RESEARCH ARTICLE

Calibration of genetic coefficients for blackgram using DSSAT-CROPGRO model

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Abstract

Blackgram is an important pulse crop in India, but abiotic stresses and poor management often limit its productivity. This study, for the first time, optimized genetic coefficients for 12 blackgram genotypes, providing a valuable resource for accurate simulation and crop modelling applications. Crop simulation models such as Decision Support System for Agrotechnology Transfer (DSSAT-CROPGRO) are valuable tools for evaluating varietal responses under diverse environmental conditions. However, accurate simulation requires genotype-specific genetic coefficients, which are largely unavailable for blackgram, limiting the effective application of such models. To address this gap, we calibrated and validated the CROPGRO-Drybean model under rainfed conditions during the *Kharif* season (2022-23) at the Main Agricultural Research Station (MARS), University of Agricultural Sciences (UAS), Dharwad. Genetic coefficients were optimized for 12 blackgram genotypes (DBG-5, DBG-19, DBG-31, DBG-33, DBG-34, DBG-93, DBG-16, DBG-96, DBG-90, DBG-95, DBG-61 and DU-1) using 3 replicated datasets from two sowing dates (May 30 and June 27) for calibration and the remaining two other sowing dates (June 13 and July 18) for validation. Results showed that simulated values closely matched with observed data, with deviations within ± 10 %. Phenological deviations ranged from 0 % to + 2.4 % for anthesis and - 1.3 % to + 1.3 % for maturity, while grain yield deviations ranged from - 3.1 % to + 5.8 %. Model performance was further supported by low root mean squared error (RMSE) values (0 - 1.41 days for phenology, 16.97 - 127.28 kg ha^{-1} for yield) and consistently high index of agreement (d = 0.889 – 1.0).

Keywords: blackgram; calibration; CROPGRO; drybean; DSSAT

Introduction

Blackgram (*Vigna mungo* L.) is one of the important pulse crops cultivated extensively in various agroclimatic zones of India. The productivity and growth of blackgram are intricately linked to prevailing weather conditions and agronomic management, besides genetic characters of the genotypes (1). Fluctuations in temperature, variations in rainfall patterns and other meteorological factors significantly influence the crop's development and yield, as they directly affect its genetic potential and physiological expression (2). In the context of climate change, where excess rainfall, droughts and other weather extremes pose constant challenges, accurate crop modelling becomes imperative.

Crop simulation models play an important role in modern agriculture by predicting crop growth under diverse environmental conditions, identifying production constraints and evaluating adaptation strategies (3, 4). The Decision Support System for Agrotechnology Transfer (DSSAT) ecosystem is one of the most widely used frameworks

worldwide, integrating soil, crop, weather and management processes for applications ranging from precision management to regional climate impact assessments (5). In particular, the CROPGRO model within DSSAT has been widely applied to legumes such as soybean, chickpea and groundnut in India (3, 6, 7) and more recently to mungbean and Indian bean (8). DSSAT has also been applied to blackgram under projected climate scenarios, demonstrating its potential (9). However, these applications remain limited to a few cultivars and environments, highlighting the absence of genotype-specific coefficients across diverse soils and regions.

This limitation is particularly critical for blackgram, which is predominantly grown under rainfed conditions in semi-arid India, where frequent moisture stress, late sowing and low input use make production highly vulnerable to climate variability. Expanding DSSAT use for blackgram is therefore essential to improve yield prediction and guide climate-resilient management. Conducting robust field experiments across multiple environments is often resource-intensive and time-consuming, whereas crop simulation models such as DSSAT

provide an efficient alternative. To run the model for any crop in a given location, however, genotype-specific coefficients are essential. Once optimized, these coefficients can be applied to a range of applications, including sowing window analysis, yield gap estimation and future climate impact assessments. Calibration and validation are essential steps in crop modeling to optimize genotype-specific coefficients and ensure model accuracy. Calibration involves adjusting genetic coefficients so that simulated values closely match observed field data, while validation assesses model performance against an independent dataset (8). Therefore, this study was undertaken to address this gap by calibrating and validating the CROPGRO-drybean model for 12 blackgram genotypes under rainfed conditions in north interior Karnataka, to develop reliable genetic coefficients for future modeling applications.

