Adapting the CROPGRO Model to Simulate Growth and Yield of Spring Safflower in Semiarid Conditions

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ABSTRACT

The importance of safflower (*Carthamus tinctorius* L.) is increasing as a low input, stress-tolerant oilseed crop around the world. Adapting a crop growth model for safflower will help to assess the feasibility of this crop under diverse environmental conditions with relatively limited field experimentation. The objective of the project was to adapt the Decision Support System for Agrotechnology Transfer (DSSAT) Cropping System Model (CSM-CROPGRO) to simulate growth and seed yield of spring safflower. The CROPGRO template approach was used, and parameters in species and cultivar files were developed based on safflower literature and calibration to field data. The entered base temperatures for photosynthetic, vegetative, and reproductive processes of safflower ranged from 0 to 5°C while corresponding optimum temperatures varied from 19 to 40°C. Simulated results were compared with observed data collected from field experiments conducted at Clovis, NM, during 2013 and 2014. The model predicted the crop life cycle (anthesis and harvest maturity date) with relative root mean square error (RRMSE) of 0.07. Average plant biomass, head mass, head number and seed number were satisfactorily simulated when compared to observed values. Seed yield, averaged over irrigation treatments and years, was predicted as 1963 kg ha^{-1} compared to measured value of 1902 kg ha^{-1} with RRMSE of 0.12. Reasonable prediction of phenology, growth, and yield by the model adapted for safflower suggested that the CROPGRO-safflower model is promising to simulate safflower production in semiarid climates. However, further testing of the CROPGRO-safflower model under different environments is needed.

I N THE SEMIARID SOUTHERN HIGH PLAINS (New Mexico and West Texas), where water resources are declining, it is important to identify drought-tolerant crops for sustainable agriculture. Safflower is an annual oilseed crop mainly grown for high quality edible oil and birdseed (Koutroubas et al., 2009). It is well adapted to arid and semi-arid regions of the world. The deep taproot system is able to extract water up to a depth of 220 cm and xerophytic spines contribute to drought and heat tolerance of safflower (Dajue and Mündel, 1996). In addition to low water consumption, the inclusion of safflower in the cropping system of the southern High Plains could increase the local production of vegetable oil and protein-rich meal for dairy livestock.

Multi-year and expensive experiments are needed to verify the adaptability of a particular crop in a region. Performance of a new crop in the region interacts with many factors such as seasonal irrigation availability, rainfall, sowing time, solar radiation, and temperature. However, it is impossible to investigate all possible combinations derived from these factors in the field. Mechanistic crop simulation models are valuable tools to optimize crop management strategies and facilitate extrapolation of results from single site experiments to other similar agro-ecological sites. Crop models can be used to assess the effects of land-use changes on crop productivity to simulate environmental risks and to evaluate alternative crop management practices for alleviating these risks.

The importance of crop models, as research tools to assess risks associated with various management strategies, has increased in the last few years. Many crop models have been assessed for decision making in different locations where soils and climate differ. The CROPGRO is a process-based mechanistic model that predicts crop growth based on weather, plant, soil, and management inputs (Boote et al., 1998a, 1998b, 2010; Hoogenboom et al., 1992; Jones et al., 2003). It is a generic model in the sense that there is one common FORTRAN code to predict the growth of a number of different grain legumes including soybean [*Glycine max* (L.) Merr.], peanut (*Arachis hypogaea* L.), dry bean (*Phaseolus vulgaris* L.) (Boote et al., 1998a, 1998b), faba bean (*Vicia faba* L.) (Boote et al., 2002),

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Abbreviations: DSSAT, Decision Support System for Agrotechnology Transfer; SLA, specific leaf area; LAI, leaf area index; PD, photothermal days; RRMSE, relative root mean square error.

velvet bean [*Mucuna pruriens* (L.) DC.] (Hartkamp et al., 2002a, 2002b) as well as non-legume crops such as tomato (*Lycopersicon esculentum* Mill.) (Scholberg et al., 1997). This adaptability of the CROPGRO model to different crops is possible because the model uses external data files that define species and cultivar traits (Jones et al., 2003). The CROPGRO species file for each given species defines base temperature (Tb) and optimum temperature (Topt) for development processes (e.g., rate of emergence, rate of leaf appearance, reproductive progression) and growth processes (photosynthesis, leaf expansion, pod addition, seed growth, etc.). In addition to cardinal temperatures, the species file also contains coefficients and other relationships for photosynthesis, tissue composition, and growth and maintenance respiration (Boote et al., 2002). Cultivar files in the CROPGRO model include the effect of daylength with two parameters that define critical daylength of each cultivar and slope of daylength sensitivity that slows or speeds up development depending on daylength.

Modeling crop growth and yield of safflower, being a minor crop, has not been an attraction to researchers so far. However, increased pressure on natural resources is bringing more attention to low input crops such as safflower. Therefore, the objective of this study was to adapt a process-based crop model to simulate growth and seed yield of spring safflower. To fulfill this aim, the template files for the CROPGRO-soybean model in the DSSAT were selected as a starting point, on the advice of model developers. The OILCROP-SUN model for sunflower (*Helianthus annuus* L.) is available in the DSSAT, but it is an older DOS-based legacy model that is not being actively coupled to new DSSAT software features (G. Hoogenboom, personal communication, 2014). Safflower belongs to the same botanical family (Asteraceae) of sunflower; however unlike sunflower which has only a single head, safflower has several heads with seeds, which is another reason why it is difficult to adapt the OILCROP-SUN model for safflower. Furthermore, being a generic in nature the CROPGRO model allows introduction of a new crop with relative ease.

