CHAPTER VI

AUTOMATIC CALIBRATION OF CULTIVAR COEFFICIENTS OF PEANUT LINES FOR USE WITH THE CSM-CROPGRO-PEANUT MODEL

Introduction

Crop simulation models have been developed for agricultural policy formulation and field practices recommendations (Boote et al., 1996; Tsuji et al., 1998). Several crop growth models are currently available such as the grain cereal model CERES (Jones and Kiniry, 1986) and the grain legume model CROPGRO (Hoogenboom et al., 1994; Boote et al., 1998). These crop simulation models have been evaluated extensively in various applications, including evaluating cultivar performances (Palanisamy et al., 1995; Piper et al., 1998; Boote et al., 2003; Banterng et al., 2004; Suriharn et al., 2007), assessing the adaptation a new cultivar to a region (Hunt, 1993; Hammer et al., 1996; White, 1998; Chapman et al., 2002), studying the nature of genotype x environment interactions (Aggarwal et al., 1997; White, 1998; Piper et al., 1998; Chapman et al., 2002; Phakamas et al., 2008) and evaluating improved management options (Paz et al., 2007; Bhatia et al., 2008; Timsina et al., 2008).

For peanut, The CSM-CROPGRO-Peanut model is one of the crop simulation models that encompass the Decision Support System for Agrotechnology Transfer (DSSAT) (Tsuji et al., 1994; Hoogenboom et al., 1999; Jones et al., 2003; Hoogenboom et al., 2004). Environmental conditions, management practices, and characteristics of cultivar-specific genetic coefficients are four input data sets that are necessary for model operation (Boote et al., 1998).

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Before the application of the CSM-CROPGRO Peanut model, it is essential to first determine the cultivar coefficients if the cultivars are new breeding lines or local cultivars that have not been used previously with the model. Determination of cultivar coefficients required data set from field experiment conducted under environments that are free from both of abiotic and biotic stresses (Boote, 1999).

The CSM-CROPGRO-Peanut model uses the concept of cultivar coefficient to characterize genotypes or cultivars (Boote et al., 1998, 2003). The cultivar coefficients are crop characters that define the development, vegetative and reproductive growth of an individual genotype (Boote et al., 2003). Data from two seasons are sufficient to determine cultivar coefficients of peanut cultivars of the CSM-CROPGRO-Peanut model (Banterng et al., 2004). First flowering (R1) and harvest maturity (R8) were the two developmental stages, and full seed (R6), physiological maturity (R7) and harvest maturity (R8) are the three plant samplings that are the minimum requirement for determining the cultivar coefficients of peanut lines for use with the CSM-CROPGRO-Peanut model (Anothai et al., 2008a).

In the estimation of the cultivar coefficients of peanut lines for the CSM-CROPGRO-Peanut model, the optimization using the Genotype Coefficient Calculator (GENCALC) was performed by Anothai et al. (2008b). GENCALC is a software for automatically calibrating cultivar coefficients from cultivar trait data which has been developed to facilitate the generation of cultivar coefficients of a new cultivar (Hunt et al., 1993). A new version of this software is currently under development for incorporation into the DSSAT (Hoogenboom, personal communication). The GENCALC program was able to derive acceptable cultivar coefficients from typical data collected in standard performance trails (Anothai et al., 2008b).

A new estimation method, the Generalized Likelihood Uncertainty Estimation (GLUE), has also been developed as a method for calibration and uncertainty estimation of models based on generalized likelihood measures (Beven and Binley, 1992). The GLUE program is used to automatically estimate genotype-specific coefficients for the DSSAT crop models without intervening by user (He et al., 2010). It is a Bayessian estimation method using Monte Carlo sampling from prior distributions of the coefficients and a Gaussian likelihood function to determine the best coefficients based on the data that are used in the estimation process (Beven and Binley, 1992).

Even though the GENCALC program has been shown to give good results (Anothai et al., 2008b), a suitable sequence is required in the operation and the capability of the program depend on heuristic rules. The GLUE method, on the contrary, can be used without intervention by user. It also provides the estimates of the uncertainties of the parameters. If GLUE can be used with the CSM-CROPGRO-Peanut model, it will simplify the process in determining the cultivar coefficients, and facilitate the generation of cultivar coefficients for new cultivars. However, before using this software, its capability in estimating genotype coefficients needs to be established first. The objective of this investigation was to compare the capability of GLUE with GENCALC and manual calibration in estimating the cultivar coefficients of peanut lines for use with the CSM-CROPGRO-Peanut model.

Materials and Methods

Field experiment and data collection

Field experiments were conducted at the Field Crop Research Station of Khon Kaen University, Khon Kaen, Thailand (lat 16° 28′ N, long 102° 48′ E, 200 masl) from February to July, 2007 and from February to July, 2009. The experimental sites in the two seasons were adjacent fields. The soil type is a Yasothon series (Yt: fine-loamy; siliceous, isohypothermic, Oxic Paleustults). A randomized complete block design with four replications was used. Six peanut genotypes, i.e., KK 60-3, Tainan 9, Tifton-8, ICGV 98305, ICGV 98324 and ICGV 98330, were the treatments. Plot size was 18.2 m^2, consisting of seven rows, 5.2 m long. The spacing between rows was 50 cm and the spacing between plants was 20 cm, giving a plant density of 10 plants m^{-2}. Management practices on irrigation, pest and disease control, and nutrients were done as good as possible to obtain optimum conditions for plant growth. Lime ($CaCO_3$) at a rate of 625 kg ha^{-1} was incorporated into the soil during soil preparation. Prior to planting, nitrogen fertilizer in the form of urea was applied at a rate of 23.4 kg N ha^{-1}, phosphorus fertilizer as triple superphosphate was applied at a rate of 24.7 kg P ha^{-1} and potassium fertilizer as potassium chloride was applied at a rate of 31.1 kg K ha^{-1}.

