROPGRO-Soybean simulations for 2 years in Iowa and 2 seasons in Ohio). Boote (2011) subsequently illustrated how elevated CO_2 is assisting soybean breeders to increase yield because there are beneficial G x E responses. In retrospect, a good portion of the soybean yield increase over this period can be attributed to rising CO_2 in addition to genetic improvement and technology. Boote et al. (2010) examined the CO_2 response curves for C3 and C4 crops simulated by the CERES-based models in DSSAT and evaluated CERES and CROPGRO modeled crops against metadata on observed CO_2 response. In addition, simple ozone impact subroutines that interact with CO_2 levels were introduced into the NWheat model (Guarin et al., 2019) and the CROPGRO-Soybean model (Guarin et al., 2024).

Further collaboration with Dr. Nigel Pickering (Pickering et al., 1990, 1993, 1995) led to the development of a stand-alone program for leaf-to-canopy assimilation that also simulated hourly canopy energy balance and evapotranspiration (ET) based on first principles and thus do not require the FAO-56 engineered ET equations of Allen et al. (1998). This code was placed into the SOYGRO/CROPGRO model to enhance the ability of the model to simulate response to CO_2 (Pickering et al., 1995). The hourly energy balance code was unused for many years but was later revived, improved, and evaluated by Cuadra et al. (2021). In addition to simulating ET, this option simulates soil and canopy temperature, uses crop temperature to drive crop processes, and uses CO_2- and vapor pressure deficit-sensitive control of stomatal conductance. This is included as an option in the latest DSSAT release.

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3.2 Introduction of pest damage capabilities into DSSAT

Most crop models do not simulate pest damage from insects, diseases, or nematodes, primarily because of the difficulty of linking two models (the crop and the pest) together, thus requiring communication and feedback. We pursued a different approach whereby pest damage was described as the type of action on rates or organs (state variables) as described by Boote et al. (1981, 1983b). This was implemented in DSSAT by Bill Batchelor (Batchelor et al.,1993). For example, pest damage such as observed percent defoliation or percent necrosis of existing leaves on given dates was entered into the observed data file (File T) and read by a coupling routine in the model with interpolation between dates, and then applying that given damage to the crop to reduce a state variable (leaf area, leaf mass, leaf N, etc.) or rate (leaf photosynthesis). This approach works for all the CROPGRO-style models and some of the CERES-style models, such as CERES-Rice, CERES-Maize, CERES-Millet, CERES-Sorghum, CERES-Sugarbeet, and NWheat (Memic et al., 2020; Ferreira et al., 2021). The pest damage effect has been used frequently to reproduce leafspot damage effects on peanut growth and yield (Naab et al., 2004, 2005; Singh, M. et al., 2013). But this approach only works to explain past performance where observed damage is recorded (e.g. via scouting). There is one example of direct linkage of the PNUTGRO model to a leafspot model (Bourgeois, 1989), but unfortunately, that code did not persist. New developments in model coupling have directly linked a wheat fusarium model to the wheat simulation model for the purpose of predicting pest damage effects on yield (Fernandes et al., 2017; Pequeno et al., 2024). In this and other ongoing efforts, we are currently evaluating various methods that allow for the coupling of two or more models in order to provide opportunities for running multiple instances of two models in parallel.

3.3 Transitions from 1998 onward

DSSAT Version 3.5 was the first stable and widely-used version of CSM and the associated tools for data entry and analysis of simulations. The individual models were well-calibrated and documented in the published DSSAT book (Tsuji et al., 1998). Four volumes of reference manuals (Tsuji et al. 1994) were released with DSSAT V3.5. In 2010, four additional volumes of reference manuals were placed inside the DSSAT software shell (Hoogenboom et al., 2010). Models for individual crops and processes of water balance and N balance were well documented by chapters in the Tsuji et al. 1998 book: e.g. CROPGRO model for grain legumes (Boote et al., 1998); CERES models for cereals (Ritchie, 1998), water balance (Ritchie, 1998), soil-crop N balance (Godwin and Singh, 1998), root-tuber crops (Singh et al., 1998), DSSAT structure (Jones et al., 1998), and pests (Teng et al., 1998).

Between 1998 and into the next century, DSSAT software managed the Y2K transition beyond the 2-digit year code plus day of year to 4-digit year code plus day of year. There was a transition from DOS-based software to use Windows-style of point-and-click, even though some of the individual tools remained unchanged. Also, during this time, the code was modularized to allow the combination of multiple models into a single code base and to improve the process of adding or replacing self-contained scientific capabilities or modules. The modularization organized the DSSAT source code into the initiation of state variables, process rate calculations, integration of state variables, and output of module predictions. Modularity applied well for many subroutines (modules) such as the photosynthesis method (leaf-level versus older RUE-style), soil organic matter (CENTURY or older Godwin-style), soil water balance, soil N balance, and evapotranspiration (several methods to be discussed later). However, we had to maintain separate growth-process modules for many crops because processes for leaf area expansion, grain addition, grain growth, and tissue N mobilization differed considerably in many cases. The CROPGRO model is an exception, using a single common plant growth module for all its crop species.

4 The creation of the Cropping Systems Model (CSM)

One of the advantages of modularization is that it now allows all the crop models, including CERES-style models, to be placed into the same executable file. The Cropping System Model (CSM) was created as a single executable program, with an integrated set of computer code representing more than 40 crops. Previously, there was a different executable code for CROPGRO models separate from executables for each of the CERES models (CERES-Maize different from CERES-Rice, for example). Once all crop modules were in the same executable code, then subroutines such as soil organic matter, soil water balance, soil inorganic N balance, ET method, etc., were shared and accessible across all DSSAT-plant modules. Figure 1 shows the modular structure of the Cropping System Model, its important linkages, and how plant, soil, management, soil-plant-atmosphere, and management modules connect to a site-specific land unit module. This structure was particularly useful for incorporating the CENTURY-style of soil organic matter simulation, which was incorporated into DSSAT by Gijsman et al. (2002). With the addition of the CENTURY-style soil organic carbon (SOC) module and use of a single executable for the entire system, the capability of crop rotation/sequence was enhanced, allowing multiple crops to be simulated on the same land unit in sequence to evaluate no-tillage practices, soil C sequestration, and greenhouse gas (GHG) emissions. In 2004, with the release of DSSAT v4.0 (Jones et al., 2003), the new executable model was named the CSM. For example, the new

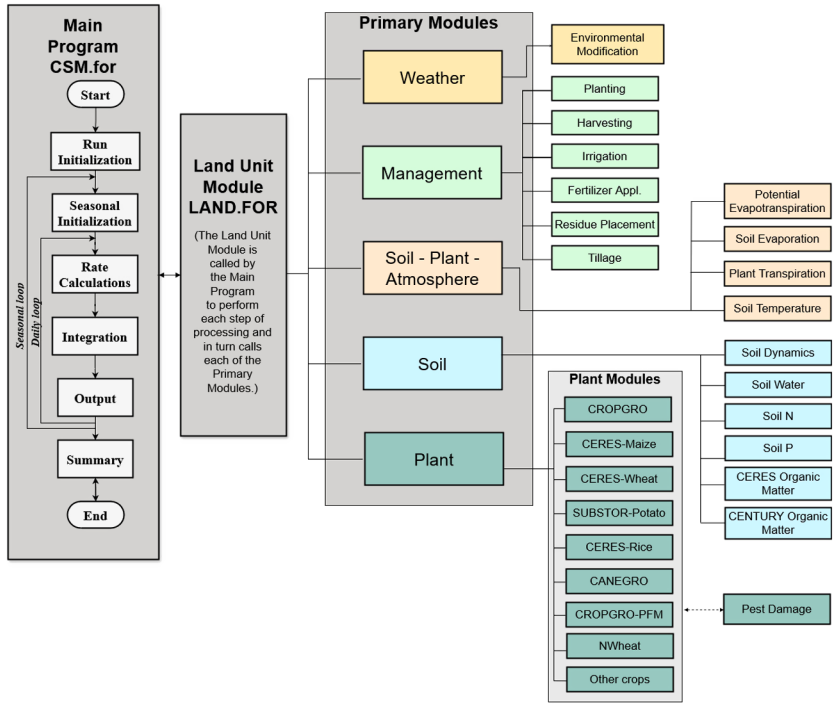

Figure 1 The modular structure of the Cropping System Model, showing important linkages, and how plant, soil, soil-plant-atmosphere, management, and weather modules connect to a site-specific land unit module.

naming of crop species is described by both model and species, such as CSM-CROPGRO-Soybean model or CSM-CERES-Maize. Figure 2 lists the many crops that are currently simulated by the Cropping System Model, with CROPGRO annual crops, CERES-style annual crops, CROPGRO-Perennial-Forage-Model crops, and other crop modules. Modeled crops shown in broken line boxes are under development.

Another advantage of modularization is that the source code was organized in such a way that each module represented a discrete scientific process or function. For example, previously in the non-modularized code, soil water content was initialized in one location of the code, rates were calculated in various places, the soil water content was updated in numerous locations in the code, and outputs were done in a separate location. With modularization, all functions associated with soil water content were done in a single module. Isolation of these processes improved transparency and allowed new programmers to more easily navigate, understand, and make advancements to the code.

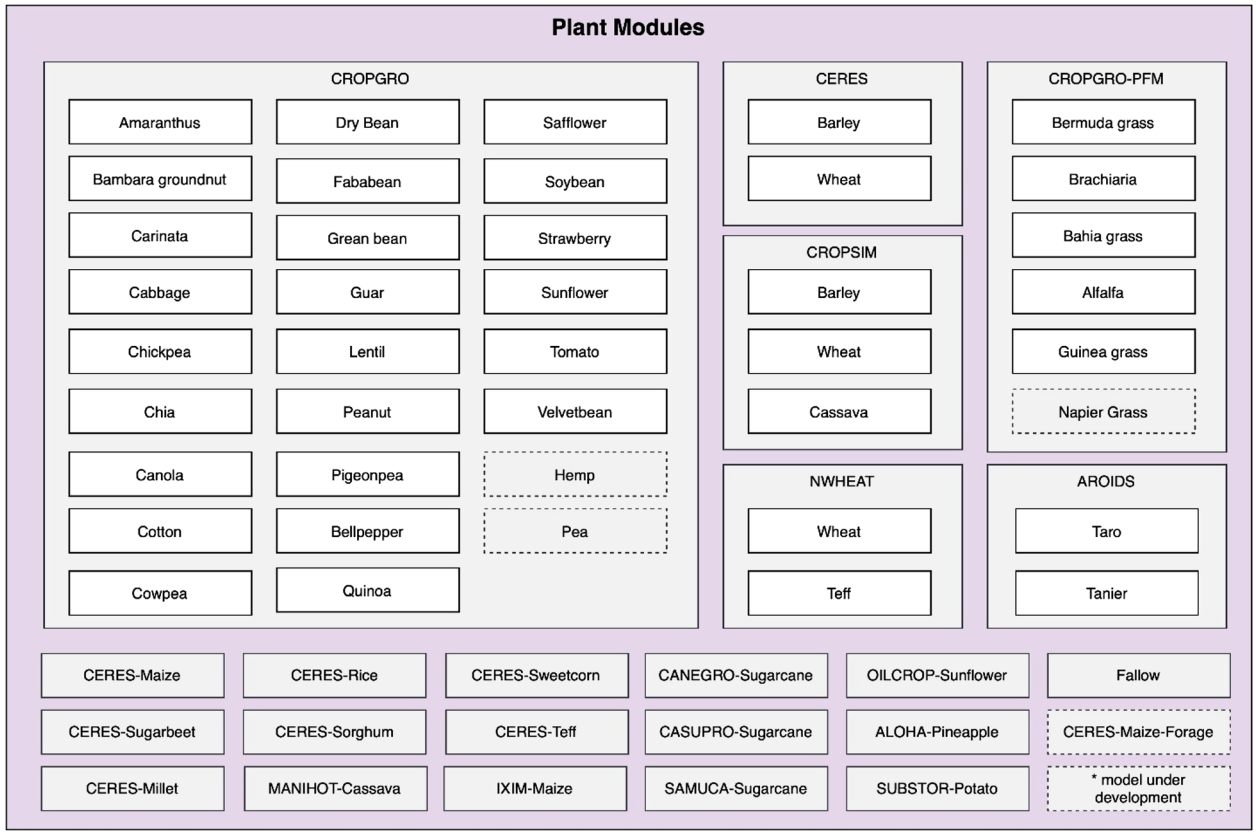

Figure 2 A listing of all the crop (plant) modules in the CSM.

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5 Adapting the CROPGRO crop growth model to simulate additional new grain crops

The generic structure of the CROPGRO model allows the addition of new crop species based only on the modification of the species, ecotype, and cultivar parameter files which are "read-in" input files. There are two informative examples of CROPGRO adaptation for grain legume crops: faba bean (Boote et al., 2002) and pigeonpea (Alderman et al., 2015). These two publications carefully describe the approach and methods to follow for adapting CROPGRO to a new species: (1) modifying tissue composition, cardinal temperature parameterization, leaf photosynthesis, etc. based on available literature information, (2) calibrating time-series growth and final yield outputs against observed time-series growth analyses (LAI, total crop mass, reproductive mass) using inverse model optimization of parameters (in the species file). Ideally, the observed growth and yield data are collected in multiple environments under conditions without water and N limitations. This approach has been quite successful. One of the concepts learned, particularly relative to the faba bean model, was the need to reparameterize many temperature responses because faba bean has much lower cardinal and optimum temperatures for processes as compared to soybean, which provided the initial template for species, ecotype, and cultivar files. It also showed that the CROPGRO model style of phenology can function for long-day as well as short-day species. The CROPGRO-chickpea model, also adapted from CROPGRO (Singh and Virmani, 1996; Hoogenboom et al., 1997; Singh et al., 2014a), is a long-day cool-season crop like faba bean. Singh et al. (2014a) updated and tested the CROPGRO-Chickpea model, particularly for temperature parameterization.