MATERIALS AND METHODS
Safflower Experimental Description

Experimental data for calibration of the model was derived from field experiments conducted at the Agricultural Science Center (ASC) of New Mexico State University during 2013 and 2014 (34°35′ N, 103°12′ W and altitude of 1348 m above sea level). The study location is characterized as semiarid climate with an annual average precipitation of 445 mm, and the mean maximum and minimum temperatures are 22 and 7°C, respectively (Singh et al., 2014). In 2013 the trial was conducted on a field following wheat, while in 2014 the trial was conducted on an adjacent field following corn. Soil type of the study site was Olton clay loam (fine, mixed, superactive, thermic Aridic Paleustoll). Soil pH was 7.3 and 7.6, and organic matter content was 1.6 and 1.9% in 2013 and 2014, respectively.

The weather data file in model was updated with the daily weather data collected from the station situated at the ASC, Clovis, NM, which was also the experimental site. Maximum and minimum air temperatures, rainfall and solar radiation were arranged in a standard format. Information of soil chemical and physical properties at different depths of the soil profile,

and soil classification was placed in the soil data file in the model. The source of soil data for the region was the USDA-NRCS-NSSC Soil Survey.

The entire experimental field was pre-irrigated with 203 mm of water in 2013 and 129 mm in 2014 to fill the soil profile emptied by previous crops of winter wheat and corn, respectively. Pre-irrigation was given, between February and April in four splits to avoid runoff, using a center pivot irrigation system set up with bubbler pads. The final 38 mm of pre-irrigation was given before planting with spray pads to create uniform seed bed moisture for the entire trial. Based on soil test results, the field was fertilized before planting with 77 kg N ha^{-1} and 28 kg P_2O_5 ha^{-1} in 2013, and 55 kg N ha^{-1} and 17 kg P_2O_5 ha^{-1} in 2014. Herbicide Treflan HFP at the rate of 2.5 L ha^{-1} was incorporated (pre-plant) into the soil for weed control in each year.

Three different spring safflower cultivars named PI8311, 99OL, and Nutrisaff were sown on 30 Apr. 2013 and 23 Apr. 2014, using a plot drill (Model 3P600, Great Plains Drill) at a row spacing of 0.15 m. However, a severe hail storm on 7 June 2014 destroyed the well-established safflower crop in the field. Hence, we replanted the whole trial on 17 June 2014. The cultivar PI8311 was selected to calibrate the model for safflower, and growth and yield data were collected. The simulation of phenology and yield of other two cultivars (99OL and Nutrisaff) was performed to check the performance of the model. Seeding rate was determined based on row spacing, seed weight, and an estimated field emergence rate of 85%. A population density of 62 plants m^{-2} was targeted. Recorded plant density for PI8311 was 48 and 37 plants m^{-2} in 2013 and 2014, respectively. The plot size was 9 by 5.5 m with three passes (11 rows per pass) in each plot. The crop was harvested on 27 Aug. 2013 and 6 Oct. 2014.

Two important growth phases were considered for irrigation treatments, that is, vegetative and reproductive. Four irrigation treatments, that is, stress at vegetative stage (V-stress), stress at reproductive stage (R-stress), rainfed, and irrigated were applied. The goal was to evaluate and predict crop response to water stress occurring at different growth stages in comparison to an unstressed irrigated crop on the one hand and to a crop stressed during most of its life cycle under rainfed conditions on the other hand. All treatment combinations were randomized into a split plot design with irrigation treatment as the whole plot and cultivar as the subplot. Every treatment combination was replicated four times for a total of 48 plots. Each experimental unit was irrigated at the same time as the irrigated treatment and same irrigation amount was given, except for skipping irrigation application at a specific growth stage.

Biomass partitioning to different plant parts was measured at a 15-d interval. Five plants were separated into leaves, stems, and heads, and oven-dried at 55°C to a constant dry weight to determine biomass partitioning. Leaf area of freshly-separated leaves was recorded every time before oven drying using a leaf area meter (LI-3000, Lincoln, NE). Plant height from the soil surface to the tip of five plants was measured at 30-d interval. At final maturity, five random plants were hand harvested to determine number of heads per plant, number of seeds per head and seed weight. An area of 2.14 m^2 was harvested with a sickle mower to record the total plant biomass production

and remaining larger area of 9.2 m² was harvested using a plot combine (Model Elite Plot 2001, Wintersteiger, Ried, Austria) for seed yield. The seed yield was converted to oven-dry weight for purposes of model simulation. Harvest index (HI) was computed as the ratio of seed yield to the total plant biomass.

Model Adaption Approach

The crop management data file was created with all the experimental details required to simulate various treatments of the experiment (site description, planting date, harvesting date, and irrigation amounts), initial conditions (soil type and conditions, soil analysis data, field characteristics, fertilizer and irrigation management, chemical applications, residue management, and harvest management) and simulation options. For cultivar-specific traits in the genetic input file, soybean maturity group 4 was used as the initial default cultivar, after which genetic coefficients for a new safflower cultivar PI8311 were estimated, including minimization of daylength sensitivities.

The approach used for model adaption for faba bean (Boote et al., 2002) and pigeonpea (*Cajanus cajan* L. Millsp.) (Alderman et al., 2015) was followed to adapt the CROPGRO model template for safflower. The basic approach to develop species and cultivar files for safflower was as follows: (i) values and relationships reported from literature were used to extent of availability (ii) optimization of additional species, ecotype, and cultivar parameters was performed based on Bayesian optimization, and simulated results were compared with data observed in field experiments conducted at Clovis, NM, during summers of 2013 and 2014. First, values such as tissue composition, Tb, and Topt for various processes were entered in the species file from the literature. Second, photothermal days (PD) were adjusted to simulate correct safflower life cycle. The main focus was to match simulated anthesis and physiological maturity dates with observed phenology in the field. Third, species and cultivar parameters that affect leaf and canopy photosynthesis were optimized by comparing simulated biomass and leaf area index (LAI) with observed values. Fourth, coefficients related to duration of flowering to first pod/head (since we are using the CROPGRO-legume model for safflower, pod and head will be used synonymously), flowering to first seed and duration of head addition were adjusted and comparisons of predicted vs. observed head growth were made. Fifth, parameters of seed size, seeds per head, seed growth, and seed filling duration were calibrated until simulated and measured seed size and seeds per head were matched. Considerable iterations among second, third, fourth, and fifth steps were required to achieve predicted values close to observed values.