Materials and Methods

Experimental site

The field experiment was conducted during the *Kharif* season (2022 -23) under the MULLaRP scheme at the MARS, University of Agricultural Sciences (UAS), Dharwad. The site is located at 15° 26' N latitude, 75° 07' E longitude and an altitude of 678 m above mean sea level. The study was carried out on deep black soils under rainfed conditions. The experimental site location is provided in Supplementary Fig. S1.

Experimental design and treatments

The field experiment followed a split-plot design with 2 factors: 4 sowing windows (i.e. D_1: 30/05/2022, D_2: 13/06/2022, D_3: 27/06/2022 and D_4: 18/07/2022) and 12 blackgram genotypes (DBG-5, DBG-19, DBG-31, DBG-33, DBG-34, DBG-93, DBG-16, DBG-96, DBG-90, DU-1 and DBG-95). Row and plant spacing were maintained at 30 cm and 10 cm respectively.

Weather data

Daily weather data, including rainfall (mm), minimum and maximum temperatures (°C) and solar radiation (MJ m^{-2} day^{-1}), were recorded at the Meteorological Observatory, MARS, Dharwad. These data were used to create the DSSAT model's weather file (.WTH) for the calibration and validation process. The table below presents the monthly weather parameters for Dharwad in 2022

(Table 1).

Soil data

The soil module within the DSSAT model requires data on soil texture, color, slope (%), pH, organic carbon (OC, %), bulk density (BD, g cm^{-3}), field capacity and permanent wilting point across different depths (Table 2). The experiment was conducted on black clay soil. Soil data were obtained from the ICAR Krishi Geoportal website (10).

Crop management and experimental files

Five datasets were prepared for DSSAT: i) A-file: Yield data and crop attributes at the time of harvest of crop. ii) T-file: Time-series data on phenology and growth stages. iii) X-file: Crop management details, including sowing date, planting method (line sowing), plant population, spacing (30 cm x 10 cm), sowing depth (5 cm), tillage operations and fertilizer applications. Fertilizer management included a basal application of diammonium phosphate (DAP, 18-46-0) at the rate of 100 kg ha^{-1}, uniformly broadcast at sowing, which supplied 18 kg N ha^{-1} and 46 kg phosphorus pentoxide (P_2O_5) ha^{-1}. No potassium (K) was applied, as the soil was rich in available K. iv) Weather file: Daily weather on Tmax, Tmin, radiation and rainfall and v) Soil file: profile depth, soil color, slope, nitrogen phosphorus potassium (NPK) content, pH, EC and soil organic matter. A schematic representation of the DSSAT model application process is provided in supplementary Fig. S2.

Calibration and validation of the DSSAT-CROPGRO model

The DSSAT-CROPGRO model was calibrated and validated using experimental data from *Kharif* 2022 for 12 blackgram genotypes. Calibration was performed with sowing dates of May 30 and June 27, while validation used June 13 and July 18. Key parameters assessed included days to anthesis, days to physiological maturity and yield at harvest maturity. In this study, calibration was carried out using the GenCalc tool integrated with DSSAT, which iteratively adjusts coefficients until simulated and observed values are in close agreement (11-13). Final acceptance of coefficients was based on predefined statistical thresholds of percent deviation within ± 10 %, Root Mean Square Error (RMSE) minimized, d-statistics > 0.8 and Normalized Root Mean Square Error (NRMSE) < 15 % across calibration environments. For validation, independent datasets

Table 1. Monthly meteorological data during the year 2022 at the MARS, UAS, Dharwad

Months	Solar radiation (MJ m^{-2} day^{-1})	Rainfall (mm)	No. of rainy days	Mean temperature (°C)	
				Minimum	Maximum
January	11.84	0.0	0	13.2	28.2
February	13.53	0.0	0	15.1	32.0
March	13.52	48.8	6	18.9	34.2
April	13.74	114.4	8	21.1	34.8
May	13.31	125.8	6	21.4	32.1
June	13.19	102.8	7	21.0	29.9
July	10.83	186.4	14	20.5	26.6
August	11.06	113.2	14	20.3	27.4
September	12.31	195.6	11	20.0	28.7
October	11.82	208.6	8	18.6	28.9
November	10.50	2.81	1	16.5	29.6
December	11.61	3.2	1	15.6	29.6
Total /Average	12.27	1101.6	76	18.51	30.16

