

# Simulation of genotype-by-environment interactions on irrigated soybean yields in the U.S. Midsouth



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## ABSTRACT

Dynamic crop models that incorporate the effect of environmental variables can potentially explain yield differences associated with location, year, planting date, and cultivars with different growing cycles. Soybean (*Glycine max* (L.) Mer.) cultivar coefficients for the DSSAT-CROPGRO model were calibrated from two growing seasons (2012–2013) comprising 58 irrigated environments (site  $\times$  year  $\times$  planting date combinations) for cultivars within maturity groups (MGs) 3 to 6 using end of season data (yield, seed weight, and seed oil and protein concentration) and previously calibrated phenology coefficients. Model accuracy after calibration of cultivar coefficients by MG (cultivars averaged within a MG) was similar compared to cultivar-specific coefficients. During the subsequent growing season in 2014 (33 environments), the model efficiency (ME) for predicting yield was 0.40, with a root mean square error (RMSE) of 571 kg ha<sup>-1</sup>. The model was less efficient predicting seed number and seed weight (ME = 0.06 and -0.06, respectively) than yield. The model was able to simulate differences in seed oil concentration across environments and MGs (ME = 0.52), but not protein concentration (ME = -0.25). The analysis of yield stability had similar slopes for the observed and predicted yield regressions against an observed environmental index (EI) that were only dependent on the MG. Simulated yields were significantly different from the observed when EI > 0, but yield differences in the highest yielding environments were still relatively small (245 to 608 kg ha<sup>-1</sup>). The results indicate an overall robust model performance in capturing G  $\times$  E responses with coefficients calibrated by MG.

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## 1. Introduction

The use of crop simulation models to predict yield of irrigated soybean (*Glycine max* (L.) Mer.) across the planting window and maturity group (MG) choices available to growers can have wide applications for identifying management strategies that optimize yield, water productivity and economic returns while minimizing risks. The accurate prediction of the soybean yield response across different planting date  $\times$  MG scenarios is critical before models can be used to study different management strategies.

Planting date and the choice of soybean MGs are two of the main factors affecting yield that have been target of numerous studies (De Bruin and Pedersen, 2008; Egli and Cornelius, 2009; Salmerón et al., 2016). Under irrigated conditions in the Midsouth, optimum planting dates can range from late March to mid-May depending on the location and MG (ranging from 3 to 6) (Salmerón et al., 2016). Planting dates after the optimum are often associated with yield reductions. When planting

dates were delayed from mid-May to beginning June, yield declined from 0.09 to 1.69% per day of delay in planting (Salmerón et al., 2016). Results from the same regional project showed that MG 4 cultivars were at the top of the yield ranking at most locations for both early and late planting dates (Salmerón et al., 2014). However, yields of MG 3 and 5 cultivars can have similar or greater yields than those of MG 4 cultivars at some locations and/or planting dates (Salmerón et al., 2016). The best MG option for a given environment should consider factors other than yield such as irrigation costs, price premiums for a given harvest date, as well as price premiums related to seed oil and protein concentration (Popp et al., 2004).

Planting date affects the timing and length of main developmental stages, and as a consequence the environmental factors that affect determination of yield components during these stages (Pedersen and Lauer, 2004). For instance, the amount of radiation intercepted, canopy photosynthesis, or crop growth rate during flowering and early pod set is related to final seed number (seeds m<sup>-2</sup>) and soybean yield (Andrade et al., 2002; Egli and Yu, 1991; Jiang and Egli, 1995; Mathew et al., 2000), and can explain yield differences associated with planting date (Egli and Bruening, 2000; Egli and Yu, 1991). The choice of MG also affects the

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timing and length of developmental stages (Egli, 1993; Salmerón and Purcell, 2016). Dynamic crop models that simulate the effect of abiotic environmental factors such as temperature, solar radiation, and daylength on growth and development on a daily basis have the potential to partially explain yield differences due to year-to-year variability as well as planting date and MG interactions on yield (Calvino et al., 2003). Moreover, crop models that integrate a plant-soil-atmosphere water balance can be used to study water requirements associated with different climates and management options (Saseendran et al., 2008) and could provide estimates of water requirements for different MG and planting date combinations.

DSSAT-CROPGRO-Soybean is a dynamic crop simulation model that incorporates algorithms describing soybean development, growth and partitioning, as well as a carbon, nitrogen and water balance (Boote et al., 1998b; Hoogenboom et al., 2012; Jones et al., 2003). CROPGRO simulates seed oil and protein concentration based on a carbon and nitrogen balance, cultivar specific target protein and oil concentrations, and considers a temperature effect (Piper and Boote, 1999). The CROPGRO model has been previously used to simulate the effect of planting date on the yield of soybean (Boote et al., 1997; Calvino et al., 2003; Egli and Bruening, 1992) (the last citation with an earlier version, SOYGRO), and to study the effect of management strategies and environmental conditions on soybean productivity and irrigation requirements (Peart et al., 1995). However, the model has not been previously tested for its accuracy predicting seed oil and protein concentration across different environments.

CROPGRO-Soybean requires calibration of 18 cultivar-specific variables usually referred to as “cultivar coefficients” that are related to cultivar differences in sensitivity to photoperiod and temperature for development, growth, partitioning, as well as target oil and protein concentrations (see more details in Boote et al., 1998b). Calibration of cultivar coefficients for new cultivars in CROPGRO requires experimental data across several environments, detailed measurements during the growing season for biomass, leaf area and/or yield, and a stepwise optimization procedure to estimate coefficients (see example for pigeonpea in Alderman et al., 2015). The need of calibration of cultivar coefficients for new cultivars can limit the use of complex crop models. As a result, there is increasing interest in models that perform well with a limited number of input coefficients (Setiyono et al., 2007 and 2010) and in approaches that allow calibration with phenology and end of season data (Archontoulis et al., 2014; Irmak et al., 2000; Mavromatis et al., 2001). Cultivar coefficients calibrated from typical information from soybean performance trials enabled CROPGRO to reproduce the observed yield ranking and much of the genotype  $\times$  environment ( $G \times E$ ) interactions (Mavromatis et al., 2001). Predictions of developmental stages with cultivar coefficients derived from soybean relative MG and plant growth habit provided similar accuracy to those with cultivar specific coefficients (Salmerón and Purcell, 2016). The aim of this study was: (i) to test the accuracy of DSSAT-CROPGRO for predicting yield, yield components and seed oil and protein concentration using generic cultivar coefficients based upon MG and calibrated for the conditions in the

Midsouth, and (ii) evaluate the model applicability for reproducing observed  $G \times E$  interactions.