Bayesian Optimization Approach

The selected parameters were estimated using a hybrid algorithm (written in FORTRAN) including a Gibbs sampler (Casella and George, 1992) and the Metropolis–Hastings algorithm (Chib and Greenberg, 1995) used in Bayesian analysis. The Bayesian approach is a maximum likelihood optimization method that considers each parameter as random variable with its own distribution. The approach was aimed to estimate the mean of this distribution based on prior knowledge, a set of observed data, and a log-likelihood function. The possible distribution of the candidate parameters based on prior knowledge (previous studies and literature) is known as the prior distribution. The prior distribution for each parameter was assumed to be uniform. The Bayesian approach estimates parameters by selecting the set of values of the parameters that maximize the likelihood function. The process was repeated for each parameter, and care was taken to make sure that the generated candidate parameter was within the range of values (minimum to maximum) reported in the literature. More detailed information of the Bayesian approach can be found in Alderman et al. (2015).

Statistical Evaluation

After optimization, the simulated data were compared with the observed time-series and end-of-season data by using model evaluation statistics. The Willmott Agreement Index (*d*) (Willmott et al., 1985) is a measure of agreement between general trends in simulated and observed data. The *d* value was calculated using the following equation:

$$d = 1 - \left[\frac{\sum_{i=1}^{n} \left(P_i - O_i \right)^2}{\sum_{i=1}^{n} \left(\left| P_i' \right| + \left| O_i' \right| \right)^2} \right] \quad 0 \leq d \leq 1 \qquad [1]$$

where *n* is the number of observations, P_i is the predicted value for the *i*th measurement, O_i is the observed value for the *i*th measurement, $\overline{O}$ is the the overall mean of observed values, and $P_i' = P_i - \overline{O}$ and $O_i' = O_i - \overline{O}$. The index varies between 0 and 1, with a value of 1 indicating perfect agreement between predicted and observed data.

A second model evaluation statistic used in this study was the relative root mean square error (RRMSE), which was computed using the following equation:

$$\text{RRMSE} = \frac{\sqrt{\sum_{i=1}^{n} \left(P_i - O_i \right)^2 \big/ n}}{\mu} \qquad [2]$$

where *n* is the number of observations, P_i is the predicted value for the *i*th measurement, O_i is the observed value for the *i*th measurement, and μ is the mean of all observed values. The RRMSE is always positive and has no upper limit. The RRMSE equal to 0 indicates perfect agreement between observed and predicted data.

RESULTS AND DISCUSSION
Setting Cardinal Temperatures and Phase Durations for Vegetative and Reproductive Development

The species file of the CROPGRO model requires four points of cardinal temperatures [base temperature (Tb), first optimum (Topt1), second optimum (Topt2) and maximum (Tmax)] to calculate crop development. Very little data showing the effects of temperature on growth and development of safflower were available. In one study, an increase in germination was noticed as the temperature was raised from 5 to 30°C and the maximum germination was found at 28°C (Balashahri et al., 2013). However, a significant decrease in percent germination was observed at a temperature lower than 5°C and higher than 30°C. Experimental

Table 1. Cardinal temperatures-base (Tb), first optimum (Topt1), second optimum (Topt2), and maximum (Tmax) used for growth processes of safflower and soybean in the CROPGRO model.

Growth/Development process	Safflower				Soybean			
	Tb	Topt1	Topt2	Tmax	Tb	Topt1	Topt2	Tmax
	°C							
Rate of node expression	3	28	30	38	7	28	35	45
Progress to anthesis	3	28	32	43	6	26	30	45
First seed to maturity	3	28	38	45	−48	26	34	45
Light saturated leaf photosynthesis, LFmax† vs. current temp.	5	35	40	45	8	40	44	48

† LFmax, light-saturated maximum leaf photosynthetic rate.

Table 2. Genetic coefficients of safflower as defined in the cultivar file of the CROPGRO model, after calibration, and compared to soybean.

Genetic coefficients	Safflower	Soybean
Critical long (safflower) daylength above which reproductive development progresses as rapidly as possible with no daylength effect (CSDL) (h)	23.00	13.09
Slope of the relative response of development vs. photoperiod (PP-SEN) (1 h^{-1})	0.001	0.290
Time between emergence and flower appearance (EM-FL) (PD†)	17.0	19.4
Time between first flower and beginning head (FL-SH) (PD)	3.0	7.0
Time between first flower and beginning seed (FL-SD) (PD)	15.0	15.0
Time between beginning seed and physiological maturity (SD-PM) (PD)	30.0	34.0
Time between first flower and end of leaf expansion (FL-LF) (PD)	20.25	26.00
Maximum leaf photosynthetic rate at 30°C, 350 µL L^{-1} CO_2, and high light (LFMAX) (mg CO_2 m^2 s^{-1})	2.20	1.03
Specific leaf area of cultivar under standard growth conditions (SLAVR) (cm^2 g^{-1})	200.0	375.0
Maximum size of full leaf (SIZLF) (cm^2)	115.0	180.0
Maximum fraction of daily growth that is partitioned to seed + shell (XFRT)	0.55	1.00
Maximum weight per seed (WTPSD) (g)	0.04	0.19
Seed-filling duration for seed cohort under standard conditions (SFDUR) (PD)	29.0	23.0
Seeds per head at standard growth conditions (SDPDV) (no. head^{-1})	22.25	2.20
Duration of head addition under standard conditions (PODUR) (PD)	17.0	10.0
Threshing percentage [seed (seed + shell) $^{-1}$]THRSH	51.3	77.0
Fraction protein in seeds (SDPRO) [g (protein) g (seed) $^{-1}$]	0.140	0.405
Fraction oil in seeds (SDLIP) [g (oil) g (seed) $^{-1}$]	0.330	0.205

† PD, photothermal days.