Adapting CROPGRO for a new crop requires both extracting crop-specific information from the scientific literature, as well as inverse optimization of model parameters to best simulate time-series growth and development of the crop. Figure 3 shows simulated and observed LAI, canopy height, canopy width, leaf, stem, pod, and total aboveground mass of faba bean cultivar Alameda grown under irrigation and relying on N-fixation during 1986–1987 season in Cordoba, Spain (Boote et al., 2002). The GBuild graphical program of DSSAT not only plots the simulated and observed data, but also computes goodness-of-fit statistics (RMSE and D-statistic) as shown in Fig. 3. The model calibration process, after setting compositions, cardinal temperatures and approximate life cycle, involved iteratively modifying species, ecotype, and cultivar parameters to maximize the D-statistic averaged over all crop output variables over six treatments in this case (including N-fertilized and second season treatments). Averaging is acceptable for the D-statistic because it is a type of normalized statistic. The RMSE was evaluated per output variable averaged over all treatments because of different magnitudes (LAI different from leaf mass, for

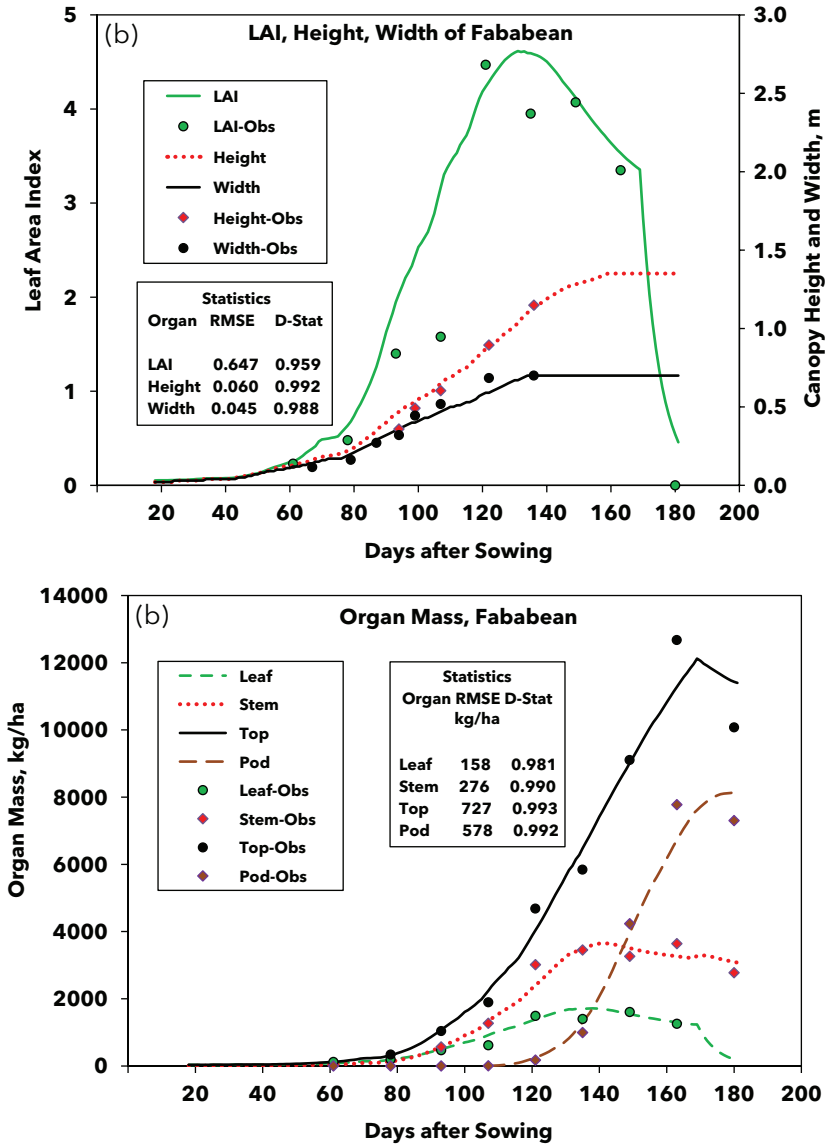

Figure 3 Comparison of simulated (lines) and observed (symbols): (A) leaf area index, canopy height, canopy width, (B) leaf, stem, total aboveground mass, and pod mass over time for faba bean cultivar Alameda sown December 10, 1986 and irrigated at Cordoba, Spain as simulated by CROPGRO-Fababean model. Statistics (RMSE and D-statistics) are shown.

example). The goal was to minimize RMSE for each output variable as well as maximize the D-statistic and to approach the observed time-series means. The regression coefficient R^2 is not used and should never be used for time-series evaluation as it suffers from "part-whole" effect going from small to large masses over time. Final yield and its components are included with the time-series data and are only sparsely and separately evaluated. Obviously, modifying given species and genetic parameters affects different aspects of the time-series output. Even cardinal temperatures and day-length sensitivity on life cycle and cardinal temperatures on processes can be modified away from sparse literature values based on simulations of sowing date effects (see Confalone et al., 2011).

Crops added to DSSAT since v3.5 that use the CROPGRO-template and adaptation approach include chickpea (Hoogenboom et al., 1997), tomato (Scholberg et al., 1997; Boote et al., 2012), cowpea (Boote unpublished, 1998), mucuna or velvetbean (Hartkamp et al., 2002), faba bean (Boote et al., 2002), cotton (Pathak et al., 2007; Boote unpublished, 2010; Thorp et al. 2014; Boote unpublished, 2024), canola (Deligios et al., 2013), pigeonpea (Alderman et al., 2015), safflower (Singh et al., 2015; Steberl et al. 2019), quinoa (Präger et al., 2019), chia (Mack et al., 2020), carinata (Boote et al., 2021), strawberry (Hopf et al., 2022), amaranthus (Nkebiwe et al., 2022), guar (Boote et al., 2023), lentil (Qi et al., 2024), bambara groundnut (Karunaratne et al., 2024) sunflower (Boote, unpublished, 2014), green bean (Boote unpublished, 2009), cabbage, and pepper. See the list of crops in Fig. 2. All the CROPGRO-type crops share the same source code, with differences in physiology and genetics being specified by different species, ecotype, and cultivar files.

Adapting CROPGRO to the various new crops basically followed the same approaches as described above. Minor issues with new data and new crops have suggested over time where minor code modifications were needed. For example, chia is a very small-seeded crop (Mack et al., 2020), which required a code change in the model to allow very small seed size. That change in itself was relatively easy, but the modified code resulted in a conflict with a hard-coded limit on how small early LAI was allowed to be, and when that coded limit was removed, then seed size (and plant population) resulted in having a greater impact on initial leaf area index. Consequently, one of the older parameters (SIZELF) no longer has any important effects on early LAI.

Quinoa provides another example of a recently adapted crop following the CROPGRO template. Figure 4A, 4B, and 4C illustrate LAI, total aboveground crop mass, and grain harvest index (HI) as affected by four sowing dates in 2016 at Stuttgart, Germany. For this region, early sowing was considerably delayed by cool temperatures, while the crop progressed and grew more rapidly with later sowing dates. This exercise demonstrated the need and value of setting cardinal temperature values for crop developmental phases (germination, time

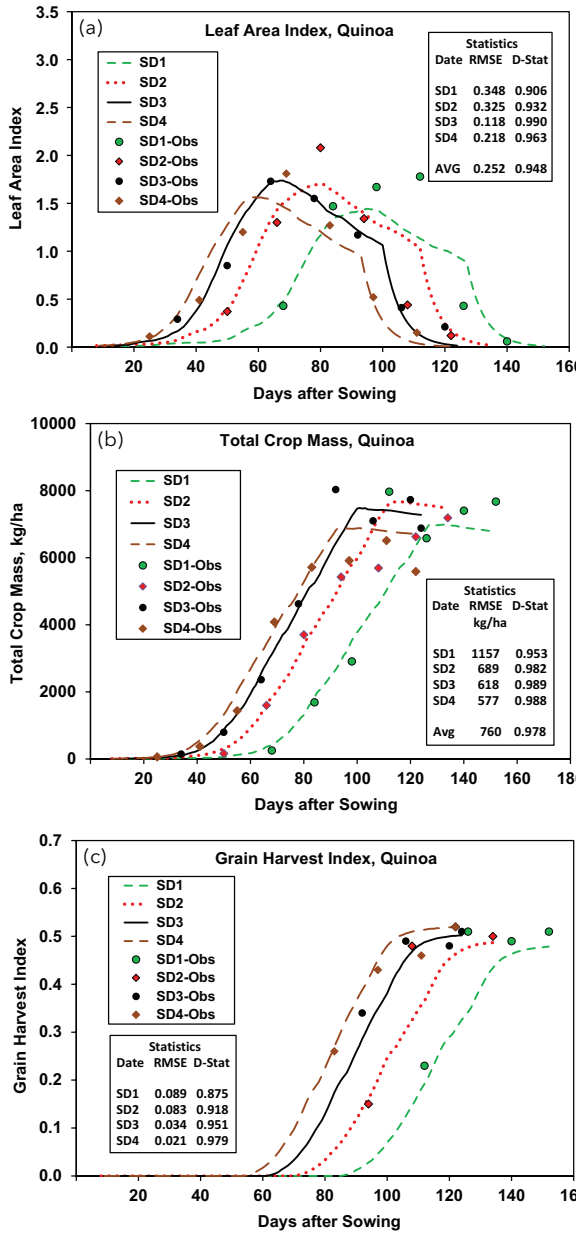

Figure 4 Comparison of simulated (lines) and observed (symbols): (A) leaf area index, (B) total aboveground crop mass, and (C) grain harvest index for quinoa cultivar Jesse sown on four dates (SD) (March 17, April 4, April 20, and April 27) in 2016 and grown under irrigation at Stuttgart, Germany as simulated by CROPGRO-Quinoa model. Statistics (RMSE and D-statistics) are shown. Simulations based on model adaptation and data of Präger et al. (2019).

to anthesis and time to maturity) as well as leaf expansion, photosynthesis, and grain growth processes. See Boote et al. (2018) for discussion of cardinal temperatures for different species.

6 Adaptation of CROPGRO for vegetables, multi-harvest, and fresh weight production

One of the early attempts was to adapt CROPGRO to simulate tomato (Scholberg et al., 1997; Boote and Scholberg, 2006; Boote et al., 2012). This was unique in three ways: (1) tomato is a non-legume, (2) it produces fruits that are fleshy with very small seeds, and (3) it is marketed on the basis of fruit fresh weight. The latter required adding code to CROPGRO to predict dry matter concentration (water concentration is the complement) of the fruit, which allowed simulated fruit dry matter yield to be converted to fresh weight (Boote and Scholberg, 2006).

The adaptation of CROPGRO for strawberry (Hopf et al., 2022) required the creation of a multi-harvest feature to allow repeated harvest of fruits concurrent with continued flowering and fruit set. CROPGRO already had the capability for continued flowering and fruit-set (it simulates daily addition of cohorts of flowers and fruits until the crop reaches a full fruit load or carrying capacity), but it did not allow simulation of periodic harvesting. New source code was added to allow harvesting of fruits as they reached harvestable fruit age on a 3 or 4-day harvesting interval typical of strawberry (or any chosen interval). An important aspect is how this uses the already existing XFRUIT cultivar parameter, which is defined as the limit on the fraction of daily assimilate allocated to reproductive growth. XFRUIT was coded to differentiate indeterminate cultivars of peanut and cotton that continue leaf growth through maturity. An XFRUIT less than 1.0 allows the CROPGRO-Strawberry model to continue to add new reproductive sinks for 6 to 7 months because a full-fruit load is not attained. Continued harvesting is accounted for so that the model never stops adding flowers and fruits. The multi-harvest feature can be used for periodic harvests for CROPGRO-Green Bean, or for CROPGRO-Tomato for indeterminate 18-month tomato production in greenhouses, although, as of this publication, it has not been tested for long-cycle greenhouse tomato production.

Four DSSAT models for vegetable crops, CROPGRO-Tomato, CROPGRO-Strawberry, CROPGRO-Green Bean, and CERES-Sweet-Corn feature the ability to simulate water concentration of fruits or sweet corn ears and fresh weight yield prediction. The three CROPGRO-style models simulate water concentration of tomatoes or fruits as a function of fruit age and output total fresh weight production and dry matter concentration as well as fresh weight per fruit, which is a quality aspect. The CERES-Sweet Corn model simulates a fixed dry matter concentration of ears and outputs total fresh market yield at

the time of harvest. Other vegetable models in DSSAT include cabbage and green pepper, although fresh weight output has not yet been developed for these models.

7 The CROPGRO Perennial Forage Model (CROPGRO-PFM)

The CSM was originally designed to only simulate annual crops, where the only carryover variables were for soils (e.g. soil water and nitrogen) if simulated in crop sequence/rotation. The CSM remained that way until code was added by Stuart Rymph, Ph.D. graduate student at the University of Florida, to simulate perennial forage growth (Rymph, 2004). He modified code of the CROPGRO model by adding state variables to represent reserve storage tissue (rhizome, taproot, stem base) and reserve concentrations, with rules for partitioning to storage tissue and rules for mobilizing reserves (total non-structural carbohydrates (TNC) and Nitrogen) to drive re-growth as well as rules for re-filling reserves. The mobilization and re-fill functions depend on LAI, current photosynthesis rate, current reserve TNC concentration, and day-length-linked dormancy. The model is designed for multi-harvest (few to many harvests over decades), which requires an MOW file that specifies the harvest dates, the amount of living stubble remaining, the percentage leaf of remaining stubble, and a "re-staged" node number on tillers. The CROPGRO-PFM model has been adapted for brachiaria (Pedreira et al., 2011; Pequeno et al., 2014, 2018; Santos M. G. et al., 2019, Santos M. L. et al., 2022), bermudagrass (Pequeno et al., 2018), guineagrass (Lara et al., 2012; Brunetti et al. 2021), and bahiagrass (Rymph, 2004; Smith et al., 2023). These are all tropical grasses with C-4 photosynthesis, which required minor adaptation to leaf photosynthesis equations. For C-4 photosynthesis, the leaf internal CO_2 to ambient CO_2 (C_i/C_a) ratio was reduced from 0.7 (C-3) to 0.4 (C-4) and the specificity for CO_2 versus O_2 (*tau* in literature) was increased by a factor of 10 (C-4) which greatly reduced the response to rising CO_2. The model was also adapted for alfalfa a C-3 legume (Malik et al., 2018, Jing et al. 2020).