Table 2. Physical and chemical properties of black clay soil in the Dharwad district for simulation

Soil layer (cm)	Horizon	Sand (%)	Silt (%)	Clay (%)	Stones (%)	Soil root growth factor	Bulk density (g cm^{-3})	Saturation (cm^3 cm^{-3})	Field capacity (cm^3 cm^{-3})	Lower limit (cm^3 cm^{-3})	OC %	pH
0-30	Ap	10	45	45	0	1.00	1.31	0.476	0.433	0.269	0.65	7.4
30-60	AB	10	45	45	0	0.8	1.31	0.476	0.433	0.269	0.65	7.4
60-90	AB	10	45	45	0	0.75	1.31	0.476	0.433	0.269	0.65	7.4
90-120	BssC	10	45	45	0	0.7	1.31	0.476	0.433	0.269	0.65	7.4

from the contrasting sowing windows were used, representing multi-environment conditions within the season.

Model evaluation

The model's performance was evaluated by calculating the percentage deviation between simulated and observed values for phenology and grain yield. A deviation within ± 10 % indicates a good simulation, while deviations greater than +10 % or less than -10 % are considered overestimations and underestimations respectively (14). The following formula is used to calculate the percent deviation,

$$\text{Percent Deviation (\%)} = \frac{Si - Oi}{Oi} \times 100 \qquad (1)$$

Where, S_i = Simulated value; O_i= Observed value

Other model evaluation statistics used include the Index of agreement (d), RMSE and NRMSE.

Index of agreement (d): It ranges from 0 (no agreement) to 1 (perfect agreement), indicating how well the model's output matches observed data (15).

$$\text{Index of agreement (d)} = 1 - \frac{\Sigma(Si - Oi)^2}{\Sigma(|Si - \bar{O}| + |Oi - \bar{O}|)^2} \qquad (2)$$

Where, $\bar{O}$ = Mean of observed values.

RMSE measures the average magnitude of error and is sensitive to large errors (16).

$$\text{RMSE} = \sqrt{\frac{\Sigma(Si - Oi)^2}{n}} \qquad (3)$$

Where, n = Number of observations

NRMSE expresses RMSE as a percentage of the mean observed value, making it useful for comparing error magnitudes across different variables or units (17).

$$\text{NRMSE (\%)} = \frac{RMSE}{\bar{O}} \times 100 \qquad (4)$$

Results and Discussion

Calibration and derivation of genetic coefficients

The calibrated genetic coefficients for different blackgram genotypes were obtained using the GenCalc tool and are presented in Table 3 and supplementary Table S1 (18). These coefficients were fine-tuned iteratively to achieve optimal alignment between simulated and observed values, ensuring accurate representation of growth and development in the CROPGRO model. Notably, variations were observed across genotypes in traits such as photoperiod sensitivity (PPSEN), days from emergence to flowering (EM-FL) and seed-filling duration (SFDUR), reflecting the genetic diversity among cultivars. Compared to the original genetic coefficient, the calibrated values exhibited improved precision in parameters influencing phenology, biomass accumulation and yield formation. The optimized values will enhance the model's ability to predict crop performance under different environmental conditions, aiding in better genotype selection and agronomic decision-making (12).

Model calibration and validation for phenology (days to anthesis and maturity)

A close agreement between simulated and observed values was noted for days to anthesis and physiological maturity across all genotypes during both calibration and validation phases. Most genotypes showed a difference of within ± 1 day for days to anthesis, with percent deviations ranging from 0 % to 2.4 % (Table 4), except for DBG-34 at the May 30 sowing date during calibration, which had a 5 % deviation with a 2-day mean difference (i.e. 43 and 41 days after sowing (DAS) respectively) (supplementary Table S2). Similarly, for days to physiological maturity, a difference of within ± 1 day was observed, with percent deviations ranging from -1.3 % to +1.3 % (Table 4). Some genotypes exhibited slightly higher deviations, up to ± 2.5 %, at specific sowing dates (supplementary Table S2). The 1:1 scatter plot for days to anthesis (Fig. 1a) and physiological maturity (Fig. 1b) revealed that most data points aligned closely along the 1:1 line, visually confirming a strong correlation and minimal bias between simulated and observed values across genotypes. Regression analysis showed moderate to strong agreement (days to anthesis: R^2 = 0.70 calibration, 0.21 validation; physiological maturity: R^2 = 0.77 calibration, 0.51 validation), consistent with previous DSSAT studies where