Table 3. Parameters as defined in the ecotype file of the CROPGRO model for safflower and soybean, after the calibration process.

Variable	CROPGRO parameter	Safflower values	Soybean values
Rate of appearance of leaves on the main stem	TRIFL	0.36	0.32
Relative width of ecotype in comparison to the standard width per node defined in the species file	RWDTH	0.85	1.00
Relative height of ecotype in comparison to the standard height per node defined in the species file	RHGHT	0.85	1.00
Time from first flower to last leaf on main stem	FL-VS	7.00	26.00
Time between physiological maturity and harvest maturity	R7-R8	26.00	12.00

Table 4. Comparison between observed and simulated crop life cycle and crop variables at maturity averaged over four treatments of 2 yr, and the relative root mean square error (RRMSE).

Crop variable	Observed mean	Simulated mean	RRMSE
Anthesis day, dap†	58	57.5	0.07
Harvest maturity day, dap	115	121	0.06
Plant biomass, kg ha^{-1}	5227	6941	0.35
Head mass, kg ha^{-1}	2126	1644	0.42
Head number, no m^{-2}	365	345	0.36
Seed number, no m^{-2}	8358	7650	0.38
Harvest index	0.39	0.29	0.25
Seed yield, kg ha^{-1}	1902	1963	0.12

† dap, days after planting.

results showed no germination of safflower seeds below 3°C and above 38°C. Hence, temperatures of 3, 28, 30, and 38°C were used as Tb, Topt1, Topt2, and Tmax, respectively, for rate of emergence and rate of leaf appearance (Table 1). A report on certified seed production of safflower described that safflower can tolerate temperature exceeding 37°C at flowering; however temperature of 32°C or more affects pollen shedding (AOSCA, 2012). Knowles and Miller (1965) reported that safflower can tolerate temperature up to 43°C at flowering; however, they also found that yields were highest in the years when temperatures were in the range of 24 to 32°C. Weiss (1971), observed a low percentage of fertilized florets at a day temperature of 32°C as compared to day temperatures of 25 or 30°C. Based on these studies, temperatures of 28 (Topt1), 32 (Topt2), and 43 (Tmax) °C were used for progress to anthesis (Table 1). Zimmerman (1972) conducted an experiment, using low (31°C), medium (38°C), and high (43°C) temperatures at flowering, and reported that the head development in anthesis and preanthesis were the most sensitive to temperature. He further suggested that on completion of fertilization, safflower was able to tolerate higher temperatures at late reproductive stage. Based on Zimmerman's findings, temperatures of 28, 38, and 45°C were assumed as Topt1, Topt2, and Tmax respectively, for rate of progress from anthesis to maturity (Table 1). A Tb of 3°C was used for reproductive development to be consistent with vegetative processes.

The CROPGRO model can model both long and short day cultivars, but in our case we initially attempted simulations with long daylength effect that requires specification of a critical maximum long daylength, at which progress to anthesis is most rapid, and a slope of daylength sensitivity that decreases rate of progress at shorter daylengths. Safflower is a day-neutral, long day plant (Johnston et al., 2002) and is grown in different times (spring/summer/fall) around the world. Hence, safflower was modeled here as a day neutral plant in the CROPGRO model. A maximum long daylength of 23 h was assumed and an apparent insensitivity of 0.001 (PPSEN) was used (Table 2). Our target was to set the CROPGRO model to predict beginning seed (R5) in the model corresponding to safflower-observed anthesis (R1) because heads appear before flowering in safflower, and seed growth commences very soon after flowering in safflower. Thus, the sum of two CROPGRO cultivar phase durations, EM-FL and FL-SD, are required to reach safflower-observed anthesis. The EM-FL and FL-SD were 17 and 15 PD, respectively. The time between physiological maturity (R7) and harvest maturity (R8) was set to 26 d to match simulated harvest maturity with the observed values (Table 3). The RRMSE values for predicting anthesis (which is beginning seed in the CROPGRO model) and maturity dates were 0.07 and 0.06 d, respectively (Table 4).

Parameterizing Tissue Composition, Nitrogen Mobilization, and Senescence

Safflower seed contains 50% carbohydrate, 14% protein, 33% lipid, and 3% ash (Sinclair and De Wit, 1975). Compositions of different tissues were modified in the species file for safflower based on literature values (Table 5). Being cultivar traits, seed protein (SDPRO) and seed lipid (SDLIP) were entered in the cultivar file (Table 2). Seed protein value (SDPRO) in cultivar file should match standard protein concentration of seed (SDPROS) and growth protein concentration of seed

Table 5. Modified tissue composition (kg kg^{-1} tissue dry weight) values for safflower in species file of the CROPGRO model.