The CROPGRO-PFM operated as a standalone executable for more than 10 years and was brought into DSSAT V4.7 in 2017. Introducing CROPGRO-PFM into the existing DSSAT code required code adaptation to bring in the unique subroutines needed for perennial forages and their harvesting. There is no final "end-of-season" output for the CROPGRO-PFM model because outputs occur periodically for few to many harvests, which list harvest dates, herbage mass, percent leaf of herbage, and crude protein of herbage, along with residual stubble and LAI. Those outputs go to the standard PLANTGRO.OUT, but they are also summarized in a new FORAGE.OUT file. The model does not mature or die but rather must be terminated in the harvest section of the management

File X, although there are species-file rules for freezing temperatures that kill above-ground leaf and stem tissue. The CROPGRO-PFM is recommended to be simulated only with the CENTURY-style of soil organic matter mineralization because dying organs (aboveground organs and roots) contribute to fresh organic matter whether on the surface or in the soil. Santos et al. (2022) used the model to evaluate decades-long simulations of brachiaria pasture in Brazil, testing various scenarios of fertilization and animal manure return to the soil.

Figure 5 illustrates the dynamics of LAI and aboveground biomass of alfalfa over multiple cutting harvest cycles during two years in Spain (Malik et al., 2018). In this example, alfalfa was sown from seed in the fall and harvested

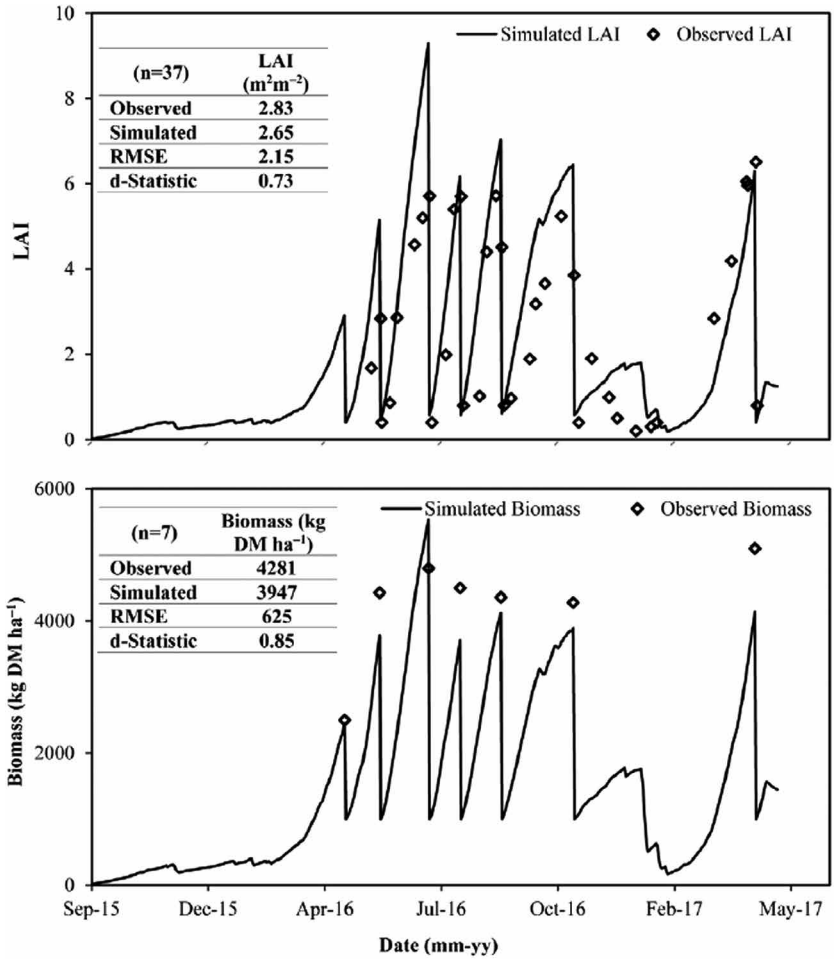

Figure 5 Comparison of simulated (lines) and observed (symbols) leaf area index (LAI) and crop biomass simulated over time at Almudevar, Spain, with the CROPGRO-PFM-Alfalfa model (with permission, Malik et al., 2018).

six times in the following season. Alfalfa has considerable taproot mass (up to 5000 kg ha^{-1}) that contains up to 20% total non-structural carbohydrates and relies considerably on rapid TNC mobilization to drive re-growth because the residual LAI is very small after cutting. Freeze kill occurred about February 2017, thus partially reducing above-ground biomass.

For some perennial tropical grasses such as Tifton-85 bermudagrass (Pequeno et al., 2018), establishment is by transplanting. Tifton-85 bermudagrass is a type of hybrid that has both above and below-ground stolons/rhizomes that store considerable TNC reserves and is harvested on approximately 4-week intervals during warm-season to provide high quality forage. As shown in Fig. 6, rapid re-growth is dependent on both residual LAI as well as mobilization of TNC reserves as reported by Alderman et al. (2011a, 2011b) and simulated by Pequeno et al. (2018).

The CROPGRO-PFM template approach should be applicable for new forage crops such as ryegrass and clover. However, each forage species requires its own unique species file, which additionally contains the relationships and parameters for growing storage organs, rate of mobilization of reserves, rate of re-fill of reserves, and degree of daylength-induced shift in partitioning to

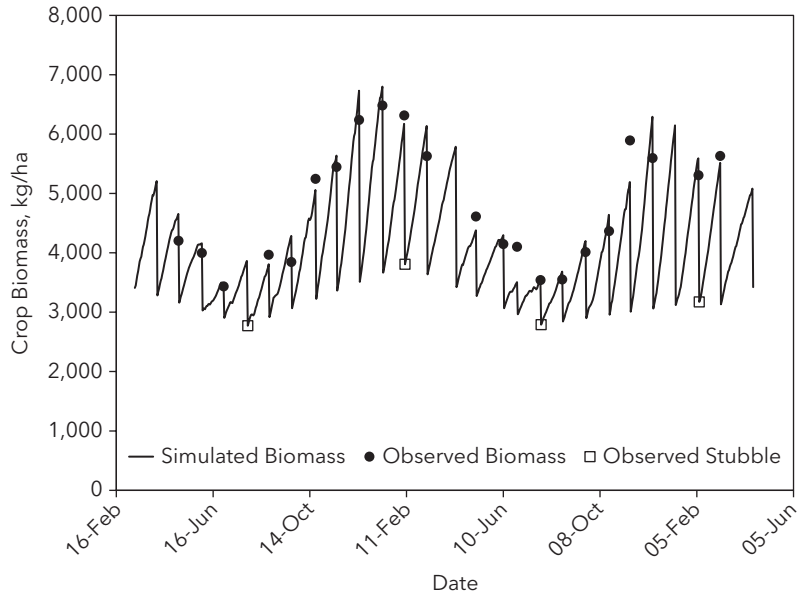

Figure 6 Tifton 85 bermudagrass biomass simulation harvested every 28 days from April 2011 to April 2013 in Piracicaba, SP, Brazil. The solid symbols are the aboveground biomass (stubble plus herbage) prior to herbage harvests, and the open symbols are the residual stubble mass measured after harvests on some dates (data from Pequeno et al., 2018).

storage. The cultivar and ecotype files have less importance than for the typical DSSAT annual crops.

8 Adding CERES-style and non-CROPGRO models for new crops

Another approach for adding new crops to the CSM code is to add completely new crop modules. This approach is more appropriate when the growth or phenological characteristics of a new crop differ greatly from those described in the CROPGRO template. In this case, both model coding and calibration of parameters are required. The CERES-Sweet Corn model (Lizaso et al., 2007) and the CERES-Sugarbeet model (Anar et al., 2019) are examples of crop modules added to CSM following the style of CERES models. Other models in CSM were adapted from an existing model to use the modular format of CSM (Jones et al., 2001), such as ALOHA pineapple (Zhang and Bartholomew, 1993; Zhang et al., 1997; Vásquez-Jiménez et al., 2024), CANEGRO sugarcane (Singels et al., 2008; Jones and Singels, 2018), and NWheat (Asseng et al., 2000; Kassie et al., 2016). NWheat was used as a template for a teff model (Paff et al. 2019), and there is also a CERES-Teff model (U. Singh, unpublished, 2024). The CROPSIM model (Hunt and Pararajasingham, 1995) was added to DSSAT-CSM as a template model for wheat, barley, and cassava. The CROPSIM template was used to develop a new crop model specific to cassava called MANIHOT (Moreno-Cadena et al., 2020; Moreno-Cadena, 2021).

9 Modeling genetics in DSSAT-CSM

CERES-style crops externalize genetic parameters in species, ecotype, and cultivar files; however, some species' genetic attributes remain in the source code, such as allometric relationships of partitioning to growth stage. The genetic attributes of the CROPGRO crops are contained only in the species, ecotype, and cultivar files. For CROPGRO-style crops with its single generic source code, the species file contains parameters and relationships for sensitivity of processes (leaf appearance rate, rate of reproductive progress, photosynthesis, respiration, leaf area expansion, protein mobilization, pod addition, and seed growth rate) to temperature, along with compositions, N effects on photosynthesis, and many other parameters. The species file and the ecotype file are reserved for modification by the model developers, and model users need only modify the cultivar file to mimic different cultivars within a crop species.

The cultivar file, for example, contains critical photoperiod parameters, photothermal durations (or degree-day units) required to reach given growth stages, along with other traits such as photosynthesis, determinacy, leaf appearance rate, seed size, seed fill duration, and seed composition.

The number of cultivar coefficients varies, depending on the crop module that is being used. For instance, the CERES-Maize model includes 6 cultivar coefficients, while the CROPGRO model includes 18 cultivar coefficients. For the CERES models, phase durations (photoperiod sensitivity and the duration of various phases in the life cycle) affecting time to flowering and maturity are given as degree-day units. For CROPGRO models, phase durations affecting reproductive stages and maturity are computed as photothermal days (ptd). The photothermal days accumulated in one calendar day are typically less than one, modified when the hourly temperature is less than optimum and the day length is greater than the critical short day length (CSDL) in the case of short-day species. Genotype-specific parameters (GSPs) in crop models are artificial constructs to mimic genetic traits; at present, they are not well linked to real genes or QTL, although some preliminary efforts are underway as described later in the chapter.

Typical GSPs are shown in Table 1 for three life cycle type cultivars of CERES-Maize and IXIM-Maize. A longer life cycle with later flowering and later maturity appear to give somewhat greater grain yield and biomass for this location in Iowa. The values of P1, P2, and P5 determine the life cycle duration of maize, although there are minimal effects of daylength (P2) for the Iowa location. The G2 is the maximum possible grain number per plant, and G3 defines the kernel growth rate during linear grain filling. PHINT is phyllochron interval per leaf, and smaller values cause faster leaf appearance and greater leaf area index (LAI). IXIM-Maize is an alternate maize model in DSSAT developed by Lizaso et al. (2011, 2022) which requires two additional GSPs for its more mechanistic leaf area growth. IXIM also has a leaf-to-canopy hedgerow light interception and photosynthesis and someday may replace CERES-Maize as the DSSAT default maize model.

The GSPs for four different CROPGRO species (Table 2) play a major role in setting the life cycle and productivity of these legumes, as shown in Fig. 7A and Fig. 7B, but crop differences are also a function of parameters and relationships in the species file. Cowpea had the shortest life cycle with rapid onset of pods and grain, with shorter time from first seed to physiological maturity (SDPM) as well as very short individual seed growth duration (SFDUR), and for those reasons, cowpea had the lowest grain yield. Three of the crops are short-day types, while peanut is not sensitive to daylength (PPSEN=0.00). Pigeonpea had the latest onset of grain growth because of its strong daylength sensitivity (PPSEN=0.71). Despite a longer life cycle than soybean, pigeonpea yield was similar to that of soybean. By contrast, peanut had the highest grain yield attributed not only to its long-life cycle, but also to its extended duration from first seed to physiological maturity (long SDPM) along with long indeterminate pod addition (PODUR) and long single grain growth duration (SFDUR). These traits, along with its higher leaf photosynthesis led to higher grain yield for

Table 1 Definitions of genotype-specific parameters (GSP) for CERES-Maize and IXIM-Maize models with example values and simulated life cycle and yield for Short (2500 growing degree-days (GDD)), Medium (2600 GDD), and Long (2700 GDD) season cultivars (when sown in Ames, Iowa).

GSP Name	Cultivar coefficient definition	Short 2500 GDD	Medium 2600 GDD	Long 2700 GDD
P1	Thermal time from emergence to end of juvenile phase during which plant is not sensitive to photoperiod (GDD†)	160	190	215
P2	Days delay in development per hour increase in photoperiod above the critical short photoperiod (d/h)	0.400	0.500	0.500
P5	Thermal time from silking to physiological maturity (GDD)	800	840	880
G2	Maximum possible number of grains (kernels) per plant	730	800	840
G3	Grain (kernel) filling rate during linear grain filling under optimum conditions (mg kernel^{-1} day^{-1})	8.6	8.5	8.4
PHINT	Phyllochron interval, thermal time between successive leaf tip appearance (GDD)	39.0	39.0	39.0
AX††	Leaf area of largest leaf (cm^2 leaf^{-1})	680	720	800
LX††	Leaf longevity of most long-lived leaf, from 50% expansion to 50% senescence (GDD)	760	780	800
Simulated Output for CERES-Maize†††				
Time to anthesis (days after sowing)		70	73	78
Time to maturity (days after sowing)		122	129	140
Maximum leaf area index		4.01	4.60	5.13
Grain yield (kg ha^{-1})		11504	12957	13601
Final total biomass (kg ha^{-1})		21470	23315	24645

† Degree days above Tb = 8C. Computed with T_{mean} = (Tmax + T_{min})/2.
†† Additional GSPs for IXIM-Maize.
††† Simulated anthesis, maturity, maximum leaf area index, grain yield, and final biomass, for three hypothetical cultivars, sown April 27, 1999 at 8 plants m^{-2}, 224 kg N ha^{-1} on a Clarion soil at Ames, Iowa.