Table 3. Key genetic coefficients of CROPGRO that vary among blackgram genotypes

Genotypes	PPSEN	EM-FL	FL-SD	SD-PM	LFMAX	SFDUR
ECOTYPE – ANDDET						
Original genetic coefficient (VAR# A 195)						
	0.020	28.00	9.20	21.50	0.990	17.50
Calibrated genetic coefficients						
DBG-5	0.0122	34.83	12.86	18.36	0.980	22.00
DBG-19	0.0175	35.00	12.78	18.96	0.980	22.00
DBG-31	0.0146	35.00	12.86	19.03	0.980	22.00
DBG-33	0.0175	35.00	12.78	18.07	0.995	21.09
DBG-34	0.0175	35.00	12.78	18.96	0.995	21.00
DBG-93	0.0146	35.00	12.86	19.03	1.000	18.70
DBG-16	0.0175	35.00	12.63	19.10	0.980	22.00
DBG-96	0.0115	34.39	13.00	21.41	0.980	21.34
DBG-90	0.0100	34.42	12.66	18.55	0.980	22.00
DBG-95	0.0115	34.39	13.00	19.60	0.980	22.00
DBG-61	0.0144	34.20	12.78	22.66	0.980	20.87
DU-1	0.0175	35.00	12.78	18.07	0.980	21.35

Coefficient code and genetic coefficient description (units): PPSEN- Slope of the relative developmental response to photoperiod over time (positive for short day plants) (1 hr^{-1}), EM-FL- Duration from plant emergence to flower appearance (photothermal days), FL-SD- Duration from first flower to first seed (photothermal days), SD-PM- Duration from first seed to physiological maturity (photothermal days), LFMAX- Maximum leaf photosynthesis rate (mg CO_2 m^{-2} s^{-1}) and SFDUR- Seed filling duration for pod cohort at standard growth conditions (photothermal days).

Table 4. Calibrated and validated values for days to anthesis and physiological maturity of different genotypes (average across sowing dates)

Genotypes	Calibration 2022						Validation 2022					
	Days to anthesis			Days to physiological maturity			Days to anthesis			Days to physiological maturity		
	Simulated	Observed	% D	Simulated	Observed	% D	Simulated	Observed	% D	Simulated	Observed	% D
DBG-5	43	43	0	77	77	0	43	43	0	77	78	-1.3
DBG-19	44	44	0	78	79	-1.3	43	43	0	78	79	-1.3
DBG-31	44	44	0	78	78	0	43	43	0	78	78	0
DBG-33	44	43	2.3	77	77	0	43	44	-2.3	77	77	0
DBG-34	44	43	2.3	78	79	-1.3	43	44	-2.3	78	79	-1.3
DBG-93	44	44	0	78	79	-1.3	43	42	2.4	78	78	0
DBG-16	44	44	0	78	78	0	43	44	-2.3	78	79	-1.3
DBG-96	43	43	0	80	81	-1.2	43	43	0	80	81	-1.2
DBG-90	43	43	0	77	77	0	43	43	0	77	76	1.3
DBG-95	43	43	0	78	79	-1.3	43	44	-2.3	78	79	-1.3
DBG-61	43	42	2.4	81	81	0	42	43	-2.3	81	81	0
DU-1	44	43	2.3	77	77	0	43	43	0	77	78	-1.3