## 2. Material and methods

### 2.1. Experimental data from multi-location field experiments

Multi-location field experiments were conducted across the Midsouth at seven locations in 2012 and nine locations in 2013 and 2014 (Table 1). The experimental design was a split-plot, with planting date as the whole plot factor, MG as the second factor (3, 4, 5 and 6), and four cultivars nested within each MG. At each location there were four planting dates every year that ranged from 21 March to 17 July across the whole study, with the exception of Fayetteville that had one single planting date (Table 1). A total of 16 commercial cultivars were used each year (four within each MG), with some of them being replaced by a cultivar within the same MG from one year to another (Table 2). All MG 3 and 4 cultivars exhibited an indeterminate growth type habit, and MG 5 and 6 cultivars exhibited a determinate one (except for an indeterminate MG 5 cultivar, AG5332). The row spacing and soil textural class at each location are summarized in Table 1. The plot size was 6 m long with four single or twin rows. Seeding rate was 35 seeds  $m^{-2}$ . All experiments were furrow or sprinkler irrigated according to the net evapotranspiration demand, calculated with a daily balance of crop evapotranspiration, precipitation, and irrigation (Purcell et al., 2007). Weather data (daily minimum and maximum temperature and precipitation) were obtained from nearby weather stations. Solar radiation was estimated from latitude, altitude, day of year, and daily temperatures using WeatherMan in DSSAT. The two central rows of each plot were harvested (4.9 to 6 m) and grain moisture was measured. Yield and weight of 100 seeds were expressed on a dry weight basis for model comparisons. Ratings of sudden death syndrome (binomial) and stem canker (binomial) were taken when disease incidence was present at specific environments, and were used to remove plots with a biotic stress from the dataset. Similarly, MG 6 cultivars planted late in the most southern locations were removed from the dataset when there was severe insect and fungal disease incidence. Oil and protein concentrations from harvested seed subsamples were analyzed using near-infrared spectroscopy (Foss Instruments, model 1241, Eden Prairie, MN).

Experimental yield data were analyzed with PROC GLM (SAS, v.9.2, SAS Institute, Inc., Cary, N.C.), where year, location, planting dates, MG, cultivars (nested within MG and year), and their interactions were considered as fixed effects. Blocks were grouped in two sets that shared the same planting date and MG treatments to simplify harvest. Set and block (nested within set) and their interactions with the fixed effects were considered as random effects. The sum of squares from the analysis of variance was grouped by sources of variation related to environment (year, location, planting date and their interactions), MG and its interactions with environmental sources of variation, and cultivars within MG and year (cultivar (MG\*year)) and its interactions with

**Table 1**  
Locations, latitudes, range of planting dates, soil type, row spacing, and soil type.

Location	Lat (°N)	2012	2013	2014	Row sp. (cm)	Soil series
Columbia, MO	38.9	–	4/22–6/25	4/23–6/27	76	Mexico silt loam
Portageville, MO	36.4	4/2–6/12	4/9–6/20	4/22–6/17	76	Tiptonville silt loam
Fayetteville, AR	36.1	6/7	6/8	6/17	48	Captina silt loam
Milan, TN	35.9	–	4/22–6/25	4/24–7/3	76	Routon silt loam
Keiser, AR	35.7	3/30–6/8	6/13–7/17	4/23–6/5	19 twins on 97	Sharkey silty clay
Verona, MS	34.2	3/21–6/7	4/23–6/17	4/23–6/17	20 twins on 97	Leeper silty clay loam
Rohwer, AR	33.8	3/29–6/26	4/26–6/28	4/21–6/30	48 and 19 twins on 97	Hebert silt loam
St. Joseph, LA	32.0	4/6–6/1	4/29–6/12	4/24–6/19	51	Sharkey clay
College St, TX	30.6	3/26–5/25	4/9–5/30	4/9–6/2	38	Westwood clay loam

**Table 2**

Soybean cultivars used within each maturity group (MG) for each growing season and relative maturity group (rMG) provided by the seed companies.

MG	2012		2013		2014	
	Cultivar	rMG	Cultivar	rMG	Cultivar	rMG
III	5N342R2	3.4	5N342R2	3.4	5N342R2	3.4
	RT 3644	3.6	R2 36X82N	3.6	R2 36X82N	3.6
	P93Y72	3.7	P93Y72	3.7	P39T67R	3.9
IV	P93Y92	3.9	P93Y92	3.9	P93Y92	3.9
	42-M1	4.2	42-M1	4.2	42-M1	4.2
	P94Y40	4.4	P94Y40	4.4	P46T21r	4.6
V	AG4732	4.7	AG4732	4.7	AG4730	4.7
	REV49R11	4.9	REV48R33	4.8	REV48R33	4.8
	AG5332	5.3	AG5332	5.3	AG5332	5.3
VI	AG5532	5.5	AG5532	5.5	AG5532	5.5
	P95Y50	5.5	P95Y50	5.5	P54T94R	5.4
	P5811RY	5.8	P5711RY	5.7	P5711RY	5.7
VI	6202-4	6.2	6202-4	6.2	AG6534	6.5
	P96M60	6.6	AG6132	6.1	AG6132	6.1
	AG6732	6.7	AG6732	6.7	AG6730	6.7
	HBKR7028	7.0	P6710RY	6.7	P6710RY	6.7

environment. The percentage of sum of squares in the model explained by each group of sources of variation was calculated by dividing the total sum of squares in the model and multiplying by 100.

## 2.2. Calibration of growth cultivar coefficients

The DSSAT model v. 4.5.1.023 was used for this study. A detailed description of the processes in CROPGRO is provided in [Boote et al. \(1998b\)](#). DSSAT-CROPGRO has a total of 18 cultivar coefficients related to growth, photosynthesis, and partitioning that usually require calibration at the cultivar level ([Table 3](#)). Cultivar coefficients related to phenology (CSDL, PPSEN, R1PPO, EM-FL, FL-SH, FL-SD, SD-PM) were previously calibrated and evaluated for the same genotypes and environments ([Salmerón and Purcell, 2016](#)), or estimated from previous research ([Grimm et al., 1994](#); [Grimm et al., 1993](#); [Piper et al., 1996](#)). The estimation of phenology coefficients based on rMG and plant growth habit provided similar accuracy to cultivar specific calibrations ([Salmerón and Purcell, 2016](#)), so cultivar coefficients related to phenology were estimated using the same approach in this study ([Table 3](#)). For the calibration of the remaining 12 cultivar coefficients, end-of-season data from 2012 and 2013 across all locations and treatments ( $n = 25$  to 58 for each

cultivar) were used. The experimental data used for calibration included: harvest yield ( $\text{kg ha}^{-1}$  in dry weight), unit seed weight (g per unit seed), and oil and protein concentration in seed. Protein concentration was converted to nitrogen concentration by dividing by a conversion factor of 5.64 ([Mariotti et al., 2008](#)).

The Generalized Likelihood Uncertainty Analysis (GLUE) optimization tool included in DSSAT ([He et al., 2009](#)) was used to estimate coefficients that minimize the error in the prediction of the observed end-of-season data across all environments. The calibration of oil and protein coefficients (SDLIP and SDPRO) was implemented outside of the GLUE interface but following the same methodology described in [Beven and Binley \(1992\)](#). Given the large number of growth coefficients to calibrate ( $n = 12$ , [Table 3](#)), the number of randomized sets of cultivar coefficients that could be generated was very large (for 5 randomized values within each coefficient there would be a total of  $5^{12}$  or >244 million possible combinations). Therefore, the chance of obtaining a set of coefficients with physiological relevance that minimized prediction error would be very low if a large number of coefficients were optimized simultaneously. For this reason, we used a sequential approach to calibrate the complete set of cultivar coefficients related to growth ( $n = 12$ , [Table 3](#)) with data availability limited to yield, seed growth, and oil and protein concentration ([Table 4](#)). The sequential calibration was comprised of eight steps, where only up to three coefficients were calibrated at a time ([Table 4](#)). The whole sequential calibration was repeated a second time. Initial values for the coefficients at the beginning of the calibration procedure were based on MG ([Boote et al., 2001](#)). The upper and lower limits allowed for each cultivar coefficient were set based upon values from [Boote et al. \(2001\)](#) ([Table 4](#)). One exception was the maximum seed weight (WTPSD) in which the lower limit was reduced from 0.15 to 0.13  $\text{g seed}^{-1}$  in Step 8, and for Step 6 and 8 in the second calibration. The number of simulations within each step (number of randomized sets of coefficients) was increased with the number of coefficients being optimized and ranged from 100 to 20,000 simulations ([Table 4](#)).