Table 2 Definitions of GSP for the CROPGRO model with values for soybean (cv. Bragg), pigeonpea (cv. 76W), peanut (cv. Florunner), and cowpea (cv. CAL # 5).

GSP name	Genotype-specific parameter definition	SoybeanMG 7 Bragg	Pigeonpea76W	PeanutGeorgia Green	CowpeaCAL # 5
CSDL	Critical short daylength below which reproductive development progresses rapidly with no daylength effect (h)	12.33	12.94	11.84	12.80
PPSEN	Slope of the relative response of development to photoperiod with time (1/h)	0.320	0.71	0.000	0.264
EM-FL	Time from emergence to first flower appearance (ptd †)	19.5	32.7	21.2	23.5
FL-SH	Time from first flower to first pod (ptd †)	10.0	17.4	9.2	3.8
FL-SD	Time from first flower to first seed (ptd †)	15.2	24.1	18.8	6.0
SD-PM	Time from first seed to physiological maturity (ptd †)	37.6	37.7	74.3	24.8
FL-VS	Time from first flower to last leaf on main axis – from Ecotype file (ptd †)	9.0	11.3	68.0	8.0
FL-LF	Time from first flower to end of leaf expansion (ptd †)	19.0	28.9	88.0	7.0
TRIFOL	Rate of node appearance at opt. temp (node td^{-1}) – in Ecotype file	0.32	0.80	0.35	0.45
LFMAX	Maximum leaf photosynthetic rate at 30 °C, 350 ppm CO_2, and high light (mg CO_2 m^2 s^{-1})	1.00	1.10	1.40	1.00

(*Continued*)

Table 2 Definitions of GSP for the CROPGRO model with values for soybean (cv. Bragg), pigeonpea (cv. 76W), peanut (cv. Florunner), and cowpea (cv. CAL # 5).

GSP name	Genotype-specific parameter definition	SoybeanMG 7 Bragg	Pigeonpea76W	PeanutGeorgia Green	CowpeaCAL # 5
SLAVR	Specific leaf area of cultivar under standard growth conditions ($cm^2\ g^{-1}$)	355.	320.	260.	250.
SIZLF	Maximum size of full leaf (compound leaf) (cm^2)	170.	171.	18.	260.
XFRT	Maximum fraction of daily growth partitioned to seed + shell	1.00	0.95	0.92	1.00
WTPSD	Genetic potential weight per seed (g)	0.17	0.18	0.69	0.14
SFDUR	Seed filling duration for pod cohort (ptd †)	24.0	24.6	40.0	9.0
SDPDV	Seeds per pod, standard growth conditions (# pod^{-1})	2.00	3.89	1.65	6.4
PODUR	Duration of pod addition (ptd †)	10.0	17.3	24.0	16.0
THRSH	Threshing percentage, maximum % of seed to seed+shell	78.0	74.0	80.0	83.0
SDPRO	Potential seed protein (fraction)	0.400	0.224	0.270	0.300
SDLIP	Potential seed lipid (fraction)	0.200	0.015	0.510	0.065

† ptd, photo-thermal days.

peanut compared to soybean and pigeonpea. The peanut and pigeonpea are non-senescing types of legumes that retain green LAI to maturity, whereas soybean has rapid grand senescence of its LAI at the end of its life cycle (Fig. 7A). Notice also that cultivar types within species are allowed to have different seed protein and oil concentrations (Table 2).

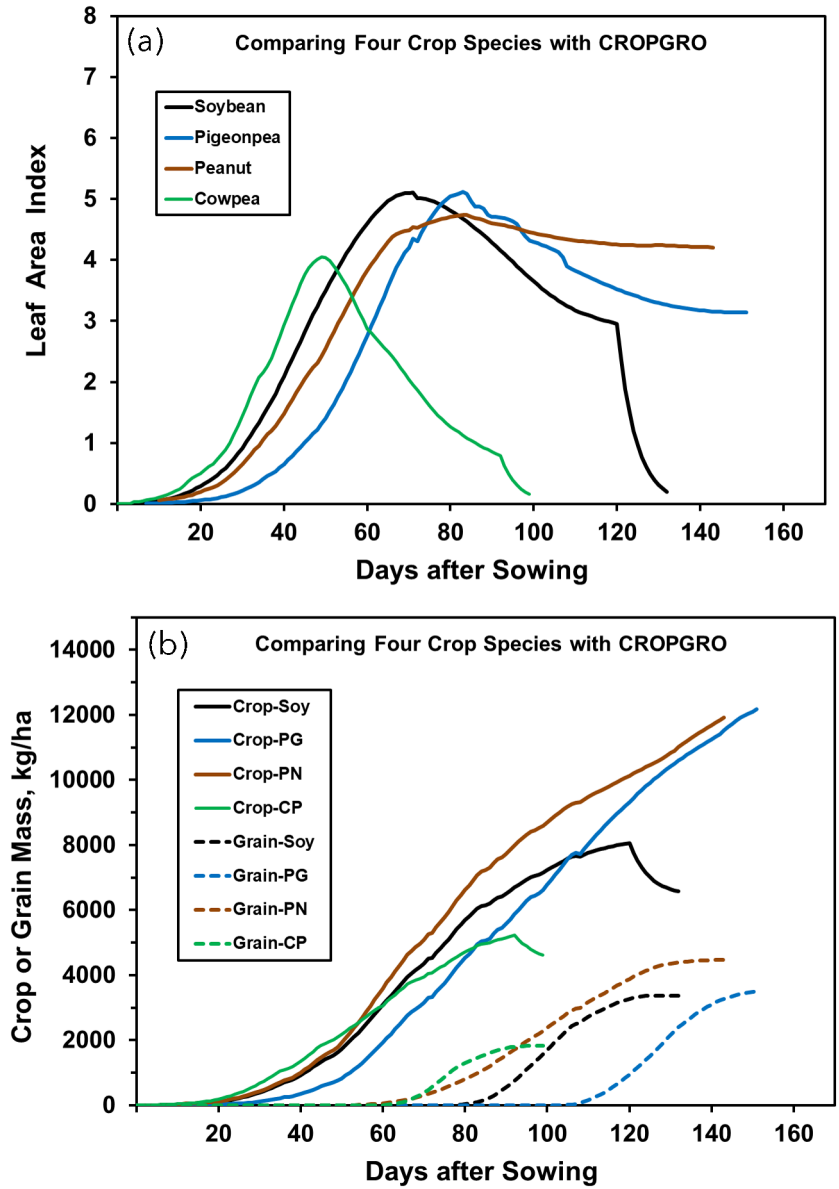

Figure 7 (A) Leaf area index and (B) total crop mass and grain mass, as simulated by CROPGRO for four grain legumes (soybean, pigeonpea, peanut, and cowpea) in 1984 at Gainesville, FL (files and observed data are in DSSAT release, data courtesy of C. E. Maliro (1986)).

10 Major processes modeled in DSSAT-CSM: water balance processes

This and the following sections on processes modeled in the CSM are adapted from Hoogenboom et al. (2019a) with minor updates.

All the crop models in DSSAT-CSM share the same soil water balance subroutines. On a daily basis, the soil water balance is computed by adding irrigation and rainfall and subtracting surface runoff, drainage, plant transpiration, and soil evaporation. Within a soil column, soil water is redistributed by vertical drainage, capillary rise, and tillage. Rainfall is supplied as a user input in weather files. Irrigation is specified in the experimental details input file, which supplies information about the type of irrigation, the efficiency of water supply, and the amount of irrigation applied. Partitioning of rainfall to infiltration and surface runoff is based on the Natural Resource Conservation Service (NRCS) curve number approach (Ritchie, 1998).

Drainage of soil water follows the tipping bucket approach for layered soils with only one-dimensional flow (Ritchie, 1998). Successive soil layers are defined by the lower limit (wilting point), drained upper limit (field capacity), and saturated volumetric soil water content. Downward water movement within the soil depends on a soil drainage factor (fraction per day), limited by the saturated hydraulic conductivity of soil layers. There is a present effort to develop a two-dimensional soil water model in DSSAT for use particularly with plastic mulch bed horticultural crops.

Evapotranspiration (ET) depends on total potential evapotranspiration (ETp) demand using any one of several options: Priestley-Taylor (Priestley and Taylor, 1972), FAO-56 (Sau et al., 2004 modification of Allen et al., 1998), ASAE-standard FAO-56 for short grass or tall grass (DeJonge and Thorp, 2017) and a new hourly energy balance option (Cuadra et al., 2021). The Priestley-Taylor option requires only standard weather data input, whereas the FAO-56 and hourly energy balance options additionally require wind speed and dewpoint temperature as input. After ETp is calculated, it is partitioned to the potential transpiration of the crop canopy (Tp) or potential evaporation of the soil (Ep) as a function of the LAI and an energy extinction coefficient (Kep). Kep is different from, and should be lower than, the extinction coefficient of LAI for photosynthetically active radiation. The parameter Kep can differ for each crop in CROPGRO, but it is more complex for the CERES crops where a "mixed" function is derived from the extinction of photosynthetically active radiation. The actual soil water evaporation depends on the potential Ep and the soil water content of the top layer, using the Ritchie (1972) method with constant and square root of time falling rate stages. The former soil water evaporation method (Suleiman and Ritchie (2003); Ritchie et al. (2009)) has been discontinued as the DSSAT default after experience testing against

flux site ET experiments showed simulated soil Es that was too high (Kimball et al., 2023). Soil Es is also influenced (decreased) by the degree of prior crop residue cover, which must be set correctly in the crop management file. Moreover, decomposition of surface residue occurs when the CENTURY-style of SOC is used, but decomposition (disappearance) does not occur with the Godwin and Singh SOC method. Actual simulated transpiration of the crop, Ts, is the minimum of the potential Tp or the root water uptake. Potential root water uptake from successive layers follows the approach described by Ritchie (1998), and it is dependent on root length density and the fraction of available soil water content in each layer. Total root water uptake is then integrated over all layers, and transpiration is reduced if potential root water uptake is less than potential Tp. The daily photo-assimilation is reduced as a function of the ratio of actual transpiration (Ts or root uptake) to potential Tp, using a 0-1 drought stress factor called SWFAC. Expansive processes (leaf area expansion, height increase, canopy width increase) are reduced somewhat sooner by a similar factor called TURFAC. The SWFAC and TURFAC factors also influence partitioning to roots, nodule growth, N-fixation, and phenology (accelerate progress after seed-set). See Boote et al. (2008) for a review of water balance, evapotranspiration, and simulation of water stress effects in the CROPGRO model.

11 Major processes modeled in DSSAT-CSM: nitrogen (N) balance processes

Soil nitrogen dynamics in DSSAT's CSM (Godwin and Singh, 1998; Singh and Porter, 2019) are handled in the soil inorganic N module and in two soil organic matter modules. In the inorganic N module, a mass balance accounts for all additions of inorganic N to the soil, all processes transforming N from one type to another, and all removals of inorganic N from the soil column. Additions of inorganic N are from fertilizer applications and from mineralized N resulting from the decomposition of organic matter. Fertilizer applications are defined in the experimental details file and include the date applied, fertilizer type, amount of N applied, application method, and the depth and percentage of incorporation into the soil. Slow-release fertilizers, nitrification inhibitors, and urease inhibitors can also be specified.

Daily transformations of nitrate, ammonium, and urea are computed based on process rates of nitrification, denitrification, ammonia volatilization, and urea hydrolysis. Removals of inorganic N from the system are based on plant uptake, immobilization related to organic matter processes, leaching, and N gas losses due to ammonia volatilization, denitrification, and nitrification. Gaseous emissions of N_2O, NO, and CO_2 are computed based on organic matter decomposition, nitrification, and denitrification processes. The partitioning

of denitrification and nitrification into N_2O, NO, and N_2 comes from DayCent (Del Grosso et al., 2001), as adapted by Peter Grace (Cheryl Porter, personal communication, 2024). For flooded rice systems, in addition to the processes listed above, the model simulates the chemical and biological processes occurring in the floodwater.

Two options are available in DSSAT for the computation of soil organic matter dynamics: the original CERES-based module (Godwin and Singh, 1998) and the CENTURY-based module (Gijsman et al., 2002). See also the review by Singh and Porter (2019). The main difference is the inclusion of surface fresh organic matter and three pools of soil organic matter in the CENTURY model. The more complex CENTURY model allows more control over initialization of stable C pools and, therefore, overall decomposition dynamics, but it also requires additional input data, which are difficult to obtain. These routines interact with the inorganic N and P modules by computing the transformation of organic N and P into inorganic forms as a product of mineralization. Conversely, immobilization can remove inorganic N and P from the soil and reduce plant-available nutrients.

11.1 Plant N processes in DSSAT-CSM

The details of modeling plant N uptake in DSSAT-CSM vary between the individual crop modules, but for all crop modules, N uptake is computed as the minimum of N demand and N supply (Singh and Porter, 2019). The potential N supply from the soil profile is a function of root length density, nitrate and ammonium concentrations, and soil water in each soil layer (Godwin and Singh, 1998). Soil N supply is influenced by environmental factors such as soil temperature, soil moisture, soil pH, mineralization of organic matter, and management of N fertilizers and organic amendments. Root morphology, root architecture, and root length density may limit the ability of the crop to access the N supply.