Compound	Tissue	CROPGRO parameter	Safflower values	Source of data
Carbohydrate	Seed	PCARSD	0.470	Sinclair and De Wit (1975)
	Shell (hull)	PCARSH	0.600	Nagaraj (1993)
	Leaf	PCARLF	0.405	Fredeen et al. (1991)
	Stem	PCARST	0.572	Evon et al. (2007)
Protein	Seed	SDPROG	0.140	Sinclair and De Wit (1975), Weiss (1983), and Latha and Prakash (1984)
	Shell (hull)	PROSHG	0.150	Nagaraj (1993)
	Leaf	PROLFI	0.356	Soybean model
	Stem	PROSTG	0.150	Evon et al. (2007)
Lipid	Seed	PLIPSD	0.330	Sinclair and De Wit (1975)
	Shell (hull)	PLIPSH	0.050	Evon et al. (2007)
	Leaf	PLIPLF	0.025	Soybean model
	Stem	PLIPST	0.010	Evon et al. (2007)
Lignin	Seed	PLIGSD	0.020	Kohler et al. (1966) and Saunders (1970)
	Shell (hull)	PLIGSH	0.152	Nagaraj (1993)
	Leaf	PLIGLF	0.070	Soybean model
	Stem	PLIGST	0.169	Evon et al. (2007)
Mineral	Seed	PMINSD	0.020	Calculated/Assumed
	Shell (hull)	PMINSH	0.035	Guggolz et al. (1968)
	Leaf	PMINLF	0.094	Soybean model
	Stem	PMINST	0.049	Evon et al. (2007)
Organic acid	Seed	POASD	0.020	Calculated/Assumed
	Shell (hull)	POASH	0.013	Calculated/Assumed
	Leaf	POALF	0.050	Soybean model
	Stem	POAST	0.050	Soybean model

(SDPROG) in species file. These tissue compositions are fractions of dry weight in the different plant organs. Sum of the different compounds for a particular plant organ, such as protein (PROLFI), carbohydrate (PCARLF), lipid (PLIPLF), lignin (PLIGLF), organic acid (POALF), and mineral (PMINLF) must be equal to 1.00. Some of the shell, leaf, and stem compositions for safflower were based on sunflower values. Therefore, minor modifications in tissue compositions from literature were needed to match the sum to 1.00, and organic acid fractions were calculated by deducting the sum of other particular values from 1.00. As required by the model, we set the maximum leaf N composition at 5.7% (0.356 protein), the normal at 2.2% (0.140 protein) and the final at 1.8% (0.112 protein). Maximum and final N values were used from the soybean model and normal N value was calculated from protein content based on the reference of Seiler (1984).

The CROPGRO model simulates leaf senescence based on remobilization of N and carbohydrates in addition to crop aging and drought stress. SENRTE (leaf mass in grams that is lost per gram of protein mobilized) was increased from 0.80 to 1.00 to get more senescence in the late crop life cycle to match with the observed values. This was coupled with increase in NMOBMX (the maximum rate of protein mobilization from vegetative tissues during reproductive growth) from 0.17 to 0.20 that caused more rapid loss of leaf area index (LAI), leaf mass, stem mass, and whole plant mass. This also helped to lower head mass and seed yield that were initially overpredicted by the model.

Parameterizing Photosynthesis Rate and Sensitivity to Temperature

Little is known on the effects of temperature on leaf and canopy photosynthesis of safflower in the literature. Hence, sunflower references were used to approximate Tb and Topt for safflower photosynthesis. Maximum light-saturated photosynthetic rates of sunflower were reported to increase as temperatures increased from 5 to 35°C (Paul et al., 1990). Mark and Tevini (1996) reported that increased growing temperature from 28 to 32°C for sunflower resulted in higher net photosynthetic rates per plant. Based on the above data, Tb, Topt1, Topt2, and Tmax values for light-saturated leaf photosynthesis were set in the model as 5, 35, 40, and 45°C, respectively (Table 1). The CROPGRO model also has a relative effect of minimum night temperature (Tmin) that affects next day's leaf photosynthesis. We presumed that safflower and soybean have similar sensitivity to night temperature as both crops can withstand high temperatures as well as relatively cool nights. Soybean asymptotic function response that starts reducing photosynthetic rate at Tmin of 19°C and approaching zero rate at Tmin of 0°C was used for safflower.

For comparison, the respective Tmin values are 4 and 22°C for peanut, –2 and 14°C for faba bean, and 0 and 16°C for dry bean. Maximum leaf photosynthetic rate (LFMAX) was modified based on optimization to predict accurate biomass and productivity (Table 2).

Calibrating Traits Affecting Canopy Expansion Processes

Leaf growth parameters such as specific leaf area (SLA) at emergence (FINREF), at early vegetative phase (SLAVR = SLAREF) and leaf area per trifoliate leaf at fifth node (SIZREF) were modified from soybean, to better predict the rate of leaf area expansion (Table 6). The species file of the CROPGRO model needs an upper and lower limit of SLA (SLAMAX and SLAMIN, against limiting low and saturating high solar radiation, respectively) to set the SLA of a given species. These limits were set at 650 and 110 $cm^2 g^{-1}$. The SLA of cultivar (SLAVR) was calibrated to 200 $cm^2 g^{-1}$ (Table 2). Observed SLA averaged on four treatments was 112 $cm^2 g^{-1}$ in 2013 and 71.25 $cm^2 g^{-1}$ in 2014. Predicted SLA was similar to observed SLA in 2013 with d-statistic of 0.70 (Fig. 1A), however the model over predicted the SLA in 2014 with d-statistic of 0.41 (Fig. 1B). The RRMSE for predicting SLA was 0.24 in 2013 and 0.75 in 2014.