Gypsum ($CaSO_4$) was applied to the soil surface at a rate of 312 kg ha^{-1} at 45 days after emergence (DAE). Pest and diseases were controlled by weekly applications of carbosulfan [2-3-dihydro-2,2-dimethylbenzofuran-7-yl (dibutylamino-thio) methylcarbamate 20 % w/v, water soluble concentrate] at 2.5 l ha^{-1}, methomyl [S-methyl-N-((methylcarbamoyl) oxy) thioacetimidate 40 % soluble powder] at 1.0 kg ha^{-1} and carboxin (5,6-dihydro-2-methyl-1,4-oxath-ine-3-carboxanilide 75 % wettable powder) at 1.68 kg ha^{-1}. A drip-irrigation system was installed for supplying water throughout crop cycle. Before planting, the field was irrigated to reach field capacity (FC) up to a depth of 60 cm. The soil water content was maintained uniformly at FC from planting until harvest, and moisture content was controlled to be within 1% difference from FC.

Crop development was recorded for the dates of planting, emergence (VE), R1 and R8, following the minimum data requirement for the determination of cultivar coefficients for the CSM-CROPGRO-Peanut model as suggested by Anothai et al. (2008a). Final pod yield, final seed yield, final biomass, final seed size, seed harvest index and shelling percentage were measured at maturity from harvest area of 7.5 m^2 for each plot. Harvested plant samples were depodded, and fresh weights of pods and stover were recorded. A sub-sample was also taken from each plot, and fresh weights of pods and stover excluding roots were measured. The sub-sample was oven-dried at 80°C for 48 h or until reaching a constant weight and dry weights of pods and stover were obtained.

Soil samples were collected at two locations in the individual fields before planting at the depths of 0-15, 15-30, 30-45, 45-60, 60-75 and 75-90 cm. They were analyzed for texture, bulk density, soil moisture, pH, organic matter, exchangeable potassium and phosphorus and nitrogen concentration. Weather information, i.e., daily solar radiation, maximum and minimum air temperatures and rainfall, were obtained from the meteorological station at Khon Kaen University.

Manual calibration

The CSM-CROPGRO-Peanut model uses 15 cultivar coefficients (Table 1) to define growth and development characters or traits of a peanut cultivar (Hoogenboom et al., 1994; Boote et al., 2003). The default values for cultivar coefficients of the cultivars NC 7 and TMV 2 were used as initial values for the calibration of the large-seeded cultivar KK60-3 and the small-seeded cultivars ICGV 98305, ICGV 98324, ICGV 98330 and Tainan 9, respectively. The initial values for cultivar coefficients of Tifton-8 which were provided in PNGRO045.CUL of DSSAT version 4.5 were used for calibration of this cultivar. The cultivar coefficients of the individual peanut genotypes were calibrated to fit the experimental data from the two growing seasons following the procedures described by Boote (1999). However, in this study, we made an effort to provide fairness for all methods. Thus, the end of crop cycle data, i.e., final pod yield and final biomass, were exclusively considered in the Manual calibration as these data were used by another two methods for deriving the cultivar coefficients. Hence, in the Manual calibration, the EVALUTE.OUT file appearing in the CSM-CROPGRO-Peanut model was specifically examined for finding the optimized cultivar coefficient values. Therefore, some steps recommended by Boote (1999) were skipped.

Table 1 Cultivar coefficients of the CSM-CROPGRO-Peanut model.

Abbreviation	Definition	Unit
CSDL	Critical short day length below which reproductive development progresses with no daylength effect	h
PPSEN	Relative response of development to photoperiod with time	h^{-1}
Phenology parameters		
EMFL	Time between plant emergence and flower appearance (R1)	photothermal day
FLSH	Time between first flower (R1) and first pod (R3)	photothermal day
FLSD	Time between first flower (R1) and first seed (R5)	photothermal day
SDPM	Time between first seed (R5) and physiological maturity (R7)	photothermal day
FLLF	Time between first flower (R1) and end of leaf expansion	photothermal day
Growth parameters		
LEMAX	Maximum leaf photosynthesis rate at 30°C, 350 vpm CO_2, and high light	mg CO_2 m^{-2} s^{-1}
SLAVR	Specific leaf area of cultivar under standard growth conditions	cm^2 g^{-1}
SIZLF	Maximum size of full leaf	cm^2
XFRT	Maximum fraction of daily growth that is partitioned to seed and shell	fraction
WTPSD	Maximum weight per seed	g
SDPDV	Average seed per pod under standard growing conditions	no. pod^{-1}
SFDUR	Seed filling duration for pod cohort at standard growth conditions	photothermal day
PODUR	Time required for cultivar to reach final pod load under optimum conditions	photothermal day