Crop N demand differs with the growth stage of a crop, with higher critical tissue N concentrations early, and therefore, N demand per unit of growth is higher during early crop growth and development. N demand is driven by plant growth rate, growth stage, and tissue N status as a function of the growth stage (Godwin and Singh, 1998). Total crop N demand is the summation of all deficiency demands from various plant organs plus the demand by new growth. For legumes simulated with the CROPGRO model, when the supply of N is less than the demand, carbohydrates are directed to nodule growth and N-fixation to meet the crop N demand via N-fixation (Boote et al., 1998; Boote et al., 2009). The N-fixation rate is influenced by soil temperature, plant water status (TURFAC), and soil aeration (Boote et al., 2009). When the N supply is less than N demand, vegetative tissues are grown at lower N concentrations. If this condition persists, N deficiency symptoms arise, resulting in a reduction in LAI, reduced photosynthesis (growth and yield reduction), and accelerated senescence.

12 Major processes modeled in DSSAT-CSM: inorganic soil phosphorus (P) processes

The CSM inorganic soil P module maintains state variables for labile, active, and stable forms of phosphorus (Singh and Porter, 2019). Transformation between the pools assumes first-order kinetics with rate constants computed based on soil chemical and physical properties. Additions to the system are from fertilizer application and mineralization due to decomposition of organic matter. Removal of P from the system is from plant uptake and immobilization of P by microbes to meet decomposition demand. Tillage events will redistribute soil P in the layers affected.

The computation of plant available P assumes that soil P is relatively immobile and that only soluble P in close proximity to roots is available for uptake. The soil column is partitioned into root and non-root volume zones using a species-dependent "effective" root radius parameter and the dynamically-varying root length density to define the root zone volume for P uptake. Pools of labile, active, and stable P are maintained separately for root and non-root soil zones. As roots proliferate, mass of soil and nutrients are transferred from non-root to root soil zones, making more P available to the plant with higher root density. Soluble P is a proportion of labile P calculated daily and is dependent on soil water content, labile P, and soil texture in each layer. This soluble P in the root zone is the daily P supply available for potential root uptake. Soil P initialization is critical to a successful simulation of P processes, but data are often difficult or expensive to obtain. Labile P is computed from measured extractable P soil tests using an expert system that depends on the laboratory extraction method used and soil characteristics.

12.1 Plant P processes in DSSAT-CSM

Modeling P demand is similar to that of crop N demand (Singh and Porter, 2019). Each day demand for each plant part is calculated as the amount of P required to bring tissue concentration up to a stage-dependent optimal concentration, plus the demand for new growth. This demand can be met through the soil's P supply and by mobilization of P to grain from vegetative, pod, or root tissue. P uptake is defined as the minimum of supply and demand. The amount of P taken up by roots may be further limited by a species-dependent minimum vegetative N:P ratio, thus limiting P uptake when vegetative N concentrations are low. When supply falls short of demand, P stresses occur affecting rates of photosynthesis, vegetative and reproductive growth, and senescence.

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13 Using DSSAT-CSM to evaluate genetic improvement and adaptation to climate change

The GSP, and even ecotype and species parameters can be varied to evaluate hypothetical genetic improvement, often relative to future climate changes, such as drought stresses, rising temperatures, and/or CO_2 increases. Examples of simulating the effects of different cultivar traits have been described for soybean (Boote and Tollenaar, 1994; Boote et al., 1998, 2001, 2002; Boote, 2011), maize (Boote et al., 2001; Tesfaye et al., 2018), peanut (Putto et al., 2013; Singh, P. et al., 2013; Narh et al., 2015; Boote et al., 2021), chickpea (Boote et al., 2013; Singh et al., 2014a), sorghum (Singh et al., 2014b), and pearl millet (Singh et al., 2017).

Several important principles must be followed for evaluating genetic improvement: (1) First, can the model simulate a given trait and is variation in a given GSP within a reasonable range relative to literature information or plant breeder advice (Boote et al., 2002; Boote, 2011)? For example, RUE is often considered a genetic trait (Martre et al., 2024), but many scientists consider RUE to be constant for a given species. So, increasing RUE often shows large yield increases, but is that reasonable? (2) Comparison should be made against a standard cultivar that is already calibrated for a given location (Tesfaye et al., 2018; Martre et al., 2024). (3) Do reasonable traits exist, and are they appropriate for the desired environmental factors and has the model been previously tested against those factors such as elevated CO_2 or temperature?

13.1 Genotype by environment Interactions (sensitivity to climate change, temperature, and CO_2)

Yield improvement with single and multiple GSP trait combinations were simulated with the CROPGRO-Peanut model using 15 years of rainfed weather in Ghana under a hypothesized increase in CO_2 and +3 °C increase in temperature (Table 3). The short-season cultivar Chinese had been well calibrated for multiple seasons in Ghana, and the soil water-holding characteristics were also well established by comparison to observed data (Naab et al., 2004; Naab et al. 2005). Because Chinese is a short-season cultivar with a relatively low LAI, yield increased 4.2% with delayed flowering (+10% EM-FL) and increased 9.0% with longer grain-filling duration (+10% SD-PM), and 12.4% with both traits combined. Likewise, with a relatively low LAI, an increase in photosynthesis (+10% LFMAX) caused a 7.3% increase in yield. Moreover, combinations of four traits, such as delayed flowering, longer grain fill, greater partitioning, and higher photosynthesis, were additive and increased yield by 24.7%. In fact, the response to these combined GSPs is modest, as genetic improvement of newly-released cultivars in Ghana indicates 76–80% yield improvement over

Table 3 Simulated peanut seed yield response to GSP trait combinations under two CO_2 levels, +3 °C temperature increase, and combination of 500 ppm CO_2, +3 °C and 20% less rainfall (RF), using CSM-CROPGRO-Peanut model. The crop was grown rainfed with 15 years of weather at Wa, Ghana. With permission from Boote et al. (2021).

GSP trait modified†	Ambient CO_2 380 ppm	CO_2 500 ppm	+3 °C temp	+3 °C 500 ppm−20%RF
Chinese (90-d std) (kg ha^{-1})	1841	2248	1553	1770
			% change in yield	
+10% LFMAX (leaf Ps)	7.3	6.4	6.9	5.4
+10% Specific Leaf Area	0.5	0.5	0.5	0.0
+10% EMFL	4.2	3.6	4.3	3.9
+10% SDPM	9.0	8.3	**12.6**	**12.4**
+10% EMFL and +10% SDPM	12.4	11.1	**16.1**	**14.6**
+10% WTPSD (wt/sd)	0.7	0.8	0.7	0.5
-10% Pod Adding Duration	0.1	0.7	3.9	3.6
+10% XFRT (partitioning)	3.4	3.8	5.3	5.7
+10% SIZLF (veg. vigor)	1.5	1.4	0.9	0.8
EMFL, SDPM, XFRT	16.5	15.5	**21.3**	**19.7**
EMFL, SDPM, LFMAX	20.4	18.0	22.7	20.3
EMFL, SDPM, XFRT, LFMAX	24.7	22.6	**28.6**	**25.8**

Bold font signifies genotype by environment interaction for some GSPs.

this Chinese cultivar (Narh et al., 2015). A strong G x E interaction is present for temperature. Three of the traits (delayed flowering, longer grain-filling, and greater partitioning) increased yield more under the +3 °C temperature scenario than under ambient conditions. Under future climate change, a temperature increase of this magnitude is probable and would cause a shorter life cycle, which the increased EM-FL and increased SD-PM help to offset. The peanut model simulates that the rate of pod addition and partitioning are reduced under elevated temperature (Prasad et al. 2003; Boote et al., 2018), and the genetic increase in partitioning helps to recover pod addition under +3 °C scenario. The peanut yields of this cultivar in this region are low for multiple reasons: un-improved short-cycle cultivar, water stress, low soil fertility (SLPF <1.0), as well as leafspot occurrence.

Table 4 Grain yield response to varying GSPs, simulated for 22 years for Annigeri chickpea grown under either rainfed or irrigated conditions at Patancheru, India. Sown on September 29 (day of year 302) on a very fine montmorillonitic clay soil, starting at field capacity. Simulated with the CSM-CROPGRO chickpea model as developed by Singh and Virmani (1996) and modified by Singh et al. (2014a). Table used with permission from Boote et al. (2013).

Cultivar GSP modified	Rainfed		Irrigated	
	Mean yield	Percent change	Mean yield	Percent change
	kg/ha	%	kg/ha	%
Standard simulation (Annigeri)	773		2614	
Rooting/SLW/LFMAX traits				
+10%, rate of root depth progression	791	2.3	2614	0.0
+10% leaf photosynthesis (LFMAX)	783	1.3	2961	13.3
+10% specific leaf weight (SLW)	916	**18.5**	2328	**−10.9**
Life cycle traits				
10% longer from emergence to anthesis	669	**−13.5**	3016	**15.4**
10% longer seed-fill (first seed to maturity)	787	1.8	2893	10.7
Seed size/partitioning				
10% larger potential seed size	746	**−3.5**	2709	**3.6**
10% faster pod addition	774	0.2	2717	3.9

Strong G x E interactions of GSP traits with water supply (Table 4) are simulated with the CSM-CROPGRO-Chickpea model for crops grown under full irrigation or under water-limited terminal drought (Boote et al., 2013). Chickpea in India is typically sown at the end of the monsoon and depends on stored residual water on high-clay soils (Singh et al., 1999a, 1999b). In this case, the target environment, irrigated versus rainfed, is critical because the responses to GSPs were often opposite and large for contrasting soil water availability. For example, the effect of increased specific leaf weight (SLW) was to decrease yield 11% under irrigation but to increase yield 18% under water limitation. Increased SLW had a negative effect on yield under irrigation because it reduced LAI and light interception. But the same higher SLW trait was beneficial under rainfed conditions because it reduced LAI, light interception, and transpiration, thus conserving water for grain growth later in the life cycle. Later flowering acted to increase LAI and gave 15.4% yield increase under irrigation but reduced yield by 13.5 % under the terminal drought. The common factor was the amount of LAI produced and the amount of soil water conserved and left at the time seed growth began. Likewise, higher photosynthesis had a much larger benefit under irrigation; while under terminal drought, it had little benefit because it increased early LAI and water extraction too much.

In a project funded by the CGIAR Research Program on Policies, Institutions and Markets and the Global Futures for Agriculture Project funded by the Bill and Melinda Gates Foundation, Tesfaye et al. (2018) used the CERES-Maize model to evaluate the yield benefits from traits for drought tolerance and heat tolerance for six regions in Eastern and Southern Africa and South Asia. The CERES-Maize model was first calibrated for local varieties at each of these sites. The drought tolerance trait was defined as greater root length density at depth along with a slight reduction in the lower limit of soil water content for the soil horizons, the latter assuming slightly more complete soil water extraction. The heat tolerance trait was accomplished by pushing up the Topt2 (highest temperature for optimal growth) and Tfailure (temperature above which no growth occurs) values on rate of grain fill (RGFILL in species file) by 2 °C. The benefits of drought tolerance, heat tolerance, and combined drought/heat tolerance were simulated over long-term weather for the six sites (Table 5). The benefits of drought tolerance varied considerably by location, being greatest in Hyderabad. Benefits of heat tolerance were generally small except for the Kiboko site, although the benefit of heat tolerance was greater under future warmer climate. Benefits of combined traits depended mostly on the value of the dominant trait.

13.2 Gene-based modeling

One of the most challenging aspects of applying the DSSAT crop models is the estimation of the GSPs, which, for all models, is required for local cultivars and hybrids prior to any real-world application. There have been efforts to bridge the gap between biotechnology, genetics, plant breeding and crop modeling using either genes or quantitative trait loci (QTLs). The first, simple, gene-based model GENEGRO, was developed by White and Hoogenboom (1996) more than 25 years ago, linking several genes to the GSPs of the dry bean model BEANGRO. Predictions of phenology were as accurate as the original model, while final yield and biomass predictions were more challenging. A similar gene-based approach was applied by Messina et al. (2006) for the E-genes of soybean, which determine the time to maturity. Like dry bean, this was successful for life cycle and somewhat less successful for grain yield. Recent developments have been based on QTLs that are directly or indirectly linked to GSPs or plant traits (Wallach et al., 2018). As the cost of mapping QTLs/genes becomes cheaper, it is expected that rapid advances can be made in this area. A future model might link QTLs/genes to traits affecting one or more growth and development processes via modules that would allow for the input of genetic data, typically from molecular markers, directly into crop models (Hoogenboom and White, 2003; White and Hoogenboom, 2003). If successful, this improvement should reduce the requirements for calibration of a new cultivar for local conditions,

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Table 5 Simulated maize yields and relative yield changes due to drought, heat, and combined drought and heat tolerance compared to benchmark maize varieties under baseline climate in Eastern and Southern Africa and South Asia (used with permission, Tesfaye et al., 2018).

Site	Benchmark	Drought tolerant		Heat tolerant		Drought and heat tolerant	
	Yield kg/ha	Yield kg/ha	% change	Yield kg/ha	% change	Yield kg/ha	% change
Chiredzi	1327	1558	17.4	1383	4.2	1626	22.5
Hyderabad	3908	6177	58.1	3930	0.6	6179	58.1
Kiboko	2395	2456	2.5	3976	66.0	4330	80.8
Matopos	3124	3156	1.0	3147	0.7	3179	1.7
Meiso	4589	4874	6.2	4615	0.6	4863	6.3
Melkasa	6026	6358	5.5	6030	0.1	6370	5.7

assuming that marker data are public and that proper phenotyping of marker effects has been done (Hoogenboom et al., 2003).

An example of common bean GSPs from genes defined in the CSM-GeneGro model (Hoogenboom et al., 2004) is illustrated here. They worked with seven genes, referred to herein as Ppd (long daylength delay), Hr (enhances effect of Ppd, requires Ppd to be present), Fin (indeterminate), Fd (early flowering and maturity), Ssz1 (seed size), Ssz2 (seed size), and Ssz3 (seed size). The following listed GSPs were computed (described by Hoogenboom et al., 2004) as a function of these genes using 0 to indicate recessive and 1 to indicate dominance nature of a given loci (the effect is implemented by entry of 0 or 1 in the allele positions in the following equations).