The rate of leaf appearance on the main stem (TRIFL) was increased from 0.32 to 0.36 leaves per thermal day (Table 3). Maximum size of the full leaf (SIZLF) was standardized to 115 cm^2 based on the leaf size obtained in the trials conducted at Clovis, NM (Table 2). To simulate LAI, FL-VS (the time from first flower to last leaf on main stem) was set to terminate the leaf development on the main stem at 7 PD after first flower (Table 3). In addition, end of leaf expansion after first flower (FL-LF) was set to 20.25 PD (Table 2). Simulated LAI in 2013 was good (slightly high) with RRMSE of 0.36 (Fig. 2A). However, the simulation of LAI in 2014 was under predicted with RRMSE of 0.45 (Fig. 2B). The average d-statistic was 0.85 in 2013 and 0.82 in 2014.

The canopy height (RHDHT) and width (RWDTH) coefficients were altered to reduce the height and width to apply to safflower (Table 3). With these calibrations, reasonable values of plant height were predicted. Simulated plant height averaged over four treatments of the 2 yr was 0.41 m with RRMSE of 0.19 as compared to observed plant height of 0.42 m (data not shown).

Calibrating Parameters Affecting Biomass Accumulation and Partitioning

Vegetative partitioning parameters were modified in the species file for the balanced allocation of dry matter to leaf, stem, and reproductive parts, leading to a better simulation of the aboveground plant biomass. Biomass partitioning to leaves

Table 6. Leaf growth parameters as defined in the species file of the CROPGRO model for safflower and soybean, after the calibration process.

| Variable	CROPGRO parameter	Safflower values	Soybean values
Specific leaf area of leaves at plant emergence	FINREF	150.0	180.0
Specific leaf area of the standard reference cultivar at early vegetative phase	SLAREF/SLAVR	200.0	350.0
Leaf area per trifoliate leaf for the leaf at the fifth node position	SIZREF	115.0	171.4
Upper limit of specific leaf area (in low light)	SLAMAX	650.0	950.0
Lower limit of specific leaf area (in saturated light)	SLAMIN	110.0	250.0
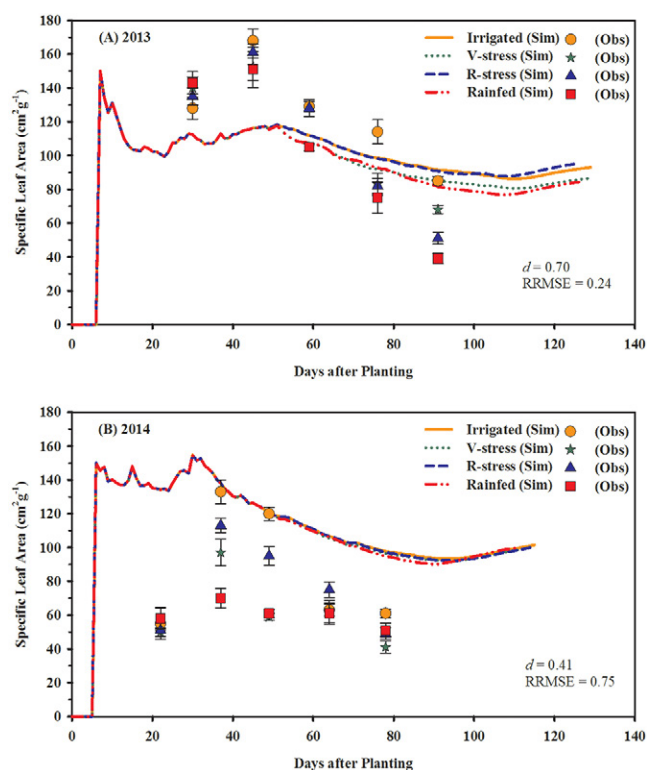
Fig. 1. A comparison of simulated (lines) and observed (symbols) specific leaf area as a function of days after planting for safflower cultivar PI8311 at Clovis, NM, in (A) 2013 and (B) 2014. Statistics shown are Willmott Agreement Index (d), and relative root mean square error (RRMSE).
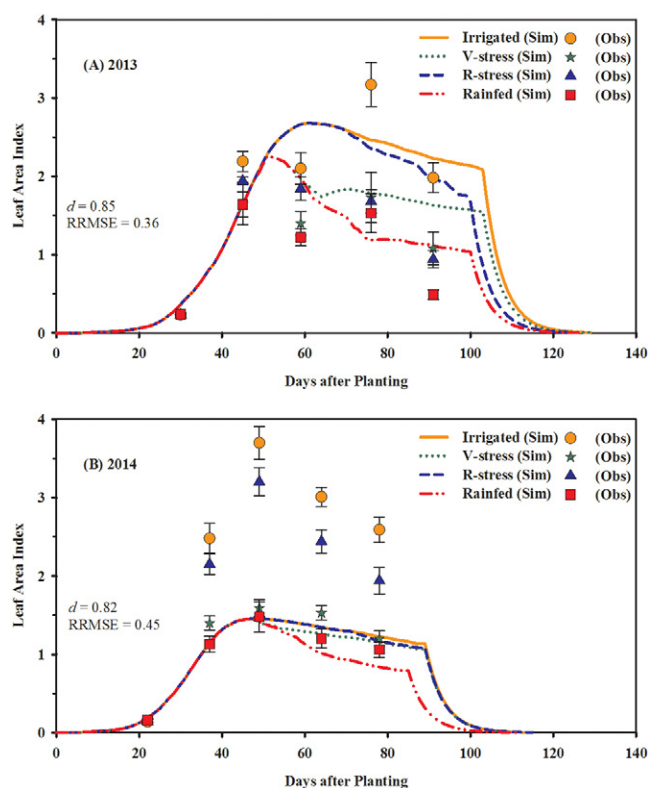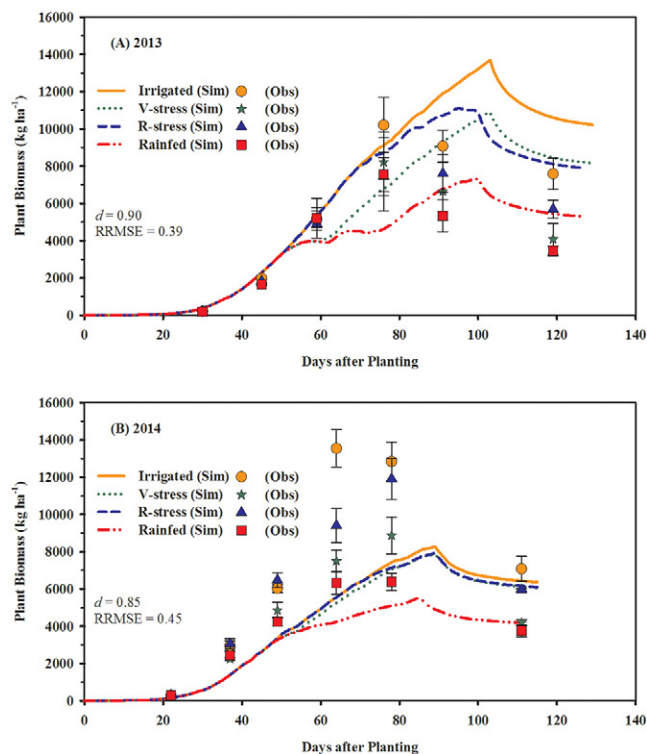