In addition to the sequential calibration approach, a simultaneous calibration of all the coefficients (except for the ones related to oil and protein concentration) was conducted to test if the sequential calibration was more efficient in reducing error in model predictions. The simultaneous calibration was conducted using GLUE to generate 200,000 sets of cultivar coefficients. Thereafter, steps 7 and 8 in the sequential calibration ([Table 4](#)) were followed to calibrate the coefficients affecting oil and protein and to allow a reduction in the lower limit of weight per seed (WTPSD) as in the sequential calibration approach. Calibrations were

**Table 3**

Calibrated generic growth coefficients by MG with data from 2012 and 2013.

Cultivar coefficients	Definition and units	Calibrated coefficients by MG			
		3	4	5	6
CSDL <sup>a</sup>	Critical short day length below which reproductive development progresses with no daylength effect (h)	13.40	13.10	12.75	12.45
PPSEN <sup>b</sup>	Slope of the relative response of development to photoperiod with time (1/h)	0.285	0.294	0.302	0.311
R1PPO <sup>b</sup>	Increase in daylength sensitivity after anthesis, CSDL decreases by this amount (h)	0.324	0.369	0.414	0.459
EM-FL <sup>a</sup>	Time between plant emergence and flower appearance (R1) (photothermal days)	17.5	17.5	21	21
FL-SH	Time between first flower and first pod (R3) (photothermal days)	6.2	7.3	7.6	8.6
FL-SD <sup>a</sup>	Time between first flower and first seed (R5) (photothermal days)	14.2	14.2	11.6	11.6
SD-PM <sup>a</sup>	Time between first seed (R5) and physiological maturity (R7) (photothermal days)	34.4	35.4	32.8	32.8
FL-LF	Time between first flower (R1) and end of leaf expansion (photothermal days)	26.0	19.2	15.0	15.2
LFMAX	Maximum leaf photosynthesis rate at 30°C, 350 $\text{vpm CO}_2$ , and high light ( $\text{mg CO}_2/\text{m}^2\text{-s}$ )	1.02	0.94	0.92	0.92
SLAVR	Specific leaf area of cultivar under standard growth conditions ( $\text{cm}^2/\text{g}$ )	368.0	359.0	359.8	395.3
SIZLF	Maximum size of full leaf (three leaflets) ( $\text{cm}^2$ )	152.2	199.3	168.2	187.9
XFRT	Maximum fraction of daily growth that is partitioned to seed + shell	0.95	1.00	1.00	0.90
WTPSD	Maximum weight per seed (g)	0.154	0.158	0.130	0.130
SFDUR	Seed filling duration for pod cohort at standard growth conditions (photothermal days)	19.0	23.9	23.6	23.0
SDPDV	Average seed per pod under standard growing conditions (seeds/pod)	2.28	2.10	2.25	2.36
PODUR	Time required for cultivar to reach final pod load under optimal conditions (photothermal days)	11.84	13.55	10.76	7.52
THRSH	The maximum percent ratio of seed/(seed + shell) at maturity causing seeds to stop growing when shells are filled	76.2	76.0	76.0	76.0
SDPRO	Fraction protein in seeds ( $\text{g}(\text{protein})/\text{g}(\text{seed})$ )	0.386	0.391	0.395	0.385
SDLIP	Fraction oil in seeds ( $\text{g}(\text{oil})/\text{g}(\text{seed})$ )	0.199	0.198	0.195	0.199

<sup>a</sup> Estimated according to [Salmerón and Purcell \(2016\)](#).

<sup>b</sup> Coefficients solved by [Grimm et al. \(1993, 1994\)](#) and [Piper et al. \(1996\)](#).

**Table 4**  
Steps followed for the sequential calibration of DSSAT-CROPGRO-Soybean.

Seq. #	Model coefficients			Target observed data	# of model runs
	Name	Type†	Range of variation allowed		
1	FL-LF	CL	15–26	Yield	15,000
	SIZLF	CL	140–200		
2	LFMAX	CL	0.92–1.17	Yield	15,000
	SLAVR	CL	355–400		
3	XFRT	CL	0.9–1	Yield	100
4	SLPF	Soil	0.78–1.00	Yield	manual
5	THRSH	CL	76–79	Yield	15,000
	SDPDV	CL	1.9–2.5		
6	SFDUR	CL	18–27	Grain unit mass Yield	20,000
	PODUR	CL	6–14		
7	WTPSD	CL	0.15–0.22	% of oil in seeds	500
	SDLIP	CL	0.17–22		
8	SDPRO	CL	0.35–0.45	% of protein in seeds	20,000
	SFDUR	CL	18–27	Grain unit mass	
	PODUR	CL	6–14	Yield	
	WTPSD	CL	0.13–0.22		

†CL: coefficient in cultivar file; SP: coefficient in species file; EC: Coefficient in ecotype file; Soil: coefficient in soil file.

performed for each cultivar in the 2012 and 2013 growing season (total of 21 different cultivars), and for observed data averaged across cultivars within each MG from 3 to 6 (total of 4 “cultivars” in this case).

Preliminary calibrations indicated a significant overprediction of yields of MG 6 cultivars. Calibrations after increasing leaf senescence of old leaves by increasing sensitivity to low irradiation (modification of ICMP and TCMP in the species file) improved yield predictions across all MG cultivars. Therefore, the calibration procedures mentioned above were performed with default model settings and with settings for increased leaf senescence (ICMP = 3.5, TCMP = 6 days).

The computation hardware at Arkansas High Performance Computer Center (AHPCC) was used for performing parallel-wise DSSAT-GLUE runs for each cultivar and MG average, for both calibration approaches (sequential or simultaneous), and for the model with default and increased leaf senescence (total of 100 simulations).

### 2.3. Estimation of soil parameters

Soil samples from all locations at different horizons were taken for particle size analysis and estimates of percent clay, silt, and sand. The soil parameters for the model related to water holding capacity, saturated hydraulic conductivity, bulk density and a root growth factor were estimated with the SoilBuild tool in DSSAT based on the particle size analysis. Given that these experiments were irrigated, water limitations were considered to be minimal. The soil photosynthesis factor (SLPF) was estimated at each location and across all cultivars as part of the sequential calibration (Table 4). Calibrated values of SLPF by location were 1 for Columbia, Fayetteville, and St. Joseph, 0.98 for Rohwer, 0.95 for Keiser, 0.93 for Milan, 0.89 for Verona, and 0.86 for Portageville and College Station.

### 2.4. Statistics for model evaluation

Statistics for evaluation of model performance were calculated for observed data averaged across repetitions only, and therefore allowing differences associated with cultivars within a MG. The root mean square error (RMSE) was calculated across all MGs and environments for each variable analyzed (yield, seed number, seed weight, seed oil and protein concentration) and also calculated across environments for each MG separately (Eq. (1))

$$RMSE = \sqrt{\frac{\sum_{t=1}^N (o_t - p_t)^2}{N}} \quad (1)$$

Where  $o_t$  is the observed variable for treatment  $t$  (cultivar (MG)  $\times$  environment combination),  $p_t$  is the predicted variable for the same treatment  $t$ , and  $N$  is the number of observations. In some cases results were expressed as a normalized root mean square error (NRMSE) by dividing by the observed average and expressing the value as a percentage.