The algorithm for calibrating the cultivar coefficients is as follows. First, the coefficient for duration of EMFL and SDPM were adjusted until the simulated days to flowering and days to maturity matched the observed. The next step was predicting the dry matter accumulation rate by finding the values of soil fertility factor (SLPF) in the soil file to derive a good fit for the mean value of top dry weight and pod for all cultivars. Then adjustment for LFMAX was made to account for the residual differences in top dry weight and pod of a cultivar. Next, the WTPSD and SDPDV were adjusted for final seed size and seeds per pod until the agreement between their simulated and observed values approached a good match. Then, the calibration of cultivars coefficients for pod and seed development (FLSH, FLSD and PODUR) was done using the onset of pod at maturity for adjusting FLSH, the onset of seed and seed harvest index for adjusting FLSD, and the onset of pod, seed, pod harvest index and seed harvest index for adjusting PODUR. After that, the SDPM was readjusted to ensure that the maturity date was correct. As the alterations of parameters affected timing and might cause the changes in seed size and seeds per pod, the WTPSD and SDPDV were, thus, re-calibrated. SFDUR was then adjusted for shelling percentage as well as pod, seed and seed harvest index, until a good fit was obtained. Then, the WTPSD, SDPDV and PODUR were re-calibrated to account for the effects of parameter alterations on the coefficients. Next, the XFRT was calibrated to produce a good match for biomass, pod, seed and seed harvest index. Finally, the adjustment of LFMAX was done again until the statistical fit revealed a good match for top dry matter, and pod and seed dry weights.

The accuracy of the procedure for estimating the cultivars coefficients was determined by comparing the simulated values of the end-of-season data of two seasons with the observed values, and by the values of the normalized root mean square error (RMSEn) (Willmott, 1982). A mean value of RMSEn averaged over multiple target characteristics was used as the criteria for determining the accuracy of the estimate of a cultivar coefficient. A low RMSEn value is desirable.

The RMSEn was computed using the following equation:

$$\text{RMSEn} = \frac{\text{RMSE x 100}}{\bar{O}} \tag{1}$$

where RMSE = root mean square error which was computed using the following equation:

$$\text{RMSE} = \sqrt{\frac{\sum_{i=1}^{n}(P_i - O_i)^2}{n}} \tag{2}$$

where P_i = predicted value of the ith measurement, O_i = observed value of the ith measurement, and n = number of measurement.

GENCALC calibration

The GENCALC program (Hunt et al., 1993) incorporated in the DSSAT Version 4.5 was used to calibrate the cultivar coefficients of the peanut cultivars with the CSM–CROPGRO–Peanut model. The default values of the cultivar coefficients of the cultivars NC 7, TMV 2 and Tifton-8 were used as the initial values as done with the Manual calibration method. The values for available cultivar coefficients varied depending on the number of simulated and observed crop measurements. The algorithm searched the output file of crop simulation model and automatically changed the values of the cultivar coefficients based on the difference between the simulated and observed values. When a good fit to each observation was obtained, it averaged the coefficients and calculated the average root mean square error (RMSE) (Wallach and Goffinet, 1987) over all the trials included in the optimization. The decision for repeating the process was based on the new candidate parameters. The calibration was considered finished when the parameters provided the lowest RMSE for a single target trait or the lowest average RMSEn for multiple target traits (Anothai et al., 2008b).

The approach, order and target traits for the optimization procedures described by (Anothai et al., 2008b) were followed. First, the coefficient for duration to first flower (EMFL) was adjusted for a good fit between the simulated and observed values of days to first flower. The next step was adjusting the values of SDPM for the simulated and observed days to harvest maturity. Then the search for LFMAX was conducted based on final biomass. Next, the WTPSD was adjusted for final seed size until the simulated and observed values were well matched. Then, XFRT was calibrated based on the values of final pod yield and final seed yield, which were the multiple targets in the calibration process. In the next step, the multiple targets of final pod yield, final seed yield and seed harvest index were used for searching a suitable PODUR. Shelling percentage was used for adjusting SFDUR until a good fit was obtained. Next, the WTPSD was recalibrated to final seed size. Then, LFMAX was readjusted for top dry matter, pod and seed dry weight. Next, shelling percentage, final pod yield, final seed yield and seed harvest index were used as the multiple targets for re-adjusting SFDUR. Next, the WTPSD was again re-calibrated. After that, the PODUR and XFRT were re-calculated for final pod yield, final seed yield and seed harvest index. Finally, LFMAX was re-adjusted of final biomass, final pod yield and final seed yield.

GLUE calibration

Calibration by the GLUE program is done automatically by the program itself. The program randomly generates parameters either phenology or growth, then selects the parameter set from the model outputs with the maximum likelihood value based on the differences between the simulated and corresponding observed data, first for phenological parameters, then for growth parameters. For this investigation, observed data for both development and growth were used for model calibration by GLUE. For development coefficients, measurement for days to first flower and days to physiological maturity were used. For growth coefficients, final grain yield, final biomass, final pod yield, unit grain weight, number of seed per pod, shelling percentage and pod and seed harvest index were used for input observation. The default values of the cultivars NC 7, TMV 2 and Tifton-8 were used as initial coefficients, the same as the Manual and the GENCALC methods. All measurements were provided in File-A of DSSAT. The program was set to run 3,000 times for all parameters, meaning that there were 3,000 runs for phenological parameters and another 3,000 for growth parameters. When the running process was finished, the derived cultivar coefficients would be shown in the output file of the program.

Evaluation of the cultivar coefficients derived by the three methods

The cultivar coefficients of all six peanut genotypes derived from end-of-season data of performance trails by the three calibration methods were evaluated against independent data sets obtained from four experiments under non-stress conditions. The experiments were conducted at the Field Crop Research Station of Khon Kaen University, Khon Kaen, Thailand during November 2003 to March 2004, October 2004 to February 2005, June to October 2005, and December 2005 to April 2006. End-of-season data from all four experiments were used to evaluate end-of-season data prediction, whereas in-season data from two experiments, i.e., November 2003 to March 2004, and October 2004 to February 2005, were used to evaluate in-season data prediction. The derived cultivar coefficients from the three methods were used to simulate days to first flower (R1), days to harvest maturity (R8), final pod yield and biomass of each genotype in four seasons, and also simulate in-season growth of biomass for the individual seasons. The manner for collecting observed data for model evaluation was the same as that used for collecting data for model calibration.