Fig. 2. A comparison of simulated (lines) and observed (symbols) leaf area index as a function of days after planting for safflower cultivar PI8311 at Clovis, NM, in (A) 2013 and (B) 2014. Statistics shown are Willmott Agreement Index (d), and relative root mean square error (RRMSE).

Fig. 3. A comparison of simulated (lines) and observed (symbols) plant biomass as a function of days after planting for safflower cultivar PI8311 at Clovis, NM, in (A) 2013 and (B) 2014. Statistics shown are Willmott Agreement Index (d), and relative root mean square error (RRMSE).

was increased in the early crop life cycle. In contrast, biomass partitioning to stem was increased in the middle of crop life cycle. With the onset of heads and seeds later in the crop life cycle, partitioning was decreased to vegetative parts. Generally, biomass samples from larger areas are more reliable (less variation) than small area samples. Hence, the magnitude of total biomass accumulation was substantially calibrated to the final harvest because sampling was done from larger land area, and less importance was given to fit the magnitude of in-season biomass. Comparison between simulated and observed aboveground plant biomass demonstrated a slight overprediction of biomass in 2013 with RRMSE of 0.39 and d-statistic of 0.90 (Fig. 3A), while an underestimation of biomass occurred in 2014 with RRMSE of 0.45 and d-statistic of 0.85 (Fig. 3B). The final simulated biomass was very close to observed value (last sample dates in Fig. 3 and Table 4). Table 4 summarizes the model predictions and RRMSEs for the crop variables measured at harvest and averaged over four treatments of the 2 yr.

Parameterizing Yield Attributes and Yield

In the CROPGRO model, heads were added after anthesis (FL-SH, time between the first flower and first head) for the duration of PODUR (time required for cultivar to reach final head load), while the number of heads carried depends on canopy assimilation (Table 2). After head addition, seeds begin growth in successive head cohorts (FL-SD, time between the first flower and first seed). There were no data available on Tb and Topt for head addition (FNPDT) and seed addition (FNSDT), hence we used default values of soybean in the
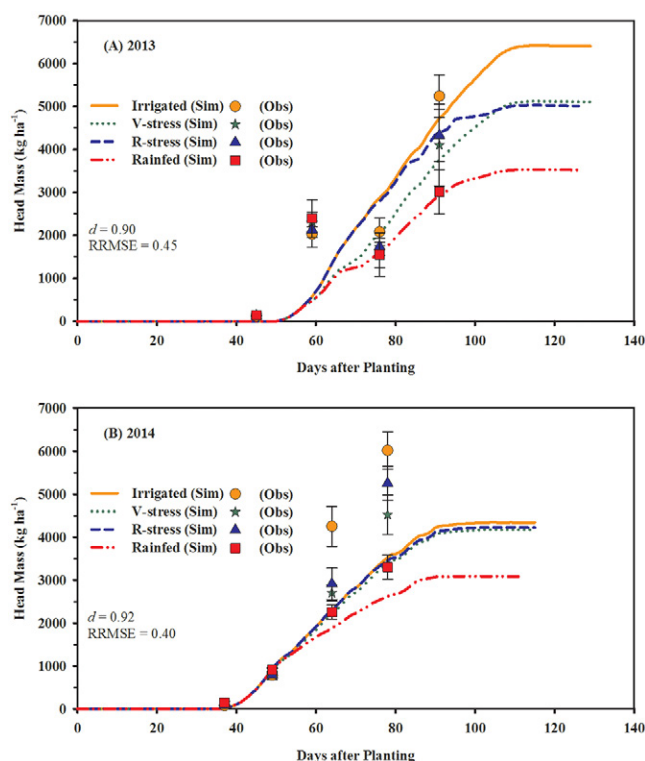
Fig. 4. A comparison of simulated (lines) and observed (symbols) head mass as a function of days after planting for safflower cultivar PI8311 at Clovis, NM, in (A) 2013 and (B) 2014. Statistics shown are Willmott Agreement Index (*d*), and relative root mean square error (RRMSE).
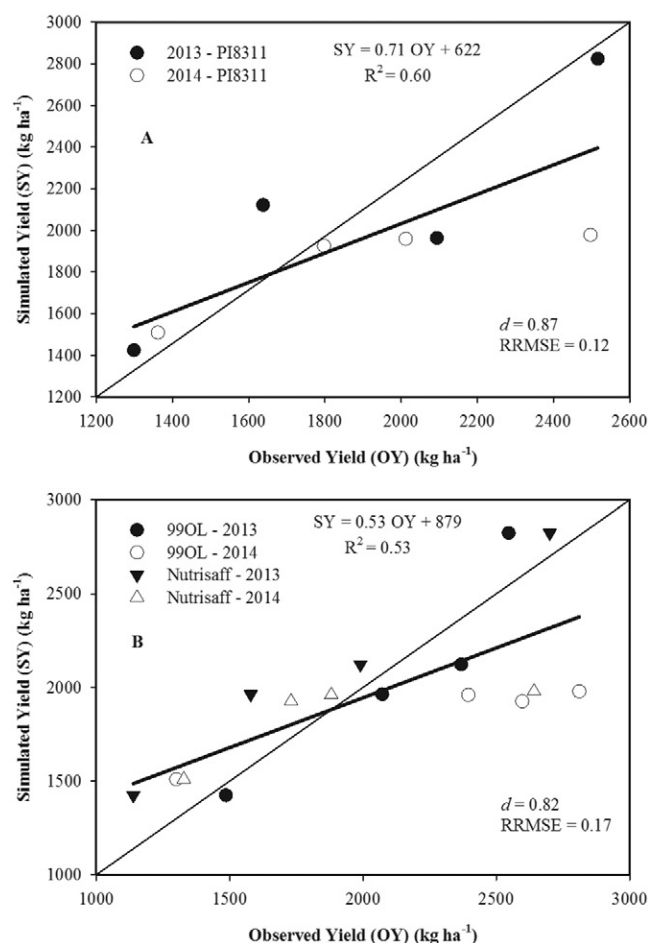
Fig. 5. A comparison of simulated vs. observed seed yield of safflower cultivar PI8311 at Clovis, NM, (A), and a comparison of simulated versus observed seed yield of safflower cultivars 99OL and Nutrisaff at Clovis, NM, (B). Statistics shown are Willmott Agreement Index (*d*), and relative root mean square error (RRMSE). The thin line represents the 1:1 line.