Similarly, the model efficiency (ME) was calculated across all environments and MGs, and for each MG separately (Eq. (2)).

$$ME = 1 - \frac{\sum_{t=1}^N (o_t - p_t)^2}{\sum_{t=1}^N (o_t - \hat{o})^2} \quad (2)$$

Where  $\hat{o}$  is the average yield across environments. Therefore, positive values of ME indicate that the model is a better predictor than the average across environments.

The different calibration of growth cultivar coefficients (a sequential or simultaneous approach with either default or increased settings for leaf senescence) were compared in their ability to minimize the NRMSE in the prediction of yield for each MG and maximize values of ME. Thereafter, the calibration that showed more accuracy in yield prediction across all MG cultivars was used to further investigate the model accuracy in prediction of all the end of season data collected for both the calibration dataset (2012 and 2013) and for the validation dataset (2014).

### 2.5. Stability analysis of the genotype $\times$ environment interaction

To evaluate the model accuracy in simulating the observed  $G \times E$  interaction, a stability analysis of the yield of each genotype across environments in 2014 was conducted. Data from the two previous growing seasons were not included in this analysis since the data were used for calibration of cultivar coefficients. Simulated yields in 2014 were obtained with coefficients calibrated by MG with the sequential approach and the model setting with increased leaf senescence. Each location and planting date combination was considered as a separate environment. Only environments containing all MGs were considered in the analysis (total of 31 environments after removing planting dates 3 and 4 from College Station due to biotic stresses). An environmental index (EI) value was calculated for each environment as the mean observed yield for that environment minus the grand mean across all cultivars and environments. Predicted and observed yields were then fit to a straight-line regression model with the EI as the independent variable. An analysis of covariance was conducted using the MIXED procedure (SAS v.9.2., SAS Institute, Inc., Cary, N.C.) where the slopes and intercepts were allowed to vary depending on the MG and the source of the data (observed or simulated). The analysis determined whether or not the MG and the data source had a significant effect on the intercept and slope of the regressions.

## 3. Results

### 3.1. Experimental conditions and observed yields

The ANOVA of the observed yield showed that the sources of variation related to environment (year, location, planting date, and their interactions) explained 47.4% of the variation in the total sum of squares. The sources of variation related to the choice of MG alone comprised 9.5% of the total sum of squares, whereas the choice of cultivar (nested within MG and year) comprised 1.9%. The sum of squares for the interaction of MG with sources of variation related to environment comprised 19.0% of the total sum of squares in the model. Finally, the interaction of cultivar (nested within MG and year) with other sources of variation related to environment comprised 9.7% of the total sum of squares in the model.



### 3.2. Calibration of growth coefficients

Different approaches for calibration of growth cultivar coefficients were compared for their accuracy to predict yield of MG 3 to 6 cultivars across all year  $\times$  location  $\times$  planting date combinations in 2012 and 2013 (Fig. 1). Cultivar coefficients related to phenology were previously estimated by MG or rMG and plant growth habit (Salmerón et al., 2016) (Table 3) and were used for all the calibrations tested in this study. Positive values of ME in Fig. 1 indicate that the model was a better predictor of yield for a given MG across location  $\times$  planting dates compared to using the average yield of the MG across environments. Results prior to calibration of growth coefficients (with generic cultivar coefficients in DSSAT v. 4.5.1.023) showed that the model was already efficient predicting yields for MGs 3 and 4 (ME = 0.51 and 0.47, respectively), but was less accurate predicting yields of MGs 5 and 6 across environments (ME = 0.03 and  $-1.10$ , respectively) (Fig. 1). After calibration of growth coefficients by MG and with default settings for model senescence, ME of MG 3 remained similar compared to using default generic coefficients in DSSAT for both the simultaneous (ME = 0.51) and the sequential calibration (ME = 0.57). Model efficiency for yield of MG 4 cultivars calibrated with default model settings for senescence was 0.66 for both the simultaneous and the sequential calibration, and thus improved compared to using default model settings (ME = 0.47). The model accuracy for yield prediction of MG 5 cultivars improved substantially after calibration (0.55 and 0.52 for the simultaneous and sequential calibration) compared to using default coefficients (ME = 0.03). Finally, yield predictions of MG 6 cultivars were improved after a simultaneous calibration (ME = 0.07), and to a greater extent with the sequential calibration approach (ME = 0.32).

Interestingly, modifying the model settings to increase leaf senescence under conditions of low irradiance greatly improved yield predictions across all MG cultivars when using default coefficients in DSSAT (ME = 0.57, 0.48, 0.53, 0.35 for MG 3, 4, 5 and 6, respectively) (Fig. 1). Calibrations after changing the model settings for increased leaf senescence also improved ME in yield prediction with both the simultaneous and the sequential calibration compared to using default model settings, with the exception of MG 4 cultivars where ME was already relatively high. Overall, a sequential calibration and model settings for increased leaf senescence were the approaches most likely to improve yield predictions across all MGs. Therefore, the cultivar coefficients calibrated by MG for the abovementioned settings (coefficients are provided in Table 3) were used to further evaluate the model accuracy in simulating the experimental end of season data and the observed  $G \times E$  interaction for the subsequent growing season. Comparison of ME in yield prediction during 2014 with default coefficient and with different calibration

approaches further confirmed that the sequential calibration under settings for increased senescence was the most consistent in maximizing ME across all MGs (Fig. 1).

Cultivar-specific calibrations were also conducted for all the genotypes in 2012 and 2013 (total of 21 different cultivars, Table 2) and calibration types (sequential vs. simultaneous, and with default and increased senescence) to compare model accuracy with cultivar coefficients estimated by MG (data not shown). The ME results from the cultivar-specific calibrations with default settings for leaf senescence were similar for the simultaneous and sequential calibration (ME averaged 0.57, 0.65, 0.44, and 0.33 for MG 3, 4, 5, and 6, respectively). Calibration of cultivar-specific coefficients under settings of increased senescence improved ME across MGs with a simultaneous calibration (ME = 0.62, 0.65, 0.54, and 0.36 for MG 3, 4, 5, and 6, respectively) and to a greater extent with a sequential calibration (ME = 0.64, 0.65, 0.58, and 0.54 for MG 3, 4, 5, and 6, respectively). Therefore, model accuracy was not substantially improved when using cultivar-specific coefficients compared to calibrations with cultivars averaged by MG (ME = 0.60, 0.64, 0.59, and 0.34 for MG 3, 4, 5, and 6, respectively). The analysis of the relationship between the calibrated cultivar-specific coefficients and the rMG provided by the seed companies (Table 2) indicated a decrease in maximum seed size (WTSP) with later maturities ( $R^2 = 0.58$ ,  $P < 0.001$ ), as well as a decrease in the time to reach final pod load (PODUR,  $R^2 = 0.32$ ,  $P < 0.001$ ). On the other hand, the rest of calibrated cultivar coefficients did not show a significant relationship with rMG (data not shown).