A comparison between the simulated values for phenological development and growth characteristics of each peanut cultivar and their corresponding observed values was a basis for the evaluation. The statistical fit parameters that included RMSEn and the index of agreement (*d*) (Willmott, 1982) were used to determine the degree of agreement. RMSEn was used to evaluate the end-of-season data prediction, and the *d* value was used to evaluate the in-season data prediction of the cultivar coefficients derived by the three calibration methods.

The value of *d* was computed using the following equation:

$$d = 1 - \left[\frac{\sum_{i=1}^{n}(P_i - O_i)^2}{\sum_{i=1}^{n}(|P'_i| + |O'_i|)^2}\right], 0 \leq d \leq 1 \qquad (3)$$

where n = number of observations, P_i = predicted value for the *i*th measurement, O_i = observed value for the *i*th measurement, $\bar{O}$ = the overall mean of observed values, $P'_i = P_i - \bar{O}$ and $O'_i = O_i - \bar{O}$

Results and Discussion

Calibration of the cultivar coefficients

The results for model calibration of phonological traits indicated that the simulated values for days to anthesis and days to maturity of the individual peanut genotypes were in a reasonably good agreement with their corresponding observed values for all three calibration methods, as indicated by the low values of RMSEn. Means for RMSEn over six peanut cultivars for the Manual calibration, the GENCALC and the GLUE methods were 0.6, 0.4 and 0.4%, respectively (Table 2). Furthermore, the mean observed and simulated values for days to anthesis were exactly the same for all genotypes and all methods (Table 2). For days to maturity, good agreements between simulated and observed values were also obtained for all three methods, with the means for RMSEn of the Manual, the GENCALC and the GLUE methods being 0.6, 0.5 and 0.6%, respectively (Table 2). Essentially, no difference between simulated and observed values for days to maturity was shown for all genotypes and all methods, except for the cultivars ICGV 98305 and ICGV 98330 in which the difference of only one day was obtained from the GLUE method.

For model calibration of end-of-season growth parameters, the simulated and the corresponding observed values for final biomass and final pod yield of the six peanut genotypes showed fairly good agreement for all the three calibration methods. The averaged values for RMSEn over six peanut cultivars of the Manual, the GENCALC and the GLUE methods for biomass were low, being 9.0, 5.7 and 13.2%, respectively, but somewhat higher for pod yield, being 27.4, 20.1 and 28.4%, respectively (Table 3). For both traits, the GENCALC method gave the lowest RMSEn values, followed by the Manual and the GLUE methods. The GENCALC method also gave the lowest RMSEn values for days to anthesis and days to maturity. These results, thus, indicated that the GENCALC method performed best in model calibration of the cultivar coefficients, followed by the Manual method and the GLUE method. However, the differences in their performances in model calibration were rather small, and all three methods gave satisfactory results in term of the agreement between the simulated and the observed values of development and growth traits.

Table 2 Observed and simulated values, ratio of observed and simulated values, mean of observed minus simulated values and the normalized root mean square error (RMSEn) for phenological characters of the individual peanut genotypes in model calibration by the three calibration methods.

Cultivar	Method	Days to anthesis					Days to maturity				
		Observed	Simulated	Ratio	Mean Diff.	RMSEn(%)	Observed	Simulated	Ratio	Mean Diff.	RMSEn (%)
ICGV 98305	Manual	30	30	1.00	0	0.0	118	118	1.00	0	0.8
	GENCALC	30	30	1.00	0	0.0	118	118	1.00	0	0.8
	GLUE	30	30	1.00	0	0.0	118	117	0.99	-1	1.2
ICGV 98324	Manual	31	31	1.00	0	0.0	122	122	1.00	0	0.8
	GENCALC	31	31	1.00	0	0.0	122	122	1.00	0	0.6
	GLUE	31	31	1.00	0	0.0	122	122	1.00	0	0.6
ICGV 98330	Manual	31	31	1.00	0	0.0	123	123	1.00	0	0.0
	GENCALC	31	31	1.00	0	0.0	123	123	1.00	0	0.0
	GLUE	31	31	1.00	0	0.0	123	124	1.01	1	0.8
Tainan 9	Manual	30	30	1.00	0	3.3	117	117	1.00	0	0.0
	GENCALC	30	29	0.98	0	2.4	117	117	1.00	0	0.0
	GLUE	30	29	0.98	0	2.4	117	117	1.00	0	0.0
KK60-3	Manual	32	32	1.00	0	0.0	130	130	1.00	0	1.2
	GENCALC	32	32	1.00	0	0.0	130	130	1.00	0	0.8
	GLUE	32	32	1.00	0	0.0	130	130	1.00	0	0.8
Tifton-8	Manual	33	33	1.00	0	0.0	136	136	1.00	0	0.7
	GENCALC	33	33	1.00	0	0.0	136	136	1.00	0	0.5
	GLUE	33	33	1.00	0	0.0	136	136	1.00	0	0.5
Average	Manual					0.6					0.6
	GENCALC					0.4					0.5
	GLUE					0.4					0.6

Table 3 Observed and simulated values, ratio of observed and simulated values, mean of observed minus simulated values and the normalized root mean square error (RMSEn) for biomass and pod yield of the individual peanut genotypes by the three calibration methods.