model. Simulated head mass for 2013 was very similar to the observed values with RRMSE of 0.45 and *d*-statistic of 0.90 (Fig. 4A), while for 2014 the model slightly underestimated head mass with RRMSE of 0.40 and *d*-statistic of 0.92 (Fig. 4B). At maturity, final head mass and head number per m^2 were closely simulated as compared to observed with RRMSE of 0.42 and 0.36, respectively (Table 4).

Final weight per seed at harvest is affected by environmental conditions and the genetic coefficient maximum weight per seed (WTPSD). Threshing percentage depends on seed divided by head wall plus seed (THRSH) and seed-filling duration (SFDUR) which is ultimately related to time from first seed to physiological maturity (SD-PM). The WTPSD, THRSH, SFDUR, and SD-PM were set in the cultivar file based on the observed data (Table 2). Similarly, maximum fraction of daily growth that is partitioned to seed plus shell (XFRT) and average seed per head (SDPDV) were calibrated in the cultivar file. The relatively low partitioning to reproductive (XFRT) compared to soybean is an indication of a degree of indeterminacy in safflower.

Seed number per m^2 and harvest index (HI) averaged over four treatments of 2 yr were well simulated by the model with RRMSE of 0.38 and 0.25, respectively (Table 4). Simulated seed yields were very consistent with the observed seed yield values with RRMSE of 0.13 in 2013 and 0.11 in 2014, and the overall *d*-statistic was 0.87 (Fig. 5A). Also, overall seed yield was very well predicted by the model with RRMSE of 0.12 (Table 4).

Model Performance

The phenology and yield of 99OL and Nutrisaff cultivars were simulated to evaluate the performance of the model with independent data. The phenology of 99OL and Nutrisaff cultivars was very well simulated by the CROPGRO-safflower model. The average simulated anthesis for both cultivars was 57 d, which was close to the average observed anthesis at 63 d with RRMSE of 0.09; similarly, the simulated harvest maturity was 120 d as compared to observed value of 117 d with RRMSE of 0.05. The simulated seed yield of the two cultivars was plotted against the observed yield (Fig. 5B). A decent relationship ($R^2 = 0.53$) between simulated and observed seed yield with RRMSE of 0.17 and *d*-statistic of 0.82 was obtained. The phenology and yield simulations, here confirmed the satisfactory performance of the model in case of cultivars that were not used in the calibration of the model.

CONCLUSIONS

The CROPGRO model for safflower was adapted to introduce a new low input crop for semiarid New Mexico. The adaption process was based on setting cardinal temperature for growth and development, entering plant tissue compositions, and optimizing cultivar traits for timing of anthesis, reproductive

partitioning and maturity. It was a bit challenging to find literature on all above aspects to adapt this model for safflower. This model can serve as a beginning platform for future researchers to integrate knowledge and to implement safflower modeling through agricultural extension for the improvement of water management strategies and food security in the region.

Overall, the CROPGRO model with modified parameters for safflower reasonably simulated crop phenology and growth variables at vegetative and reproductive stages. The CROPGRO-safflower model may be an effective tool for simulating and understanding the impact of climate change on yield of safflower when coupled with other DSSAT crop and climate models. However, this model is based on two field experiment cases and should be tested under different locations, weather conditions, planting times, and cultivars. We recognize that the model probably should be run with N balance "on" because safflower is a non-legume that depends on soil N. However, due to too much uncertainty related to soil N mineralization, and the lack of data on which to initialize NH_4 and NO_3 at planting, we turned "off" the N balance. Hence, N balance should also be explored in the later versions as we assumed no N limitation in this version. Inclusion of this model in the DSSAT will facilitate further testing of this model as future data becomes available.

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