PPSEN = 0.004 + 0.0154 Ppd + 0.036 Hr – 0.0104 Ppd Hr
EM-FL = 26.77 + 4.886 Fin – 5.88 Fd
FL-SH = 4.63 + 0.972 Ssz1 – 0.98 Ssz2 – 1.8 Ssz3
FL-SD = 10.61 + 2.028 Ssz2 – 2.1 Ssz3
SD-PM = 21.027 - 0.11 Ssz1 + 4.13 Hr
FL-VS = 7.00 + 4.76 Fin – 2.75 Ssz2 – 1.02 Fin Ssz2
FL-LF = 18.0 + 3.8 Fd – 6.9 Ssz2
SLAVR = 322 + 41 Ssz1 – 38 Ssz2 – 25.3 Ssz3
WTPSD = 0.22 + 0.21 Ssz1 + 0.07 Ssz2
SDPDVR = 5.14 - 0.2 Fin - 1.9 Ssz1 + 0.24 Ssz3

Eight less important GSPs not shown are also a function of the genes. Cultivar Porrillo Sintetico (mostly Meso-American) is Ppd, hr, Fin, fd, ssz1, ssz2, and Ssz3, while cultivar Manitou is Ppd, hr, fin, Ssz1, Ssz2, and Ssz3. Cultivar Bayo Madero is Ppd, Hr, Fin, Ssz1, Ssz2, and Ssz3. [As used here, a capital letter indicates dominant, and lower-case indicates recessive.] By changing 'Fin' to 'fin', Boote et al. (2016) created a Calima-like cultivar with Ppd, hr, fin, Ssz1, Ssz2, and Ssz3. With these genes for different cultivars, we were able to demonstrate different modeled growth dynamics with the CROPGRO-Dry Bean model based on the presence or absence of the dominant allele for those genes (where first-letter capitalization indicates the dominant allele). Fig. 8, Fig. 9 , and Fig. 10 illustrate the emergent behavior of the genes when compared to the observed growth of Porrillo Sintetico and Jatu Rong (Calima-like) cultivars grown at Palmira in 1990 by Sexton et al. (1994). Fig. 8A illustrates how genes for time to flower and determinacy affect main stem node number. Calima is the only cultivar with recessive fin, whereas the other three gene-based cultivars have dominant allele Fin, along with different photo-thermal times to flower. The simulated Calima-like gene-based cultivar closely matches the GSP-based simulations and data of main stem node number for the Jatu Rong cultivar while the simulated gene-based Porrillo Sintetico fits well the observed data and GSP-based simulations for Porrillo Sintetico (Fig. 8B). The gene-based

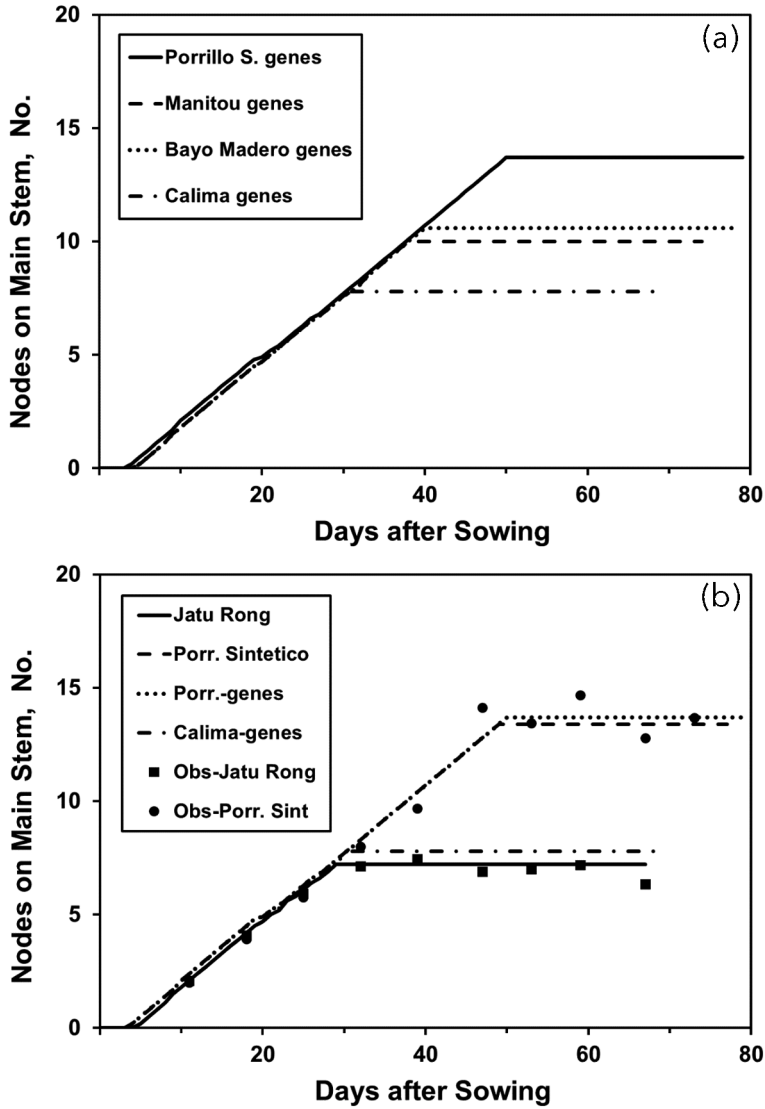

Figure 8 (A) Node number on main stem as affected by genes in four gene-based dry bean cultivars at Palmira, (B) Node number on main stem as affected by genes in two gene-based dry bean cultivars compared to data for Jatu Rong (Calima-like) and Porrillo Sintetico at Palmira (used with permission from Boote et al., 2016).

cultivars differed in their pattern of LAI (Fig. 9A), reaching a peak sooner for the Calima-like (fin) with its early flowering (Fd), followed by the gene-based cultivars with Fin but relatively mid-cycle flowering, and later peak with highest LAI for gene-based Porrillo Sintetico. Comparison to GSP-based simulations

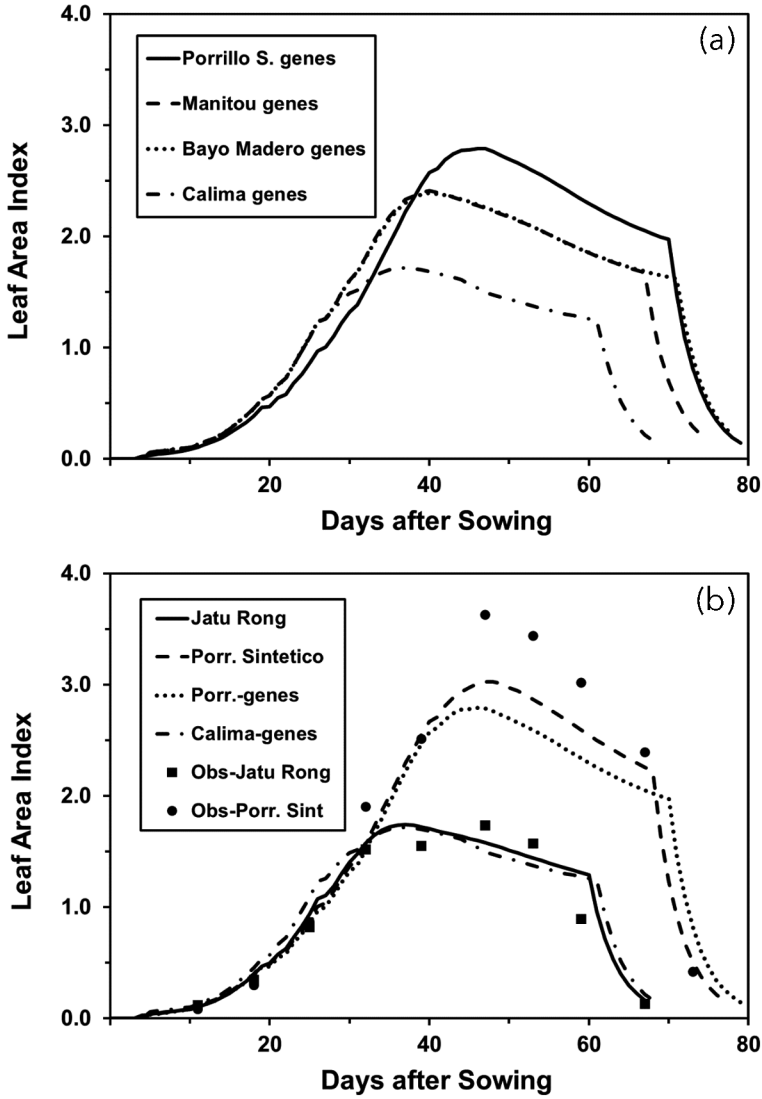

Figure 9 (A) Leaf area index as affected by genes in four gene-based dry bean cultivars at Palmira, (B) Leaf area index as affected by genes in two gene-based dry bean cultivars compared to data for Jatu Rong (Calima-like) and Porrillo Sintetico at Palmira (used with permission from Boote et al., 2016).

and real data for Jatu Rong and Porrillo Sintetico at Palmira (Fig. 9B) illustrates very similar predictions of LAI patterns for the gene-based Calima-like and Porrillo Sintetico. The four gene-based cultivars had very different total seed growth patterns (Fig. 10A), with earliest onset and lowest yield associated with the Calima-like cultivar, followed by later onset and higher seed yield for the

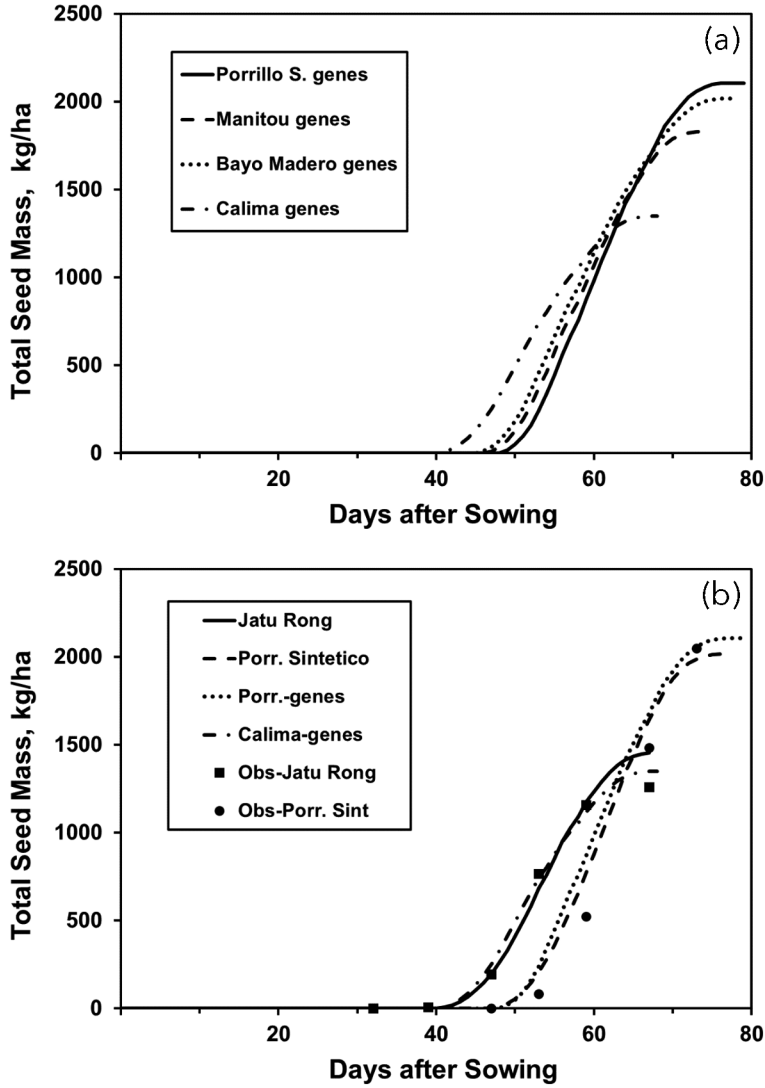

Figure 10 (A) Grain mass over time as affected by genes in four gene-based dry bean cultivars at Palmira, (B) Grain growth pattern as affected by genes in two gene-based dry bean cultivars compared to data for Jatu Rong (Calima-like) and Porrillo Sintetico at Palmira (used with permission from Boote et al., 2016).

other gene-based cultivars. For Jatu Rong and Porrillo Sintetico at Palmira, there were quite comparable simulated patterns of seed growth for the gene-based Calima-like and Porrillo-Sintetico cultivars compared to the GSP-based cultivars (Fig. 10B). These comparisons well illustrate how the resulting widely varying

growth patterns are attributed to genes that control life cycle progression and other aspects of dry bean growth.

There is a recent example of quantitative trait loci (QTLs) linked to the simulation of flowering date in dry bean (Oliveira et al., 2021). The authors investigated the effects of QTLs, environment (E), and QTL × E interactions on the rate of progress to first flower of 187 recombinant inbred lines from a bi-parental bean family grown in two seasons across five sites highly different for daylength and temperature. They identified 12 QTLs responding to daylength, maximum temperature, minimum temperature, and solar radiation that influenced rate of progress to first flower in dry bean. The allelic presence or absence of each QTL, along with regression magnitudes of each QTL and their interactions with E were set up similar to the Hoogenboom et al. (2004) example above. The integrated gene-based module in the CROPGRO-Dry bean model simulated days to first flower that agreed closely with observed values (root mean square error of 2.73 days and model efficiency of 0.90) across the five sites and 187 genotypes. The gene-based module was developed to operate in a hybrid mode in the DSSAT-CSM where the user can decide to use the original GSPs or the QTL data to simulate flowering date.