Cultivar	Method	Biomass ($kg\ ha^{-1}$)					Pod ($kg\ ha^{-1}$)				
		Observed	Simulated	Ratio	Mean Diff.	RMSEn (%)	Observed	Simulated	Ratio	Mean Diff.	RMSEn (%)
ICGV 98305	Manual	8900	8416	0.95	-484	6.6	1488	1590	1.07	101	17.8
	GENCALC	8900	8292	0.94	-607	8.3	1488	1578	1.06	89	9.9
	GLUE	8900	8406	0.95	-494	6.9	1488	1526	1.02	38	16.9
ICGV 98324	Manual	8338	8629	1.03	290	3.8	1840	1844	1.05	4	30.4
	GENCALC	8338	8121	0.97	-218	2.9	1840	2012	1.12	172	16.2
	GLUE	8338	8993	1.08	654	7.8	1840	1545	0.88	-295	33.9
ICGV 98330	Manual	8471	8463	1.01	-8	5.8	2188	2144	1.01	-44	26.9
	GENCALC	8471	8320	0.99	-150	9.5	2188	2133	0.99	-55	8.5
	GLUE	8471	9337	1.11	866	12.6	2188	2018	0.95	-170	27.7
Tainan 9	Manual	8970	8952	1.00	-17	8.1	2030	2080	1.02	50	16.3
	GENCALC	8970	9024	1.01	54	5.7	2030	2064	1.02	34	17.45
	GLUE	8970	8237	0.92	-732	11.4	2030	1919	0.94	-112	14.1
KK60-3	Manual	11806	11118	0.94	-688	6.6	2334	2071	0.94	-264	34.2
	GENCALC	11806	11305	0.96	-500	5.6	2334	2114	0.96	-220	35.0
	GLUE	11806	10336	0.88	-1470	12.9	2334	2096	0.95	-238	33.4
Tifton-8	Manual	9068	11152	1.23	2084	23.0	1422	1594	1.19	172	39.0
	GENCALC	9068	8924	0.98	-145	2.0	1422	1598	1.18	175	33.4
	GLUE	9068	11554	1.27	2486	27.4	1422	1718	1.28	295	44.5
Average	Manual					9.0					27.4
	GENCALC					5.7					20.1
	GLUE					13.2					28.4

The values of the cultivar coefficients that were derived from the three calibration methods were the same or slightly different for all phonological coefficients and some growth coefficients, but differed considerably for a few growth coefficients, particularly XFRT, SFDUR and PODUR (Table 4). Such differences were presumably the consequence of the differences in the calibration procedure of the three methods. For the GLUE and the Manual methods, the cultivar coefficients were adjusted based on the distributions with the minimum and maximum values of the individual parameters, but for the GENCALC method the values of the cultivar coefficients were allowed to go beyond the ranges given in the DSSAT.

Evaluation of the derived cultivar coefficients

The results for model evaluation using independent data sets from four experiments conducted during 2003 and 2006 showed that the simulated values for days to anthesis and days to maturity day of the six peanut genotypes were in good agreement with the corresponding observed values for all the experiments. The mean RMSEn values of the Manual, the GENCALC and the GLUE methods for days to anthesis were 7.0, 6.9 and 6.9 %, respectively, and for days to maturity were 3.5, 3.3, 3.5 %, respectively, (Table 5). The mean differences between the simulated and the observed values for days to anthesis for the three methods were all small, being two days or less. The predictions of maturity day by the cultivar coefficients that were derived by the three calibration methods were also acceptable, with the mean differences between the simulated and the observed values ranging from 0 to 7 days (Table 5). The greatest differences were for days to maturity of ICGV 98330, but the differences were high for all three methods, being 6, 5 and 7 days for the Manual, the GENCALC and the GLUE methods, respectively. Thus, all calibration methods gave the estimates of the cultivar coefficients that predicted independent data on phonological development reasonably well.

Table 4 Estimates of the cultivar coefficients of six peanut genotypes derived from the three calibration methods.