### 3.3. Prediction of yield components and oil and protein concentrations

Results for the model evaluation in the prediction of end-of-season data for the calibration dataset (2012–2013) and for the validation dataset (2014) are presented in Table 5. Observed yields ranged from 1333 to 5527 kg ha $^{-1}$  across all environments and MGs in 2012–2013 and from 1677 to 4893 kg ha $^{-1}$  in 2014. After calibration of cultivar coefficients by MG, the model was efficient in predicting yield for all MGs across planting dates and locations in 2012 and 2013 (ME = 0.34 to 0.64) with a low average bias (between  $-141$  and  $-28$  kg ha $^{-1}$ ) and a RMSE ranging from 509 to 570 kg ha $^{-1}$ . In 2014, the model was efficient predicting yields of MG 3, 4, and 6 cultivars (ME = 0.44, 0.55 and 0.29, respectively). However, the negative values of ME for the MG 5 cultivars in 2014 (ME =  $-0.26$ ) indicate that the model was less accurate in predicting yield of MG 5 cultivars across locations and planting dates than using the average yield of MG 5 cultivars across environments. The bias (predicted – observed) shows that the low efficiency in MG 5 cultivars in 2014 was due to a tendency to overpredict

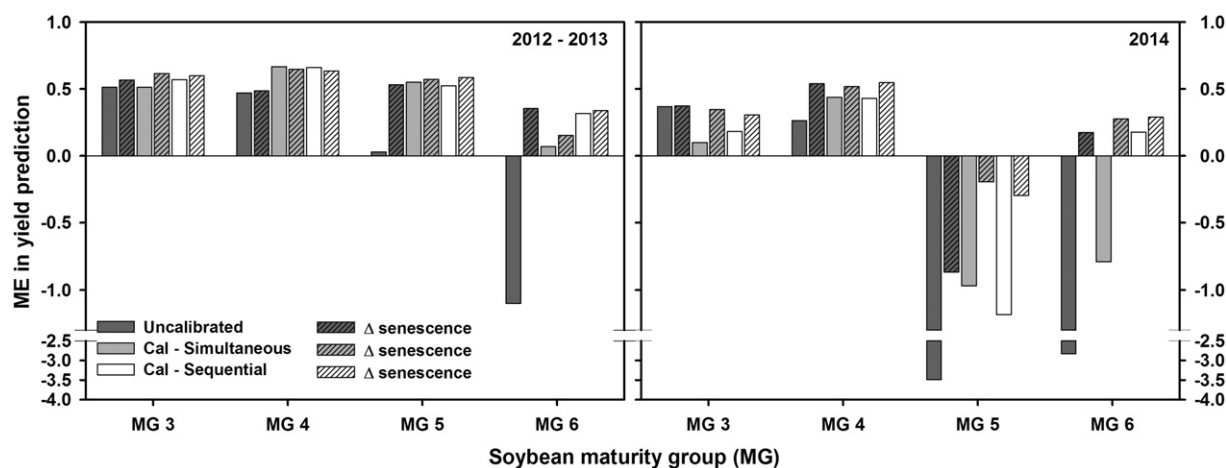


Fig. 1. Model efficiency (ME) in the prediction of soybean yield by MG (maturity group) during the growing seasons used for calibration (2012–2013) and in the following growing season (2014). Model simulations were conducted with uncalibrated cultivar coefficients (default coefficients by MG in DSSAT v. 4.5.1.023) and after a simultaneous or sequential calibration of cultivar coefficients. Results after a modification to increase senescence under low irradiance ( $\Delta$  senescence) and with default model settings are presented.

**Table 5**

Model evaluation in the prediction of grain yield ( $\text{kg ha}^{-1}$ ), seed number ( $\text{seeds m}^{-2}$ ), seed weight ( $\text{g seed}^{-1}$ ), and oil and protein concentration (%) during the calibration (2012–2013) and for an independent growing season (2014). The following statistics were calculated by comparing observed and predicted data for each cultivar and summarized by MG: bias (predicted – observed), model efficiency (ME), and root mean square error (RMSE). Simulations were performed with Cultivar coefficients calibrated by MG (Table 3). Additionally, the RMSE of model predictions with cultivar specific coefficients (RMSE<sub>CUL</sub>) is provided for the calibration dataset.

MG	2012–2013 (calibration dataset)					2014 (evaluation dataset)			
	Obs	Bias	ME	RMSE	RMSE <sub>CUL</sub>	Obs	Bias	ME	RMSE
<i>Grain yield (<math>\text{kg ha}^{-1}</math>)</i>									
3	3381	–119	0.60	552	522	3633	–196	0.44	514
4	3546	–94	0.64	514	505	3762	–52	0.55	494
5	3461	–28	0.59	509	513	3260	345	–0.26	644
6	3170	–141	0.34	570	476	2831	273	0.29	627
All	3409	–64	0.58	534	507	3394	83	0.40	571
<i>Seed number (<math>\text{seeds m}^{-2}</math>)</i>									
3	2243	–118	0.40	426	433	2465	–212	0.24	417
4	2466	–77	0.44	420	441	2666	–135	0.28	434
5	2636	7	0.52	365	417	2551	179	–0.25	481
6	2384	–81	0.07	498	389	2355	–54	–0.48	544
All	2436	–46	0.43	424	424	2515	–58	0.06	468
<i>Seed weight (<math>\text{g seed}^{-1}</math>)</i>									
3	0.151	–0.002	0.21	0.016	0.015	0.148	0.004	–0.23	0.016
4	0.144	–0.002	0.16	0.016	0.017	0.141	0.006	–0.59	0.015
5	0.129	–0.002	–0.05	0.016	0.016	0.128	0.004	–0.39	0.016
6	0.130	0.001	–0.51	0.018	0.016	0.121	0.015	–2.81	0.021
All	0.139	–0.002	0.29	0.016	0.016	0.135	0.007	–0.06	0.02
<i>Oil concentration in seed (%)</i>									
3	20.1	–0.02	0.23	0.71	0.59	20.2	–0.26	0.15	0.95
4	20.0	–0.19	0.14	0.59	0.47	19.9	–0.36	0.29	0.63
5	19.3	0.01	0.32	0.58	0.58	19.0	0.00	0.48	0.60
6	19.1	–0.05	–0.23	0.96	0.81	18.6	–0.11	0.28	0.91
All	19.6	–0.06	0.36	0.70	0.61	19.5	–0.19	0.52	0.78
<i>Protein concentration in seed (%)</i>									
3	35.2	–0.33	–0.58	1.62	1.62	34.6	–0.15	–0.22	1.54
4	35.2	0.28	–0.30	1.29	1.31	34.9	0.55	–0.19	1.00
5	35.4	0.37	–0.75	1.50	1.41	35.2	0.34	–0.41	1.21
6	35.7	–0.14	–0.54	1.41	1.16	35.3	–0.01	–0.65	1.34
All	35.4	0.06	–0.53	1.46	1.40	35.0	0.19	–0.25	1.29

yield ( $345 \text{ kg ha}^{-1}$  higher on average). Yields of MG 6 cultivars in 2014 were also overpredicted on average (bias =  $273 \text{ kg ha}^{-1}$ ), whereas yields of MG 3 and 4 cultivars were underpredicted (bias of  $-196$  and  $-52 \text{ kg ha}^{-1}$ , respectively).

The potential to minimize prediction errors with cultivar specific calibrations was quantified with RMSE<sub>CUL</sub> in 2012 and 2013. Model prediction with calibration of cultivar-specific coefficients slightly reduced the overall RMSE to  $507 \text{ kg ha}^{-1}$  compared to using coefficients calibrated by MG (RMSE =  $534 \text{ kg ha}^{-1}$ ). The most significant improvement in model predictions with cultivar-specific coefficients was for MG 6 cultivars ( $476 \text{ kg ha}^{-1}$  compared with  $570 \text{ kg ha}^{-1}$  with coefficients calibrated by MG). Further testing of model predictions with an independent group of genotypes would help further investigate the applicability of using generic coefficients based on MG rather than cultivar-specific coefficients.