% D = Percent deviation, simulated– predicted values obtained from the DSSAT-CROPGRO model, observed– actual values recorded from field experiments.
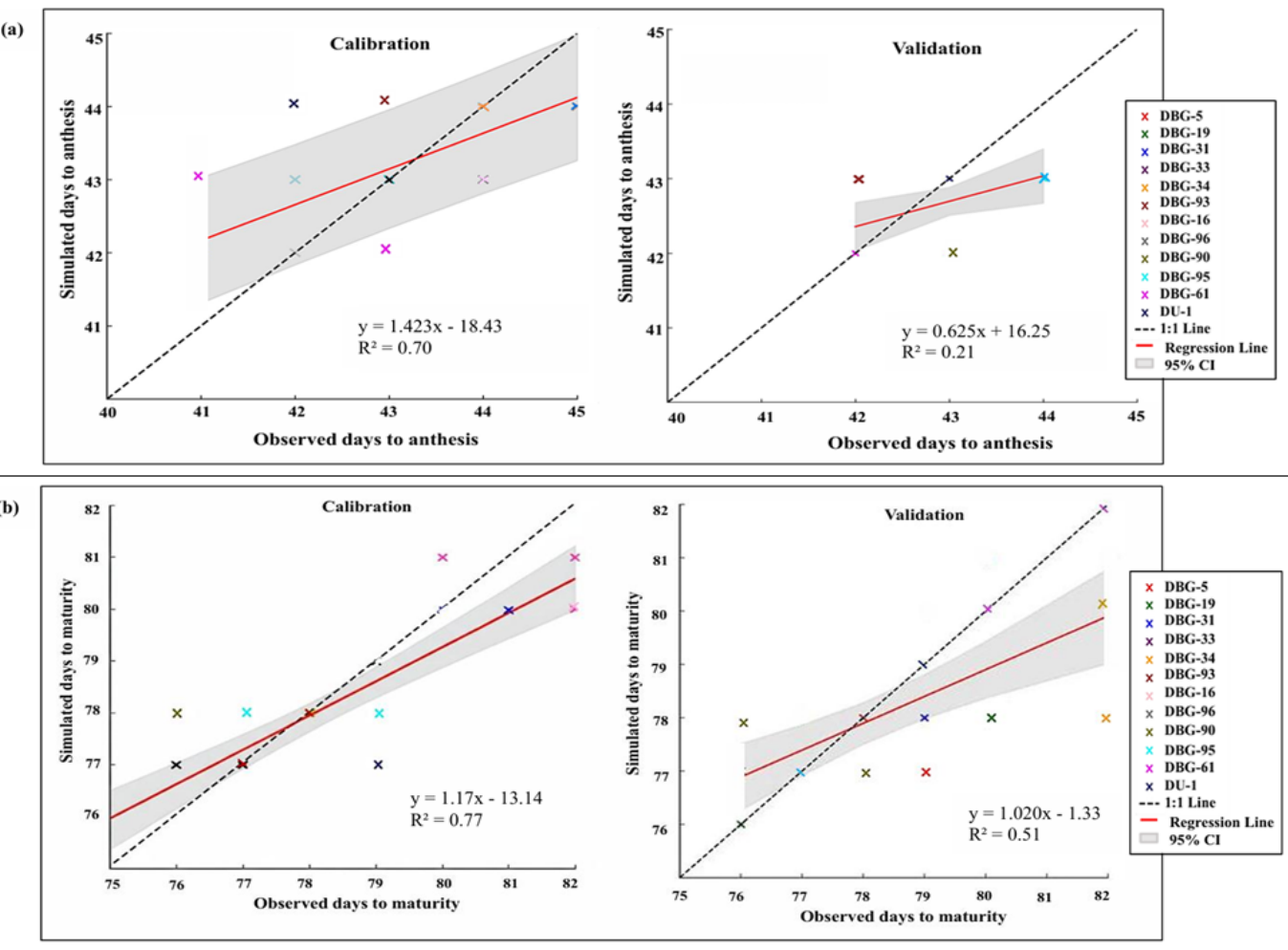

Fig. 1. Scatter plots comparing observed and simulated (a) days to anthesis (DAP) and (b) days to physiological maturity (DAP) during calibration and validation of the model. Each point represents a genotype, with colors indicating different genotypes as shown. The dashed line represents perfect agreement (1:1), while the solid red line indicates the fitted regression. Shaded bands denote the 95 % confidence intervals (CI) around the regression line. Regression equations and coefficient of determination (R^2) values are provided to indicate the goodness of model fit.

calibration generally exhibited a stronger fit than validation due to environmental and genotypic variability (19). The 95 % confidence intervals (CI) around the regression line further illustrated the statistical uncertainty of predictions. Most observed points fell within these intervals, confirming the robustness of CROPGRO simulations across genotypes. For anthesis, calibration showed a stronger correlation than validation and although the CI appeared wider in calibration, this reflected the influence of regression slope and data distribution rather than reduced accuracy, since simulated and observed values differed by only one day.