Cultivar	Method	CSDL	PPSEN	EM-FL	FL-SH	FL-SD	SD-PM	FL-LF	LFMAX	SLAVR	SIZLF	XFRT	WTPSD	SFDUR	SDPDV	PODUR	THRSH	SDPRO	SDLIP
ICGV98305	Manual	11.84	0.00	21.00	7.00	17.50	62.70	78.00	1.05	270.00	16.00	0.75	0.60	29.00	1.88	32.50	78.00	0.27	0.51
	GENCALC	11.84	0.00	20.85	7.00	17.50	62.61	78.00	1.13	270.00	16.00	0.36	0.80	34.30	1.65	11.33	78.00	0.27	0.51
	GLUE	11.84	0.00	20.82	7.80	17.90	61.17	78.00	1.03	239.00	16.20	0.65	0.80	38.29	1.65	33.01	78.00	0.27	0.51
ICGV98324	Manual	11.84	0.00	21.60	7.70	17.50	66.00	78.00	1.00	270.00	16.00	0.80	0.72	28.00	1.52	30.50	78.00	0.27	0.51
	GENCALC	11.84	0.00	21.62	7.00	17.50	65.41	78.00	0.94	270.00	16.00	0.42	0.82	30.75	1.65	8.62	76.05	0.27	0.51
	GLUE	11.84	0.00	21.94	7.30	18.10	64.41	78.00	1.02	238.00	16.60	0.64	0.95	28.86	1.65	30.18	78.00	0.27	0.51
ICGV98330	Manual	11.84	0.00	21.70	7.00	17.60	66.60	78.00	1.00	270.00	16.00	0.80	0.75	22.90	1.59	22.20	78.00	0.27	0.51
	GENCALC	11.84	0.00	21.81	7.00	17.50	66.31	78.00	0.96	270.00	16.00	0.45	0.82	31.77	1.65	10.07	75.64	0.27	0.51
	GLUE	11.84	0.00	21.67	9.90	19.70	65.39	78.00	1.01	284.00	17.10	0.67	0.81	42.60	1.65	31.94	78.00	0.27	0.51
KK 60-3	Manual	11.84	0.00	22.00	7.80	20.60	69.20	88.00	1.15	270.00	20.00	0.53	1.00	42.40	1.87	30.00	75.00	0.27	0.51
	GENCALC	11.84	0.00	21.61	8.00	20.30	69.36	88.00	1.20	270.00	20.00	0.53	1.09	38.04	1.65	27.79	75.00	0.27	0.51
	GLUE	11.84	0.00	21.76	9.40	20.00	69.71	88.00	1.08	266.00	16.10	0.58	1.10	33.37	1.65	26.50	75.00	0.27	0.51
Tainan 9	Manual	11.84	0.00	20.20	7.00	17.50	62.40	78.00	1.17	270.00	16.00	0.61	0.79	30.00	1.81	20.80	78.00	0.27	0.51
	GENCALC	11.84	0.00	19.98	7.00	17.50	62.31	78.00	1.18	270.00	16.00	0.42	0.79	24.62	1.65	9.36	72.86	0.27	0.51
	GLUE	11.84	0.00	19.86	10.00	17.10	63.33	78.00	1.04	245.00	16.00	0.63	1.03	30.02	1.65	22.07	78.00	0.27	0.51
TIFTON-8	Manual	11.84	0.00	23.00	8.10	19.70	75.00	83.00	1.00	205.00	19.00	0.78	1.36	20.00	1.66	35.50	74.00	0.27	0.51
	GENCALC	11.84	0.00	23.09	8.20	19.70	74.49	83.00	0.74	205.00	19.00	0.42	1.38	44.47	1.65	23.24	74.00	0.27	0.51
	GLUE	11.84	0.00	23.11	5.70	20.30	73.96	83.00	1.08	277.00	17.20	0.59	2.80	37.80	1.65	33.28	74.00	0.27	0.51

Table 5 Observed and simulated values, ratio of observed and simulated values, mean of observed minus simulated values and the normalized root mean square error (RMSEn) for phenological development of the individual peanut genotypes in model evaluation of the three calibration methods.

Cultivar	Method	Days to anthesis					Days to maturity				
		Observed	Simulated	Ratio	Mean diff.	RMSEn (%)	Observed	Simulated	Ratio	Mean diff.	RMSEn (%)
ICGV 98305	Manual	34	36	1.05	2	6.7	130	131	1.01	2	2.4
	GENCALC	34	36	1.05	2	6.7	130	131	1.01	1	2.4
	GLUE	34	36	1.05	2	6.7	130	130	1.00	0	2.1
ICGV 98324	Manual	35	36	1.05	2	5.5	132	136	1.03	4	4.0
	GENCALC	35	36	1.05	2	5.5	132	135	1.02	3	3.6
	GLUE	35	36	1.05	2	5.5	132	135	1.03	4	3.6
ICGV 98330	Manual	34	36	1.06	2	8.1	131	137	1.04	6	5.2
	GENCALC	34	36	1.06	2	8.1	131	136	1.04	5	4.8
	GLUE	34	36	1.06	2	8.1	131	138	1.05	7	6.0
Tainan 9	Manual	34	34	1.03	1	5.7	128	130	1.02	2	2.3
	GENCALC	34	34	1.02	0	5.1	128	129	1.01	2	2.3
	GLUE	34	34	1.00	0	5.3	128	130	1.02	2	2.5
KK60-3	Manual	36	38	1.05	2	6.9	142	145	1.02	3	2.9
	GENCALC	36	37	1.05	2	7.1	142	144	1.01	2	2.5
	GLUE	36	38	1.05	2	6.9	142	144	1.02	2	2.5
Tifton-8	Manual	37	39	1.07	2	8.8	147	152	1.03	5	4.3
	GENCALC	37	39	1.07	2	8.8	147	151	1.03	4	4.1
	GLUE	37	39	1.07	2	8.8	147	152	1.03	5	4.5
Average	Manual				1.8	7.0				3.7	3.5
	GENCALC				1.7	6.9				2.8	3.3
	GLUE				1.7	6.9				3.3	3.5

Model evaluations for prediction of growth traits were done both using independent end-of-season data from four experiments and using independent in-season data from two experiments. For the evaluation with the end-of-season data, the simulated values for final biomass of the six peanut genotypes agreed fairly well with the corresponding observed values for all three methods, with the means for RMSEn being 16.8, 17.3 and 19.7 % for the Manual, the GENCALC and the GLUE methods, respectively (Table 6). The agreement between the simulated and observed values for final biomass, however, varied considerably among peanut genotypes and calibration methods. For instance, the RMSEn values for biomass of the peanut cultivar ICGV 98305 were 8.3, 18.0 and 8.5 % for the Manual, the GENCALC and the GLUE methods, respectively, while those of the cultivar ICGV 98305 were 17.5, 9.4 and 26.5 % for the Manual, GENCALC and GLUE methods, respectively (Table 6). Nevertheless, the average values for RMSEn over six peanut cultivars for the three methods were not different, indicating that the cultivar coefficients that were derived from the three calibration methods were equally effective in predicting independent end-of-season biomass data.