Observed values for seed number ranged from 897 to  $3958 \text{ seeds m}^{-2}$  across all environments and MGs for the calibration dataset, and from 1189 to  $3517 \text{ seeds m}^{-2}$  in 2014. Observed seed number were on average greater for MGs 4 and 5 compared to MGs 3 and 6 in both the calibration and evaluation datasets (Table 5). For the 2012 and 2013 data, the model was more efficient predicting seed number of MGs 3 to 5 (ME = 0.40 to 0.52) compared to MG 6 (ME = 0.07). The overall RMSE in prediction of seed number in 2012 and 2013 was  $424 \text{ seeds m}^{-2}$  and did not improve when using cultivar-specific coefficients (RMSE<sub>CUL</sub> =  $424 \text{ seeds m}^{-2}$ ). For the evaluation dataset, the model showed a lower efficiency in general (ME = 0.06), in particular for MG 5 and 6 cultivars

(ME < 0). The RMSE in the prediction of seed number in 2014 ranged from 417 to  $544 \text{ seeds m}^{-2}$ , with the error being greater for the later maturities. On average, the model underpredicted seed number for MG 3, 4, and 6 cultivars, and overpredicted seed number of MG 5 cultivars in 2014.

Observed seed weight ranged from 0.08 to  $0.18 \text{ g seed}^{-1}$  for the calibration dataset (2012–13), and from 0.10 to  $0.17 \text{ g seed}^{-1}$  for the validation dataset. After calibration, the model was efficient predicting seed weight of MG 3 and 4 cultivars (ME > 0.16), but not for MG 5 and 6 cultivars (ME < 0) (Table 5). Overall, the model was efficient predicting seed weight across MGs and environments in 2012–2013 (ME = 0.29). However, in 2014, the model showed low efficiency in general (ME =  $-0.06$  across MGs) and within each MG (ME =  $-0.23$  to  $-2.81$ ). The RMSE in the prediction of seed weight normalized with the observed averages was 11.5% across MGs in 2012–2013, and 14.8% in 2014. Error in prediction of seed weight was therefore lower relative to prediction of yield (15.7 and 16.8% for 2012–2013 and 2014, respectively) and seed number (17.4 and 18.6%). Overall, the model was more efficient in the prediction of yield compared to prediction of seed number and seed weight.

Seed oil concentration for the calibration dataset ranged from 17.5 to 21.7%, and from 15.9 to 21.8% for the validation dataset. The concentration of oil in seeds was predicted with accuracy across MGs and environments in 2012–2013 (ME = 0.36) and for the evaluation dataset in 2014 (ME = 0.52) (Table 5). The NRMSE in prediction of seed oil concentration was low in general, averaging 3.6 and 4.0% in 2012–2013 and in 2014, respectively. Simulations with cultivar-specific coefficients in 2012–2013 only had a small improvement in prediction of seed oil concentration (NRMSE = 3.1%).

Seed protein concentration ranged from 32.2 to 37.5% in 2012–2013 and from 31.2 to 36.4 in 2014. The model was not efficient in the prediction of seed protein concentration, with negative values for ME in all cases (Table 5). However, the NRMSE was low in general, averaging 4.1 and 3.7% in 2012–2013 and in 2014, respectively. Calibrations with cultivar-specific coefficients had a small impact in the model accuracy during 2012–2013 (NRMSE = 4.0%).

### 3.4. Prediction of the $G \times E$ interaction with an independent dataset

The analysis of the yield response to an environmental index (EI) allowed a comparison of the observed and the predicted yield response of each MG across environments ( $n = 31$ ) during the 2014 growing season. The covariance model explained 74% of the yield variability after removing non-significant effects. The interaction of EI with MG and data source (observed vs. predicted) was left in the model to allow different slopes in the regression of yield with the EI for observed and predicted data. The analysis of covariance indicated that the MG choice had a significant effect on both the intercept and the slope of the regressions (Table 6). On the other hand, the source of the yield data (observed vs. predicted) only had a significant effect depending on the MG in the intercept of the regressions, and no significant effect on the slopes (Table 6). The regressions of the observed and predicted yield versus EI by MG are provided in Fig. 2.

The analysis of lsmeans at different values of the EI was used to test differences between observed and predicted yields within each MG (Fig. 2). For environments lower yielding than the average (EI <  $0 \text{ kg ha}^{-1}$ ), predicted yields were similar to observed yields for MGs 3 to 5 (Fig. 2). For MG 6, only in very low yielding environments (EI =  $-600 \text{ kg ha}^{-1}$ ) were predicted yields similar to the observed. For average to high yielding environments (EI >  $0 \text{ kg ha}^{-1}$ ), the model underpredicted yields of MG 3 cultivars, and overpredicted yields of MG 5 and 6 cultivars. Only for MG 4 cultivars were simulated yields similar to the observed across all environments. Under a very high yielding environment (EI =  $600 \text{ kg ha}^{-1}$ ), the model error predicting yields of MG 3 and 6 cultivars was reasonably small ( $-245$  and  $269 \text{ kg ha}^{-1}$ , respectively). On the other hand, simulated yields of MG 5 cultivars were  $608 \text{ kg ha}^{-1}$  higher than the observed in a high yielding environment.

**Table 6**

Analysis of covariance for the regression of soybean yield on the environmental index (EI) as an independent variable. Soybean maturity group (rMG), yield data source (observed vs. predicted by the model; O vs. P), and the interactions of both were included as factors in the model to test their effect on the intercept and slopes of the regressions.

Regression parameter	Effect	Num DF	Den DF	F value	P-value
Intercept	Maturity group (MG)	3	226	75.7	<0.0001
	MG × O vs. P	4	226	7.6	<0.0001
Slope	Environmental Index (EI)	1	226	354.04	<0.0001
	EI × MG	3	226	7.17	0.0001
	EI × MG × O vs. P	4	226	1.91	0.1089

It is interesting to note from the analysis of yield stability in 2014 that MG 3 and 4 cultivars had the highest yields on average (intercept in the regression) and were also the most responsive to changes in environment (highest values for the slopes). In contrast, MG 5 and 6 cultivars had lower yields on average and were less responsive to high yielding environments. This results in MG 4 cultivars being at the top of the yield ranking in all environments, followed by MG 3 cultivars. Only in the lowest yielding environments, did MG 5 cultivars have yields similar to MG 3 cultivars. The low intercept and slope in the regression for MG 6 cultivars placed them at the bottom of the yield ranking in all environments. The model mimicked the observed yield ranking well except for MG 5 cultivars, which were ranked before MG 3 cultivars in all environments.