For physiological maturity, the CI bands were narrow in both phases, with only minor deviations reflecting statistical variation rather than model deficiency. Overall, the CROPGRO model reliably reproduced phenological events with high precision across genotypes. The lower R^2 for anthesis during validation reflects inherent differences among genotypes but does not compromise model reliability (20), as evidenced by model evaluation statistics showing accurate prediction (RMSE: 0-1.41 days, NRMSE: 0 % - 2.33 %, d-values: 0.889-1.0 during calibration; RMSE: 0-1.0 days, NRMSE: 0 %-2.38 %, d-values: 0.917-1.0 during

Table 5. Model evaluation statistics for phenology and yield of blackgram genotypes during calibration and validation

Parameter	Calibration			Validation		
	RMSE	NRMSE	d	RMSE	NRMSE	d
Days to anthesis	0-1.0	0-2.33%	0.917-1.00	0-1.0	0-2.38%	0.917-1.00
Days to physiological maturity	0-1.41	0-1.75%	0.889-1.00	0-1.0	0-1.28%	0.944-1.00
Grain yield (kg ha^{-1})	16.97-85.56	0.62-2.92%	0.943-0.998	78.1-127.28	2.89-4.71%	0.943-0.975

RMSE= root-mean-square error, NRMSE= normalized root-mean-square error, d= Index of agreement. Ratings are as follows: Excellent- NRMSE < 10 % of mean observed; Good- 10 % < NRMSE < 20 %; Satisfactory- 20 % < NRMSE < 30 %; Unsatisfactory- NRMSE > 30 %. Very good- d ≥ 0.9; Good- d ranges between 0.80-0.89; Moderate good- d ranges between 0.25-0.49; Very poor- d < 0.25 (18).

validation) (Table 5; for detailed genotype-wise evaluation, refer to supplementary Table S3). These results are considered acceptable, as some genotypes showed zero error, while others had deviations within ± 10 %, indicating good model performance. These findings are consistent with reports of similar results for chickpea calibration and validation in Gujarat, which showed percentage errors of 8.08 % for days to anthesis and 4.34 % for days to maturity (7). Similar results were also observed during calibration of the model for different legumes, supporting its reliability (21).

Model calibration and validation for grain yield at harvest maturity

The percent deviation between the simulated and observed values of grain yield fell within the range of -3.1 % to + 5.8 % during the calibration (2022) and validation (2022) phases. These results are considered satisfactory, as the deviations remain within ± 10 %, indicating a strong agreement between the simulated and observed data. Similar findings have been reported for chickpea in Gujarat, with grain yield errors of 7.9 % and acceptable error ranges were also observed across various legumes, confirming the model's reliability (7, 21). The 1:1 scatter plot (Fig. 2) clearly depict this agreement, as the data points cluster closely along the 1:1 line during both calibration and validation, demonstrating the model's ability to simulate grain yield accurately among genotypes. Regression analysis further confirmed this relationship, with $R^2 = 0.90$ during calibration and $R^2 = 0.57$ during validation, in line with earlier DSSAT studies for pulses reporting stronger calibration fits due to environmental and genotypic variability (19). The inclusion of 95 % CI in regression plots confirmed this reliability, as most simulated-observed pairs fell within the bands. Model evaluation statistics in Table 5 reinforce this performance, with RMSE values ranging from 16.97 kg ha^{-1} to 85.56 kg ha^{-1}, NRMSE from 0.62 % to

2.92 % and d-values from 0.943 to 0.998 during the calibration phase, while in the validation phase, RMSE values ranged from 78.1 kg ha^{-1} to 127.28 kg ha^{-1}, NRMSE from 2.79 % to 4.71 % and d-values from 0.943 to 0.975, all of which indicate excellent to very good model agreement. Detailed genotype-wise model evaluation statistics for yield are provided in supplementary Table S4.