Model evaluation with end-of-season pod yield data showed fair agreements between the simulated values of the six peanut cultivars with the corresponding observed values for all calibration methods. The means for RMSEn of pod yield for the Manual, the GENCALC and the GLUE methods were 25.9, 30.7 and 33.5%, respectively (Table 6). On the average, the cultivar coefficients from the Manual method performed best in predicting pod yield, followed by those from the GENCALC and the GLUE methods, respectively. However, it was noted that all three methods gave cultivar coefficients that poorly predicted pod yield of the cultivar ICGV 98324, as shown by the rather high RMSEn values of 38.2, 46.5 and 48.6 % for the Manual, the GENCALC and the GLUE methods, respectively (Table 6). Such results might have been due to the effects of uncontrollable stresses to which this cultivar was susceptible. In four out of six cultivars, predictions of pod yield by the cultivar coefficients derived from the GLUE method were poorest, as shown by higher values of RMSEn than those from the other two methods, particularly for Tifton-8 (51.7 % RMSEn for GLUE compared to 24.3 % for Manual and 23.6 % for GENCALC). However, the cultivar coefficients from GLUE performed equally well with those from the other two methods in predicting pod yield of the cultivar KK 60-3 and gave the best prediction for the cultivar ICGV 98330 (Table 6).

For model evaluation with in-season data, the cultivar coefficients derived from the three calibration methods gave slightly different simulated values for dry matter accumulation of the four peanut genotypes. The cultivar coefficients from the Manual calibration gave higher simulated values than those from the other two methods in some cultivars, e.g., ICGV 98305, but in other cultivars, e.g., ICGV 98324, the cultivar coefficients from GENCALC gave higher simulated values, yet in other cultivars, e.g., ICGV 98330, the cultivar coefficients from GLUE gave higher simulated values than the other two methods (Figure 1). Overall, the simulated values fit well with the corresponding observed values for all calibration methods, with the *d* values being 0.93-0.99, 0.95-0.99 and 0.93-0.99 % for the Manual, the GENCALC and the GLUE methods, respectively (Figure 1), indicating that the three calibration methods gave the cultivar coefficients that were equally capable of predicting dry matter accumulation of peanut genotypes.

Table 6 Observed and simulated values, ratio of observed and simulated values, mean of observed minus simulated values and the normalized root mean square error (RMSEn) for biomass and pod yield of the individual peanut lines in model evaluation of the three calibration methods.

Cultivar	Method	Biomass					Pod				
		Observed (kg ha^{-1})	Simulated (kg ha^{-1})	Ratio	Mean Diff. (kg ha^{-1})	RMSEn (%)	Observed (kg ha^{-1})	Simulated (kg ha^{-1})	Ratio	Mean Diff. (kg ha^{-1})	RMSEn (%)
ICGV 98305	Manual	6531	6962	1.07	431	8.3	1786	1394	0.81	-392	26.0
	GENCALC	6531	7638	1.17	1107	18.0	1786	1438	0.85	-348	25.8
	GLUE	6531	6985	1.07	454	8.5	1786	1307	0.77	-478	32.3
ICGV 98324	Manual	6114	7021	1.16	906	17.5	2081	1639	0.90	-442	38.2
	GENCALC	6114	6411	1.05	297	9.4	2081	1761	1.03	-320	46.5
	GLUE	6114	7648	1.26	1533	26.5	2081	1375	0.76	-706	48.6
ICGV 98330	Manual	5950	6827	1.16	878	18.7	1676	1898	1.17	222	15.0
	GENCALC	5950	6617	1.13	668	14.5	1676	1916	1.24	240	29.0
	GLUE	5950	7722	1.32	1773	31.2	1676	1685	1.05	9	12.7
Tainan 9	Manual	6288	7354	1.18	1066	20.3	1688	1778	1.24	90	26.9
	GENCALC	6288	7365	1.18	1076	19.9	1688	1797	1.32	109	36.8
	GLUE	6288	6880	1.11	591	14.8	1688	1648	1.17	-40	32.6
KK60-3	Manual	8293	9831	1.20	1538	21.9	2060	1845	1.00	-214	24.8
	GENCALC	8293	9966	1.22	1673	23.2	2060	1890	1.01	-170	22.4
	GLUE	8293	9058	1.11	764	15.4	2060	1924	1.04	-136	23.3
Tifton-8	Manual	8862	9681	1.10	819	14.4	1521	1532	1.07	11	24.3
	GENCALC	8862	7608	0.87	-1253	18.6	1521	1426	1.00	-95	23.6
	GLUE	8862	10544	1.20	1682	21.8	1521	2065	1.45	544	51.7
Average	Manual					16.8					25.9
	GENCALC					17.3					30.7
	GLUE					19.7					33.5