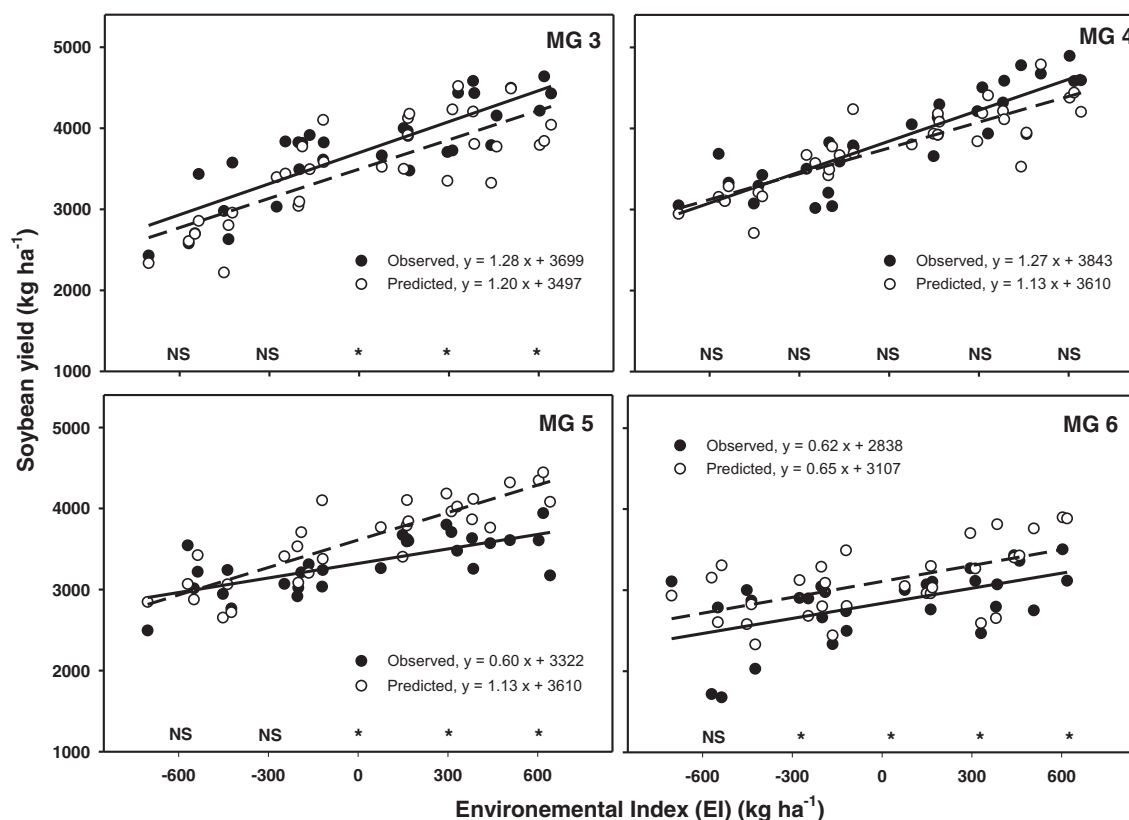
## 4. Discussion

### 4.1. Calibration of cultivar coefficients by MG

The analysis of variance for observed yields across the three growing seasons indicated that environment (year, location, planting date, and

their interactions) had the largest effect on yield variability (47.4% of the total sum of squares in the model). The percentage of the sum of squares explained by the MG alone was smaller (9.5%) compared to that of MG × environment (19.0%), indicating changes in the relative performance of MG across environments. The sources of variation related to the cultivar effect and its interaction with environment were relatively small (11.6%) compared to that explained by the environment, MG, and their interaction (75.9%). Therefore, it seemed reasonable to calibrate cultivar coefficients in DSSAT-CROPGRO by MG and test the model to predict yield differences associated with the planting date, location, and MG. The simulation results for an independent growing season indicated that the model was more efficient predicting yield than using the average yield of a MG across locations, except for MG 5, and therefore was able to partially explain the yield variation linked to environment and MG choice. A large part of the difference in yield potential among genotypes can be attributed to different environmental conditions during critical developmental stages (Egli, 1993). Hence, the ability of the model to simulate the observed timing of developmental stages across the environments and genotypes in this study (Salmerón and Purcell, 2016) was critical prior to calibrating and testing the model for yield predictions.

Calibration of DSSAT-CROPGRO cultivar coefficients usually requires detailed information collected during the season and across several environments or management systems in combination with a stepwise calibration for minimization of error in prediction of measured variables (Alderman et al., 2015; Boote, 1999). This intensive data collection and calibration can potentially allow interpretation of coefficients. For instance, calibrated cultivar coefficients for new and old cultivars grown at one location in Iowa provided understanding of the mechanisms of genetic improvement (Boote et al., 2001). In this study, the previous stepwise calibration approach was not possible since observed data were limited to end-of-season measurements. In fact, given the need



**Fig. 2.** Individual regressions of soybean yield by MG and data source (observed and predicted yield) versus the environmental Index (EI). Data were averaged across cultivars within a MG and environment. The analysis of covariance explained 74% of the total sum of squares in the model. The asterisks at different values of the EI indicate significant differences (0.05 probability level) between observed and predicted yields within a MG.



for intensive data collection and a complex non-trivial stepwise calibration, studies that calibrated DSSAT-CROPGRO cultivar coefficients related to growth are either limited by the number of locations and latitudes, by the number of planting dates, or conducted on few cultivars (Boote et al., 1997).

One alternative to intensive data collection and calibration has been the calibration with an “extensive” dataset from variety trials across a wide range of environments but with limited observed data (Mavromatis et al., 2001). Boote et al. (2001) recommended a minimum of 20–30 site-year combinations, such as 3 years over seven sites differing in latitude and planting date for this calibration approach. In this study, we initially observed large model errors with default coefficients by MG in CROPGRO, in particular for MG 5 and 6 cultivars. When we attempted to calibrate a large number of growth coefficients ( $n = 12$ ), the results indicated that a sequential calibration of 1 to 3 coefficients at a time (with 500 to 20,000 combinations of coefficients sets) was more efficient in improving yield predictions compared to a simultaneous calibration of all coefficients (with 200,000 combinations of coefficients sets). However, one limitation in the sequential procedure is that it can be dependent on the order in which coefficients are calibrated. Coefficients for complex models derived from limited end-of-season data should be interpreted with caution, since they are a result from optimizing tools to reduce prediction error and might not necessarily have a meaningful mechanistic or physiological interpretation.

CROPGRO is a source-driven model with a few exceptions (Boote et al., 1998a). The fact that predictions improved after a model modification that increased senescence suggests that there was a need for decreasing the assimilate source for late maturing MG 5 and 6 cultivars. The lower values obtained for the calibrated maximum leaf photosynthesis for MGs 5 and 6 (0.92), compared to MGs 3 and 4 (1.02 and 0.94, respectively) also support this finding. Moreover, the lower values for XFRT (fraction of assimilates to reproductive organs) obtained for MG 6 (0.90) compared to earlier maturities (0.95–1) further reduced the assimilates partitioned to reproductive organs in MG 6 cultivars. These results are consistent with a radiation interception study at two locations in Arkansas that showed higher radiation interception for MG 5 and 6 cultivars compared to MG 3 and 4 cultivars during the growing season despite that MG 5 and 6 cultivars had lower yields (Salmerón et al., 2015). The mechanism that explains the possible lower net assimilate supply to reproductive organs for late MG 5 and 6 cultivars grown across environments in the Midsouth needs further investigation.

#### 4.2. Prediction of yield components, and seed oil and protein concentration

The model was more efficient in the prediction of yield compared to prediction of seed weight ( $\text{g seed}^{-1}$ ) and seed number ( $\text{seeds m}^{-2}$ ), in particular during the independent growing season used for model evaluation (2014). During this growing season, in most cases the model failed to predict yield components with more accuracy than using the average value across environments. However, the model was still efficient predicting final yield, except for MG 5 cultivars, due to a compensation in the prediction error for seed weight and seed number.