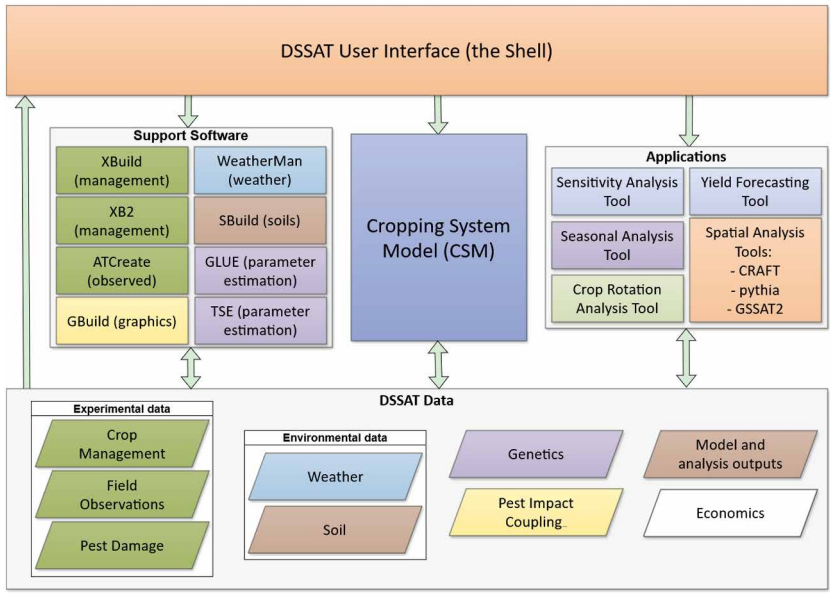

Figure 11 The DSSAT Crop Modeling Ecosystem, linking the CSM to databases, support software, and applications.

14 The DSSAT user interface

This section is adapted from Hoogenboom et al. (2019a) with updates.

The combination of different models, tools, utilities, and applications requires the development of a unique interface that provides easy access for users who may not be familiar with crop models in general, especially with the challenges of formatting input and output files. The CSM model is at the core of the DSSAT shell (Fig. 11). The shell provides the user interface to connect the CSM to the various databases (weather, soils, genetics, experiments-data, economics, pest information, and prior outputs), utility tools, and application tools. The support software allow users to create the experiments (XBuild and XB2), to create soil files (SBuild), to enter weather data (WeatherMan), to enter field observations (ATCreate), to plot model outputs (GBuild), and to estimate genetic coefficients from data (GLUE, GENCALC, and TSE). In addition, there are application programs for Sensitivity Analysis, Seasonal Analysis, Crop Rotation Analysis, Yield Forecasting, and Spatial Analysis. Yield Forecast and Climate Change applications require careful user initiative to link to their own spatial tools, climate change scenarios, and long-term weather records. DSSAT provides tools to assist users in preparing the different input files that are needed for running a model, defining the experiments and treatments or scenarios a user wants to simulate, and conducting an analysis of crop model outputs from the simulations, including comparisons with observed data for model evaluation and strategic analyses for model scenarios (Fig. 11).

In order to facilitate the interaction between the crop models, the data tools, the utilities, and the application programs, a very strict protocol is required for file naming conventions, specific file formats, and system settings that define the location and names of the model input and output files. The strict protocol has allowed programmers to develop new tools and utilities that can be easily incorporated into DSSAT based on standard input and output formats. This approach was first presented to DSSAT users in DSSAT Version 2.1 (IBSNAT, 1989) and DSSAT Version 3.0 (IBSNAT, 1993). The original design and concept are still viable in the most current version of DSSAT Version 4.8.2 (Hoogenboom et al., 2023).

14.1 Minimum data set (MDS) for crop modeling

In order to run a crop simulation model, a minimum set of input data is required. This minimum data set includes daily weather data, soil surface and soil profile information, crop management, and initial conditions at the start of the simulation. The minimum weather data include the metadata for the weather station, especially latitude, longitude, elevation, sensor height, and daily maximum and minimum temperature, rainfall, and solar radiation.

The minimum soil data include the metadata for the location where the soil conditions were measured: soil surface color, slope, drainage, and permeability, as well as soil texture, bulk density, and soil organic carbon for each individual soil horizon. Boundary or initial conditions at the start of the simulation are also very important, especially for the soil environment, requiring initial soil moisture, nitrate and ammonia for each horizon or soil layer, as well as the soil organic C, surface biomass residue, and roots of the previous crop.

The crop management data includes the crop and cultivar selection, planting date, plant density, row spacing, sowing depth, irrigation, and fertilizer inputs. For irrigated treatments and scenarios, the dates, amounts, and the type of irrigation system must be defined; for fertilized treatments and scenarios, the dates, amounts, and types of inorganic fertilizer must be defined, as well as the depth of incorporation. For organic fertilizer using plant or animal material, the type and composition of the organic fertilizer must be defined. If a crop, such as rice, tomatoes, other vegetables, and vegetatively-propagated forage, is started using transplants, the initial weight of the transplant material, age, and the temperature of the nursery must be defined. For potatoes, the weight of the seed potato is an input, for cassava, the weight and length of the stick and orientation of planting are defined; and for sugarcane, the initial cane mass is defined.

The previously listed input data for weather, soil, crop management, and initial conditions are the MDS required for running the model. But for model calibration, evaluation, and improvement, measurements of the crop and soil are required so that comparisons can be made between simulated and observed data. Depending on the research goals and objectives, measurements can include yield and yield components, detailed crop phenology, time-series crop growth analyses, and soil profile measurements such as soil moisture, nitrate and ammonia, organic carbon, and other information (Hoogenboom et al., 2012). See Boote et al. (2015) and Kersebaum et al. (2015) for discussion of quality-classification of experimental data sets for crop modeling.

14.2 Input data tools

Most researchers have their own individual standard methodology for recording experimental data in field books, spreadsheets, and other electronic media. These individual differences make it somewhat challenging to convert the measured data into a format that can be directly applied in a crop modeling system. DSSAT, therefore, provides specific tools for entering weather, soil, crop management, and observational data.

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14.2.1 XBuild

XBuild is the tool for entering crop management data that are stored in a crop management file (Fig. 11). The tool is designed so that the user first enters information that defines the field, specifically the weather station and soil profile that are associated with that experiment, followed by the crop and cultivar selection, and planting information. Initial conditions are defined in the Environmental Section of XBuild. The user can enter different levels for each management scenario, such as multiple cultivars or hybrids, different planting dates, and different input levels and application dates for irrigation and fertilizer.

14.2.2 WeatherMan

The tool called WeatherMan allows for the entry and formatting of weather data into DSSAT weather files (Fig. 11). A user can import weather data preferably from spreadsheets, but WeatherMan can also import other formats, including CSV and ASCII text files. Once the data have been imported into WeatherMan, quality control procedures can be applied to identify extreme values or extreme changes in values for two consecutive days and any missing values. A new internal database is created in WeatherMan with what is referred to as the "corrected" data. The final procedure is to export the data back into DSSAT format weather files.

14.2.3 SBuild

The soil water balance simulation in DSSAT is based on the tipping bucket approach with three key soil moisture variables, including Saturated Water Content (SAT), Drained Upper Limit (DUL), and the Lower Limit of plant extractable water (LL). There are procedures for measuring these, but such measurements are not commonly available for all experiments. The SBuild program of DSSAT allows a user to enter soil surface information, including soil color, slope, permeability, and drainage characteristics, and soil texture (percent clay and percent silt), bulk density, and organic carbon for each soil horizon (Fig. 11). SBuild then uses internal pedotransfer functions to calculate SAT, DUL, and LL for each soil horizon or layer, and it saves the information for that particular soil profile in the soil input file.

14.2.4 ATCreate

Measurement data for model evaluation can be differentiated into two types in DSSAT. The first type is referred to as the summary data and includes the key phenological stages, yield and yield components at final harvest, and other measurements that can be obtained at critical stages, such as maximum leaf

area index (LAI) or grain nitrogen concentration. The summary data are stored in File A as a single line per treatment. The second type of measurement data is referred to as time series data for growth analysis, tissue N concentrations, soil moisture content, soil nitrogen measurements, and other relevant data that can be used for model evaluation. The time series data are stored in File T and are organized by treatment and then observation date. There is also the ability to store the observations for the individual replicates. The ATCreate program allows users to enter observations either manually or by importing a spreadsheet or text file, thereby creating File A and File T for each experiment. It is important to select the appropriate header for each column of data so that the other programs within DSSAT are able to recognize the observed variables. Power-users can use spreadsheets to directly create the File A and File T, by saving as *.PRN files but correctly setting required column widths and headers for data columns, and then correctly naming the file and its internal lead line. The file called DATA.CDE holds the names of these variables (short name, long name, and units) so that header names are shared and are also readable by the graphics program and other programs in DSSAT.

15 Methods for estimating genotype-specific parameters

The DSSAT modeling system defines genotype-specific parameter (GSPs) inputs that allow a user to define characteristics of cultivars, hybrids, clones, and transplant material. As model developers, the DSSAT group is unable to provide local cultivar-specific parameters beyond those with specific experiments included in DSSAT, which means that a model must be calibrated first for local genetics, requiring some of the critical crop observations associated with the MDS described previously. Once the crop management and observational data have been entered, the specific cultivar is then calibrated, either manually (looking at the means and other statistical outputs of GBuild) or using optimization tools. The ultimate goal is to minimize the error between simulated and observed phenological dates, yield, and yield components.

Within the DSSAT Ecosystem, there are several tools that can be used for crop cultivar calibration, the *GLUE* tool, *GENCALC* tool, and TSE tool. In addition, the Sensitivity Analysis utility can also be used to improve the value of one or more GSPs by setting the range and increment for a particular GSP and by comparing simulated with observed data. A comparison of the performance of the first two tools for rice was conducted by Buddhaboon et al. (2018).

15.1 GLUE

The General Likelihood Uncertainty Estimation (GLUE) is a statistical approach that results in multiple sets of parameter values that are equally as likely as a final

solution, *but it only gives the most probable set of GSPs*. The initial evaluation of GLUE for DSSAT was made for the CSM-CERES-Sweetcorn model by He et al. (2009, 2010). To estimate the most likely values for the GSPs for a new cultivar, a user first must provide the required input files associated with weather, soil, and crop management and basic observations, especially for phenology, yield, and yield components. For more robust outcomes, at least two non-stressed treatments from different environments representing different locations, planting dates, or years are recommended. Once the model runs properly, the GSPs can be estimated with GLUE, first for phenological GSPs and then for the yield and yield component GSPs. GLUE stochastically generates each parameter set used in the optimization, therefore, each new GLUE optimization on the same data will give a slightly different set of GSPs. Running a high number of simulations gives greater confidence in the results, and it is recommended to simulate at least 10,000 runs. Caution: GLUE uses only final end-of-season data for the optimization algorithm. Therefore, if in-season growth analyses data are available, users should also look at time-series simulations and statistics (RMSE and d-statistic) available with the GBuild tool. A new version of GLUE has recently been released that allows for the use of multiple cores for parallel processing and significantly speeds up the calibration process (Ferreira et al., 2024).

15.2 GENCALC

The Genetic Coefficient Calculator or GENCALC uses a rule-based approach to determine the value for one or more GSPs (Hunt et al., 1993). In the input file for GENCALC, one or more GSPs are associated with one or more particular plant output variables. During the calibration process, these GSPs are varied to minimize the error between the simulated and observed variables. GENCALC normally optimizes the phenological GSPs first, followed by growth, and then yield components and yield for final optimization. Most crop models do not have a specific GSP that controls only yield; rather, GSPs can affect multiple yield components. GENCALC is for more advanced DSSAT users who are familiar with the GSPs of a particular model and are comfortable editing the GENCALC rules file (Anothai et al., 2008).

15.3 TSE

A third tool, TSE (Time-Series-Estimator), developed by Memic et al. (2021), makes use of time-series growth analysis data from File T as well as File A data and uses normalized root mean square error methods. The TSE optimizes user-selected GSPs against user-selected targeted crop growth variables. For an advanced user and where time-series growth data are available, the TSE Tool may offer greater capability for optimizing GSPs. The GLUE and GENCALC

tools can only use end-of-season File A data, which can result in good final yield simulations but potentially with poor outcomes for time-series simulations.

16 Model visualization tools: GBuild

For performance evaluation of the model with experimental data, visualization tools that not only provide a visual comparison between simulated and observed data but also statistical analysis are critical (Yang J. M. et al., 2014a; Yang J. Y. et al., 2014b). The main tool in DSSAT for visualization and comparison of model simulations with observed data is GBuild.

GBuild is an analysis utility for the visualization of simulated and experimental data (Uryasev et al., 2004). It gives a user the ability to easily plot graphs that are routinely used during crop model development and evaluation. The basic design of GBuild is based on a set of codes that use headers for each column of data that represents different variables. The file selection in GBuild allows a user to select one or more output files for plotting any combination of the variables and runs/treatments and then proceed to display the graph. The graphic type selection options provide different views of the simulated results and include time series, e.g. displaying the simulated data as a function of date or days after planting (DAP), and simulated data vs. experimental data. To better compare the simulated results with observations from experiments, GBuild includes statistics for time series data with emphasis on the d-statistics (Willmott et al., 1985), Root Mean Square Error (RMSE) and means for time-series data, phenological and end-of-season data, such as flowering and maturity dates, yield and yield components. The graphic output of simulated and observed data can be visualized, printed, and exported to an Excel spreadsheet along with the statistics.

17 Application programs

Crop simulation models embedded in decision support systems are very powerful tools for scenario analyses. So far, this chapter has provided an overview of the science of the crop simulation models that are included in DSSAT, as well as the tools and utilities for weather, soil, experimental inputs, observational data entry, crop model calibration, and evaluation. Once a crop model has been calibrated, the most important and useful aspects are associated with the applications. DSSAT, therefore, includes several application programs, as shown in Fig. 11.