Among 12 blackgram genotypes, DBG-61 showed the highest simulated grain yield, with an average deviation of -1.6 % (observed yield - 3342 kg ha^{-1}, simulated yield - 3290 kg ha^{-1}) during calibration and 2 % (observed yield-3230 kg ha^{-1}, simulated yield-3294 kg ha^{-1}) during validation. The genotype DBG-96 also closely followed higher yields after DBG-61, with a deviation of - 1.7 % (observed yield - 3180 kg ha^{-1}, simulated yield - 3126 kg ha^{-1}) during calibration and 2.6 % mean deviation (observed yield-3046 kg ha^{-1}, simulated yield-3124 kg ha^{-1}) during validation (Fig. 3 and supplementary Table S3). The superior yields of DBG-61 and DBG-96 can be attributed to the interaction between their slightly longer reproductive duration, particularly the extended seed-filling duration (SDPM) and efficient physiological traits. Although the reproductive phase is only 2-3 days longer than other genotypes, it allows prolonged photosynthetic activity (LFMAX), greater total assimilate accumulation and efficient partitioning of assimilates to seeds (XFRT, WTPSD; supplementary Table S1), resulting in higher grain weight. Genotypes with similar physiological traits but shorter reproductive phases and SDPM have less time to fully exploit these advantages, leading to comparatively lower yields. This highlights that small differences in reproductive duration, when combined with favorable physiological traits, can significantly influence final grain yield. These physiological traits not only enhance yield under variable environmental and sowing conditions but also make DBG-61 and DBG-96 valuable germplasm for breeding programs aimed at improving yield stability and efficiency in blackgram.
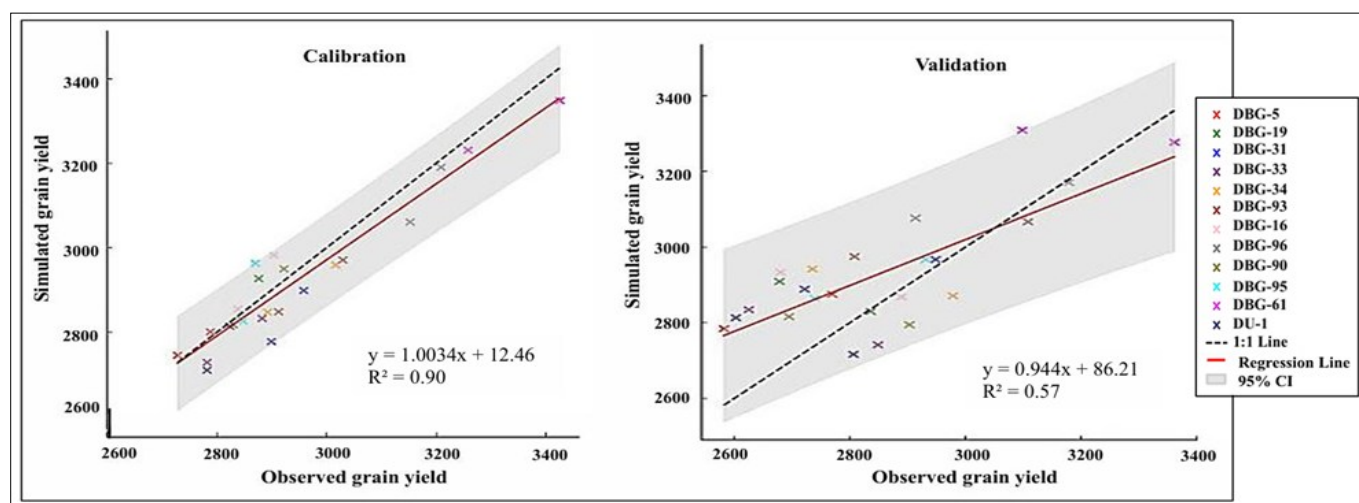