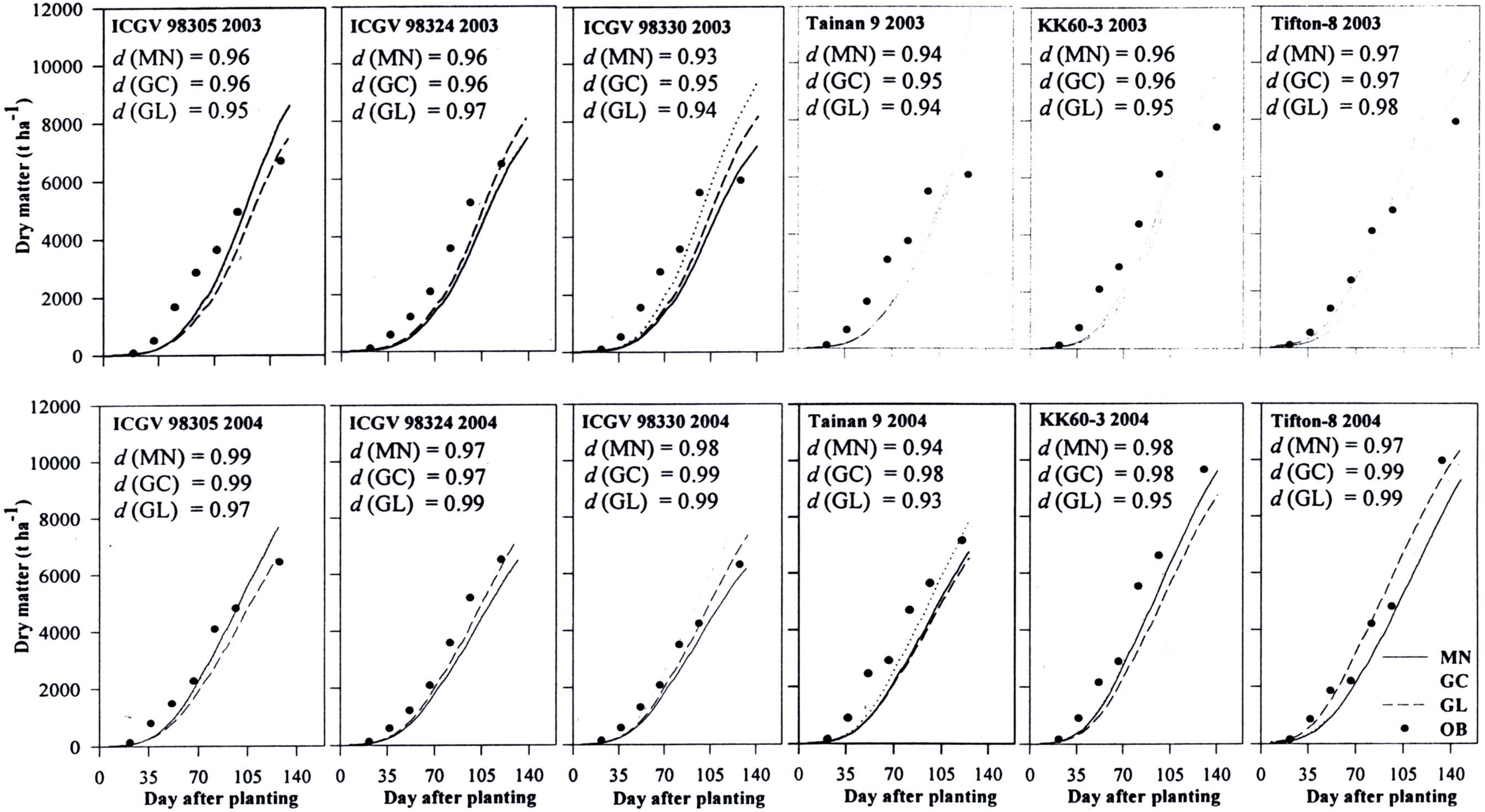

Figure 1 Simulated values for dry matter accumulation of six peanut cultivars from cultivar coefficients derived from the Manual (MN), the GENCALC (GC), and the GLUE (GL) calibration methods, the corresponding observed values (OB) from independent experiments conducted in 2003 and 2004, and the values for agreement index (*d*).

This study aimed to compare the capability of GLUE with GENCALC and manual calibration in estimating the cultivar coefficients of peanut lines for use with the CSM-CROPGRO-Peanut model. Essentially, it was intended to assess whether GLUE can be used for deriving the cultivar coefficients of new peanut lines for model applications. Since GLUE operation is simple, requires no skill in model calibration, and can be used with end-of-season data normally collected from crop performance trials, if GLUE can be used for this purpose, the opportunity for applications of the CSM-CROPGRO-Peanut model will be greatly enhanced.

The results of the present study indicated that all the three calibration methods worked reasonable well in model calibration of the cultivars coefficients for phenological development, final biomass and final pod yield of the six peanut genotypes. The derived cultivar coefficients from all three calibration methods gave simulated values of days to anthesis, days to maturity, final biomass and final pod yield of peanut genotypes that were in good agreement with the corresponding observed values that were used to derive the cultivar coefficients. The cultivar coefficients generated by GLUE were as good as those derived from GENCALC and manual calibration in model evaluation against independent data sets, both for phonological traits and for final biomass and pod yield, and with end-of-season data and in-season data. The results of the present study were comparable with those of Suriharn et al. (2007) in which model calibration was done manually using in-season time series data, and with those of Anothai et al. (2008b) in which model calibration was done with end-of-season data by the GENCALC method. The measures of agreement between simulated and observed values, i.e., mean differences and RMSEn values for phenological traits, final biomass and pod yield, from all three methods in the present study were in the same ranges as the comparable values in the studies of Suriharn et al. (2007) and Anothai et al. (2008b). Also, all the measures of agreement between the simulated and the observed values for the phonological and growth traits of the individual peanut genotypes obtained from the three calibration methods were in the acceptable ranges, with only very few exceptions for which the RMSEn values were rather high. The three calibration methods were, thus, considered acceptable and equally effective in deriving the cultivar coefficients of peanut lines for use with the CSM-CROPGRO-Peanut model.

Conclusions

The results of the present study indicated that GLUE is as effective as GENCALC and manual calibration to deriving the cultivar coefficients of peanut lines for use with the CSM-CROPGRO-Peanut model. As GLUE is software that can generate the cultivar coefficients automatically without user intervention, it can be used by anyone who can run the CSM-CROPGRO-Peanut model. The software, thus, will open up the opportunities for utilizing the CSM-CROPGRO-Peanut model in a broader range of applications.

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