17.1 Sensitivity analysis tool

In addition to evaluating the model with real-world data, it is also important to understand the response of the model to variation in a given specific input,

such as weather data, cultivars, soil data, and values for individual GSPs. This approach, in which all inputs are kept constant except for one input or GSP, is called sensitivity analysis. This DSSAT tool is called *Sensitivity Analysis* and enables the user to evaluate the model sensitivity to changes of cultivars, single GSPs, soil profiles, weather inputs for different locations or years, plant and row spacing, and various other options. Variables that have numeric values, such as planting date, can be varied using a starting value, an increment value, and the number of iterations. The program automatically creates a new experimental file ready to run with the selected sensitivity input variation. Following the simulations, the linked GBuild graphics program allows for visual analysis of simulation results and associated statistics.

17.2 Seasonal analysis tool

The *Seasonal Analysis* application allows a user to explore the effects of weather variability and to evaluate the uncertainty and risk factors associated with various management and genetic inputs (Thornton and Hoogenboom, 1994). The *Seasonal Analysis* application enables a user to simulate many hypothetical scenarios quickly and efficiently using long-term historical weather records or stochastically generated weather data. The model simulates a distribution of yields and other outputs, converting uncertainty in weather into uncertainty in yield for the specified management scenarios (Fig. 11). The seasonal analysis application works on a field scale and emphasizes weather uncertainty. Economic risks can also be estimated using the cost of inputs and prices of products, including the variability associated with these costs and prices. The application can be used to select optimal crop and variety, planting options, irrigation options, application of fertilizer, marketing options, insurance risks, policy advisement, and investments in equipment, technology, and diversification of land use. For each scenario, many weather years are simulated, with re-initialization of soil variables done at the beginning of each simulation so that the results reflect the variation in model outputs due to interannual weather variability. A graphical interface allows a user to explore distributions of outcomes for variables, including crop yields, farm profits, and environmental factors such as nitrogen leaching and irrigation requirements. The application includes graphical options such as box plots, cumulative function plots, and mean-variance plots for biophysical and economic variables. This feature allows the user to optimize management practices that will benefit the farmer and to select best management practices relative to maximum profit, minimum risk of low profit or yield, minimum degradation of the environment, or other criteria.

17.3 Crop rotation analysis tool (sequence analysis)

The *Crop Rotation Analysis Tool* (Fig. 11) is used for the analysis of crop rotation, and, in addition to weather and economic uncertainties, takes into account the effects of long-term cropping systems including changes in the soil system with respect to carry-over of soil water, carbon, nitrogen, and other nutrient components. Crop rotation analysis (or *S*equence Analysis) allows a user to produce long-term simulations of a given cropping system for predictions of farming system sustainability such as soil carbon loss, soil fertility degradation, decreasing yields, and increased greenhouse gas emissions (Thornton et al., 1995). Users can explore the sustainability of various options over a long period of time and optimize options for managing the land to sustain productivity, soil health, and natural resources. Crop rotation analysis is used to explore cropping system options based on a pattern of crops planted in sequence. Sequence Analysis/Crop Rotation differs from Seasonal Analysis in several ways. In Seasonal Analysis, soil variables are re-initiated every season, but in Sequence Analysis, soil variables are initialized only once at the beginning of a long-term, continuous simulation. In Sequence Analysis, the soil C, soil N, and soil water carry over into the next fallow or crop, thus running continuously without re-initialization. The crop rotation sequencing or patterns are flexible to create and can mimic a real observed experiment of 10-year duration, for example, with real weather. But the most common option is to use generated weather and "repeat" multiple times (30 or more) over generated weather.

The dynamics of soil organic carbon are of prime importance in these long-term simulations. In sequence simulations, soil organic carbon is "carried over" from one season to the next, and these long-term soil fertility dynamics can be analyzed. It is best to use the CENTURY-style SOC method for sequence rotations because it handles the decomposition of surface residue and senesced plant tissue, which facilitate no-tillage simulations. The initialization of soil organic carbon state variables and pools for CENTURY can be difficult, but it is very important to the predictive accuracy of the model. Methods have been developed to estimate the amount of stable, intermediate, and microbial soil carbon present in the system (Basso et al., 2011; Porter et al., 2010). The best way to estimate (optimize) the stable pool for the CENTURY-style SOC is to have a zero N fertilized treatment with knowledge of initial soil nitrate and ammonium at sowing.

17.4 Spatial analysis

The crop models in DSSAT are point-based models in that the inputs are based on site-specific information such as the weather data from a local

weather station, the soil data from a local soil profile at the experimental site, and crop management for a plot or field. For many applications, there is significant interest in understanding the variability across space for crop growth and yield. The strength of the CSM is that it can simulate at a spatial scale as small as 1 m or less for precision agriculture to ~100 km (1 arc-degree) for global simulations. The current DSSAT software does not include a specific tool for the preparation of input files and visualization of output files. However, the underlying crop model and associated input and output files with GPS coordinates can be easily integrated into other systems if the DSSAT file naming convention and file system structure are maintained. Several examples of spatial applications that use DSSAT in the background include MINK for global gridded simulations developed by the International Food Policy Research Institute (Robertson, 2017), pDSSAT for global gridded climate change applications in agriculture (Elliott et al., 2014), and CCAFS Regional Agricultural Forecasting Toolbox (CRAFT) for yield and production forecasting, climate change impact studies and agricultural risk assessment (Shelia et al., 2019).

17.5 Climate change applications

Climate change applications typically use the Seasonal Analysis Tool to evaluate 30+ years of weather (baseline weather (1990–2020), near-term future weather (2020–2050), and long-term future weather (2050–2080)). The future climate weather can be generated by multiple Global Climate Models, which vary the temperature, atmospheric CO_2, and rainfall based on hypothesized rates of GHG increase and socio-economic pathways. This exercise has been repeated many times over the past decades for many regions in the world. For a simple evaluation, a user can also use the Environmental Modifications section of the File X to vary input temperature, atmospheric CO_2, rainfall, and solar radiation relative to a baseline weather file. Climate change applications can also be done using Sequence Analysis if one wishes to evaluate long-term consequences on yield, soil degradation, and soil C sequestration (or lack thereof).

17.6 Yield forecast application

The Yield Forecast tool within DSSAT involves creating a unique type of File X designed for forecasting. The Tool allows users to estimate in-season yield forecasts using observed weather data combined with multiple realizations of future weather data to predict a range of possible outcomes for the remainder of the season for yield and other model outputs (Shelia et al., 2019; Tesfaye et al., 2023). Simulations use the observed weather data for

the forecast year up through the last observed date or a date specified by the user. After that date, the model uses either generated daily weather data or all available historical weather data to simulate an ensemble of predictions for the remainder of the season. The Yield Forecast Application synthesizes the simulations to present the range of outcomes predicted and the most probable.

17.7 Example applications

See the chapter by Hoogenboom et al. (2019) which provides several illustrative case studies of application approaches: (1) Interaction of nitrogen and water management on performance of maize (1982 maize experiment in DSSAT), (2) Impact of irrigation management on performance of soybean (1978 soybean experiment in DSSAT), (3) Seasonal strategy analysis of irrigation management on soybean over 30 seasons, (4) Sequence analysis that considers the carry-over of the prior crop's extraction of soil water on next crop or the degradation or sequestration of soil organic carbon and effect on long-term soil fertility.

18 DSSAT-CSM software development, distribution, and training

One of the unique aspects of the original IBSNAT Project was its participatory approach that encouraged scientists from different disciplines and different organizations to collaborate in support of the development of one unique DSSAT ecosystem. This network of model developers has expanded since the end of the IBSNAT Project in 1993 to include many scientists from Brazil, China, South Korea, France, Nigeria, India, South Africa, Kenya, and many other countries across the globe. The mutual support and collaboration are facilitated using an Open Source approach, in which the source code of the crop simulation models along with the tools and utility programs are freely available. Currently, the source code for the Cropping System Model can be obtained from GitHub (https://github.com/dssat/dssat-csm-os). The CSM source code is open source using the 3-Clause BSD License (BSD-3-Clause). Since 2014, the DSSAT Development Team has also facilitated biannual DSSAT Development Sprints, which are hackathons for crop modelers. During these one-week, hands-on "working" workshops, the emphasis is on crop model improvement and the advancement of application programs, tools, and utilities. These Development Sprints also provide a forum for communications and information exchange among developers, users, and others interested in modeling and decision support systems. They allow new DSSAT developers to learn the protocols and methods used.

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In the early years, the DSSAT software was sold to cover some of the administrative and development costs. In 2011, the distribution of DSSAT was converted to a free download system from the DSSAT portal (www.DSSAT.net), and since then, the interest in DSSAT has exponentially increased. There were 6,630 downloads of DSSAT Version 4.5, 6,500 downloads of DSSAT Version 4.6, and over 18,500 downloads of DSSAT Version 4.7 since November 2017. DSSAT Version 4.8 was released in April 2021 with 11,100 downloads until present (September, 2024). For the dissemination of information to the DSSAT User Network, a DSSAT Listserv is used, and currently, there are over 29,000 unique e-mail addresses of registered users. User support and documentation are also provided through the DSSAT portal (www.DSSAT.net).

Because DSSAT is such a comprehensive software program, it requires training of agricultural scientists who traditionally specialize in single disciplines and who may not be very familiar with the systems approach that encompasses multiple disciplines. Annual crop modeling training workshops have been held in the US since 1985, initially as two-week workshops and then condensed to intensive, six-day training workshops. Since 2002, these workshops have been hosted at the University of Georgia's Griffin campus, with an average of 55 international participants from universities, governmental organizations, and private industries. The rapid expansion of the DSSAT user network has also resulted in requests for international training programs across the globe, and recent workshops were held in Argentina, Australia, Germany, Indonesia, Kazakhstan, Nigeria, Philippines, Singapore, South Africa, Tanzania, Thailand, Tunisia, Türkiye, and Vietnam. In addition, some of our expert users are now DSSAT trainers, facilitating workshops in Pakistan, Indonesia, Türkiye, Brazil, China, and other countries. Ideal capacity building requires multiple workshops, starting with the basics of crop modeling and data requirements, followed by data collection for model evaluation, and finishing with model applications, the most critical part of crop modeling and decision support (Kihara et al., 2012).

19 Future trends and conclusion

19.1 Collaboration

One of the challenges of maintaining and developing scientific software platforms in agriculture is the limited availability of resources and data for software development and improvement. Many agricultural scientists are not good programmers, especially in computer languages such as Fortran, Delphi, and Visual Basic that are currently used in DSSAT. Early in the development of DSSAT and the crop models, the emphasis had been on scientists developing the crop models rather than relying on professional programmers who develop the code based on input provided by the scientists. This has

shifted in recent years with the addition of more programmers, along with an increased number of model users who want to apply models but who are lacking the hard-core scientific skills to improve model relationships. There is a general lack of emphasis on scientific model improvement in the current overall crop modeling community. Sustainable model development will require the collaboration of scientists with state-of-the-art crop-soil-systems expertise with programmers who can write scientifically sound code. DSSAT source code is Open Source and is shared on GITHUB which has allowed the DSSAT Development group to expand to a community of those interested in advancing and improving the DSSAT, including the models as well as the tools and utility programs.

19.2 Opportunities

The current agricultural production system is challenged by the increase of climate extremes and economic risks associated with climate change. At the same time, there is pressure to grow more and healthy food using sustainable practices. Among these practices, the reduction of greenhouse gas emissions and increase of soil carbon stocks are some of the major challenges that can be supported by biogeophysical models. Measuring, Monitoring, Reporting, and Verification (MMRV) efforts are demanding the scaling up of carbon stocks measured from point to plot, farm, and country. Crop models can be used to translate historical and actual crop management while assimilating remote sensing and local soil observations. Artificial Intelligence (AI) can play a valuable role in those tasks, and AI can also be trained by leveraging crop models' outputs. At the same time, technology is rapidly improving with new sensor technologies, the Internet of Things, remote sensing, genetic markers, and artificial intelligence. AI can be potentially useful to search for information and data on which to parameterize crop models. The amount of data that is being collected for agricultural production systems is exponentially expanding, providing opportunities for data analytics and the use of AI for strategic and actionable decisions. Unfortunately, much of that data is relatively superficial, e.g. remotely sensed biomass, and is lacking in depth and quality of crop physiology needed for model improvement. The promise of genetic technologies and QTL markers needs to be better linked to the genetic attributes used for cultivars in the crop models, and if done well, may reduce the need for detailed experiments for every new cultivar released. When AI is used in collaboration with these massive data sets, the DSSAT-CSM can play a major role in helping to understand the physiological relationships and interactions between Genotype, Environment, and Management (G * E * M). This can provide alternative management options that increase crop yield and quality, optimize resource use, and minimize environmental impact for

long-term sustainable agricultural production. Boote (2019) reviewed the future of crop modeling relative to potential uses and applications and the needs for model improvement. There are great opportunities as well as challenges. A new concern since that review is whether Machine Learning and AI because of their newness and popularity will short-circuit true learning and understanding of mechanistic processes in the models.

19.3 Conclusion

The DSSAT crop modeling ecosystem is one of the oldest and most widely used crop modeling platforms across the world. The success of DSSAT and the CSM is based on the inclusiveness and participatory approach employed since the original development of the CERES and CROPGRO models that led to the much-expanded Cropping System Model. The modularity of the CSM with its linkage of multiple crop models and process components in a single executable code offers much promise for future enhancement of the CSM and DSSAT. We continue to add new crops to CSM, including perennial forages and vegetables, and have added new capabilities to the DSSAT software, such as yield forecasting. The emphasis on sharing data and model code in an open-source environment has also facilitated continued model improvement. The CSM and DSSAT offer multiple application possibilities, including crop management, minimizing environmental pollution, optimizing genetic yield improvement, and evaluating the impacts of future climate change.

DSSAT with the CSM is not just a software program but an ecosystem of:

- Crop model users
- Crop model trainers
- Crop model developers/scientists
- Models for important food, feed, fiber, pasture, and fuel crops
- Tools and utilities for data preparation
- Minimum data for model calibration and evaluation
- Application programs for assessing real-world problems

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