Fig. 2. Scatter plots comparing observed and simulated grain yield (kg ha^{-1}) during calibration and validation of the model. Each point represents a genotype, with colors indicating different genotypes as shown. The dashed line represents perfect agreement (1:1), while the solid red line indicates the fitted regression. Shaded bands denote the 95 % confidence intervals (CI) around the regression line. Regression equations and coefficient of determination (R^2) values are provided to indicate the goodness of model fit.
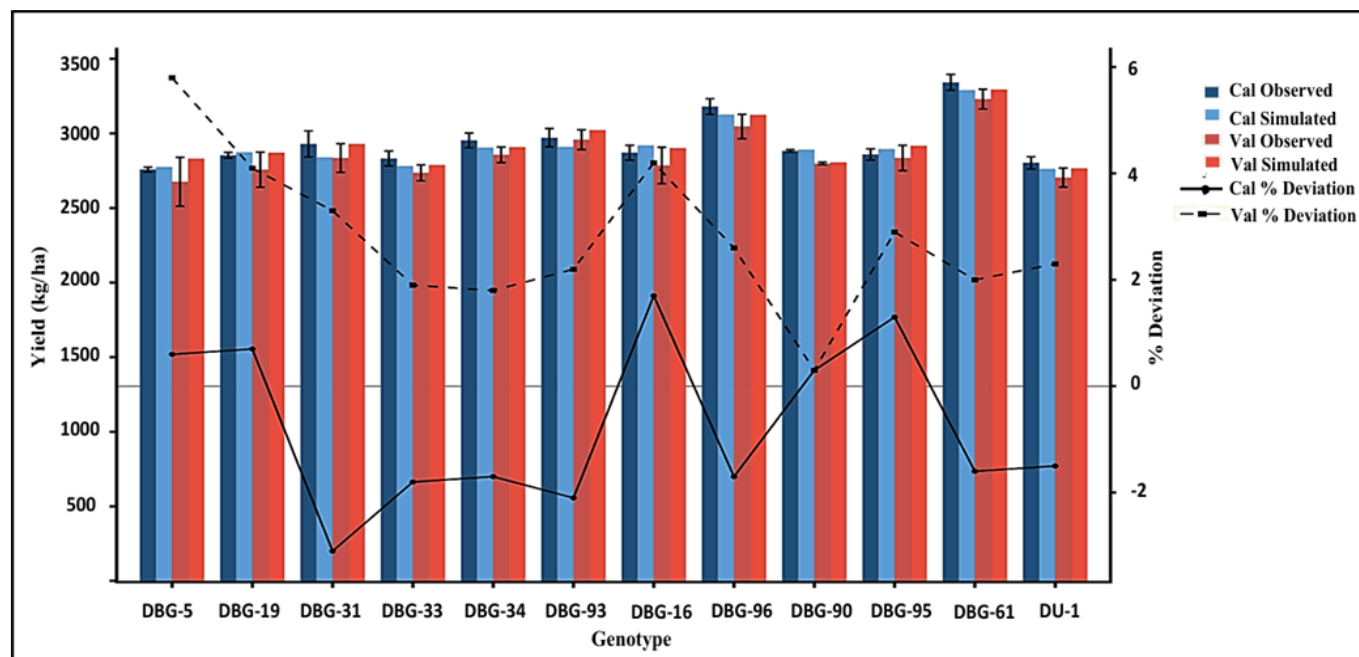
Fig. 3. Comparison of observed and simulated grain yield (kg ha^{-1}) across blackgram genotypes at harvest maturity during calibration and validation phases. Bars represent observed and simulated yields for calibration (blue shade) and validation (red shade), with error bars indicating standard deviations. Solid and dashed lines show percentage deviations between observed and simulated yields for calibration and validation respectively.

Conclusion

The genetic coefficients specific to 12 blackgram cultivars in the DSSAT-CROPGRO Drybean model were successfully optimized, with reliable performance across calibration and validation phases (RMSE < 2 days for phenology; RMSE 17-127 kg ha^{-1} for grain yield; d-index consistently > 0.94). Beyond validation, the model holds strong potential for applications in climate scenario analysis, precision agriculture and management optimization. Furthermore, the framework can be extended to other pulse crops, providing a valuable tool to support breeding strategies and enhance productivity under variable environments.

Authors' contributions

PA carried out the research work, including data collection, analysis and manuscript preparation. RHP served as the chairperson and provided overall guidance and supervision throughout the research and manuscript development. SCM and GM, as members under the MULLaRP scheme, provided input support for the experiment, offered valuable suggestions and guidance and assisted with manuscript review.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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