CROPGRO calculates potential seed growth rate for a genotype based on its maximum seed weight and duration of seedfill for pod cohort (cultivar coefficients WTPSD and SFDUR, respectively). Pod set and seed number are then estimated based on the assimilate supply and the potential seed growth rate with an approach similar to Charles-Edwards (1984) but computing a daily carbon and nitrogen balance that takes into account the effect of temperature, water, and nitrogen stress (Wilkerson et al., 1983). Genetic differences in seed growth rate in soybean are controlled by the number of cells in the cotyledons (Egli et al., 1981), and high temperatures during flowering and early pod setting ( $33/28^\circ\text{C}$  day/night temperatures) reduce cell division and seed growth rate (Egli and Wardlaw, 1980). CROPGRO accounts for a temperature effect during flowering and pod set by increasing flower abortion and reducing pod setting with a temperature function

(Egli and Wardlaw, 1980), but potential seed growth rate in the model is not modified. Temperatures during seedfill will affect potential seed growth rate in CROPGRO, and final seed size will be further influenced by an indirect effect of temperature on seedfill duration and by leaf senescence. Based on the comparisons of the processes determining yield component determination in CROPGRO with previous research, it is possible that the low model accuracy was related to not accounting for the effect of high temperatures on potential seed growth rate during flowering and early pod set. High temperatures during this period would reduce cell division and therefore potential seed growth rate before calculation of pods and seeds that can be set. This compensatory error would explain the higher model accuracy predicting yield compared to seed number and seed size.

To our knowledge, there are no prior studies evaluating the accuracy of DSSAT-CROPGRO or another complex mechanistic crop model to predict seed oil concentrations across a wide range of environments. It is interesting to note the high model accuracy predicting seed oil concentration for all the MGs across all the environments studied for an independent growing season. Moreover, the model was able to mimic how seed oil concentration decreased on average with later maturities. The model uses a carbon balance approach in which increases in predicted seed oil concentration will come at a higher energy cost and have an impact on yield. Oil concentration increases with temperature, with an optimum between  $25$  and  $28^\circ\text{C}$  (Dornbos and Mullen, 1992; Gibson and Mullen, 1996; Piper and Boote, 1999). CROPGRO incorporates a linear function that affects seed oil composition (Piper and Boote, 1999) with a base and maximum average daily temperatures of  $7.2$  and  $23.7^\circ\text{C}$ , respectively. The present research indicated that this modeling approach was efficient in predicting seed oil concentration across a wide range of environments and MGs in the Midsouth.

Model predictions of seed protein concentration had a small average bias ( $0.03$  to  $-0.55\%$ ) and a relatively small RMSE ( $1.00$  to  $1.54\%$ ). However, the model was not efficient reproducing the small changes in protein concentration observed across environments. Protein concentration in seed has a genetic component (Brim and Burton, 1979). However, when performing simulations with cultivar-specific coefficients during the 2012 and 2013 growing season, predictions of protein concentration did not improve compared to using coefficients calibrated by MG. Previous studies have shown good model agreements after calibration for prediction of seed N concentration in pigeonpea (Alderman et al., 2015) and cumulative total N in soybean (Boote et al., 1997). The response of seed protein concentration to temperature has been inconsistent for temperatures below  $28^\circ\text{C}$  (Piper and Boote, 1999; Wolf et al., 1982) and shows an increase at very high temperatures ( $33/28^\circ\text{C}$ ) (Wolf et al., 1982). CROPGRO uses a temperature function as a function of oil plus protein concentration to account for the temperature effect in protein concentration that was estimated from Piper and Boote (1999). The low model efficiency predicting protein concentration in this study could be related to not accounting well for the temperature effect during seed fill or due to inaccuracy in the N balance across environments.

#### 4.3. Prediction of $G \times E$ interactions in the Midsouth

The objective of this study was to test a complex mechanistic crop model to reproduce yield variation across locations, planting dates, and MGs in the Midsouth. The results indicated that the model was able to partially explain yield differences associated with genotype, planting date and location ( $\text{ME} = 0.40$  across all locations and environments). When evaluating model predictions by MG, the model was efficient explaining differences across locations and planting dates for MGs 3 and 4 but not for MGs 5 and 6 due to yields being overpredicted on average. The RMSE for yield prediction with cultivar coefficients calibrated by MG during the independent growing season ranged from  $494$  to  $644 \text{ kg ha}^{-1}$ . Other models with limited data input have been able to reproduce soybean yield differences across locations and planting dates in



Nebraska, Iowa, and Indiana for treatments under near-optimal conditions with a RMSE of  $460 \text{ kg ha}^{-1}$  (Setiyono et al., 2010). Previous studies testing DSSAT-CROPGRO to simulate yields across several site  $\times$  years included rainfed conditions and the effect of water limitations on yield with RMSE values ranging from  $363$  to  $559 \text{ kg ha}^{-1}$  (Calvino et al., 2003; Irmak et al., 2000; Mavromatis et al., 2001; Mavromatis et al., 2002). In the previous studies, the model accuracy was partially related to the ability of the model to simulate water balance and yield reductions under water-limitation, and only partially due to simulation of other environmental effects on yield determination and calibration of cultivar coefficients. Under the irrigated conditions in this experiment, the model was still efficient explaining part of the  $G \times E$  interaction. Moreover, for the relatively high yields in our study, the NRMSE was quite low, with values of 14, 13, 20, and 22% for MG 3, 4, 5, and 6, respectively.

The analysis of yield stability for an independent growing season also demonstrated the applicability of the model to simulate  $G \times E$  interactions. In order to use a stability analysis technique to evaluate a model performance, it is essential to perform yield regressions with an EI calculated from observed data and not from simulated data as in Mavromatis et al. (2001). For this study, the analysis of covariance indicated that the slopes of the regressions of the observed and simulated yields with EI were similar within each MG. Therefore, the model was able to reproduce the observed yield responses across environments associated with a given MG. Although the simulated yields did differ significantly from the observed yields when  $EI > 0$  in MG 3, 5 and 6 cultivars, yield differences in the most high yielding environments were still relatively small ( $-245$ ,  $269$ , and  $608 \text{ kg ha}^{-1}$  for MG 3, 5, and 6, respectively). Therefore, the stability analysis indicates an overall robust model performance in capturing  $G \times E$  responses.

## 5. Conclusion

The ability of DSSAT-CROPGRO to reproduce irrigated yield variation across locations, planting dates, and soybean genotypes has wide applications for developing decision management tools. The results indicated that the model could partially explain yield differences associated with MG, planting date and location, and was efficient reproducing yield variability across MGs and environments. Although yield was predicted well, seed number and seed weight were predicted with less accuracy. The model also predicted differences in seed oil concentration across environments and MGs but was not efficient in predicting protein concentration.

Model performance for predicting yield was similar when using cultivar-specific coefficients as when using generic coefficients based upon MGs. Although the use of cultivar coefficients calibrated by MG seemed reasonable under the irrigated conditions in our experiment and for the commercial cultivars studied, greater yield differences associated with cultivar choices within a MG might be expected when introducing more genetic variability or under water limited conditions.

Model performance was improved by increasing sensitivity of leaf senescence to low-radiation levels, especially for later MGs. Further evaluation of model simulations across environments in the MidSouth with detailed measurements during the season is needed.

The analysis of yield stability for an independent growing season with regressions of observed and predicted yields with an EI indicated that the model was able to mimic the different yield responses to changes in environment associated with the choice of MG. Although the slopes of the regressions were similar for the observed and predicted yields, for above average environments ( $EI > 0$ ) simulated yields of MG 3, 5 and 6 cultivars were significantly different from the observed. However, yield differences in the most high-yielding environments were still relatively small ( $245$  to  $608 \text{ kg ha}^{-1}$ ). Overall, the results indicated a robust model performance in capturing  $G \times E$  responses with coefficients calibrated by MG.

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