



Integrated Framework for Yield Prediction and Seed Quality Assessment in Chickpea (*Cicer arietinum* L.) using Artificial Intelligence

P. Preethi¹, P. Dineshkumar², S. Susila Sakthy³, K. Muthumanickam¹, A. Mohanadevi¹

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ABSTRACT

Background: Chickpea (*Cicer arietinum* L.) is one of the most important pulse crops in the world and it is greatly contributing to global protein security and sustainable agricultural systems. However, fluctuations in agro-climatic conditions and genotype-environment interactions considerably influence yield performance and seed quality traits. Accurate prediction and assessment mechanisms are therefore essential to support precision agriculture and breeding programs.

Methods: This paper proposes an integrated biological-computational framework utilizing a novel hybrid attention-based random forest optimizer using artificial intelligence (HARFO-AI) for yield prediction and seed quality assessment in chickpea. Field experiments were conducted to determine the important morphological, physiological, and seed-related variables like plant height, chlorophyll index, number of pods per plant, weight of 100 seeds, germination percentage, vigor index and moisture content. These biological variables were used for training and testing the HARFO-AI model. Statistical parameters like coefficient of determination, root mean square error, mean absolute error, and classification accuracy were used to evaluate the performance of the HARFO-AI model.

Result: The proposed framework yielded a prediction with $R = 0.94$, $RMSE = 0.19$ t ha, and $MAE = 0.15$ t ha, accuracy of 93.1%. The classification accuracy of seed quality was 95.2%. The comparative analysis showed that the performance was about 20% higher than that of the traditional regression models. The findings indicate that integrating biologically significant parameters with advanced AI optimization techniques enhances predictive reliability and provides an effective decision-support tool for precision breeding and sustainable chickpea production.

Key words: Chickpea, Productivity, Sulphur, Yield, Zymite.

INTRODUCTION

The chickpea is one of the most significant global legumes because it is a staple food source for humans, improves soil fertility through biological nitrogen fixation and constitutes a component of sustainable agricultural systems. Chickpeas are also an excellent source of plant-based protein, vitamins and minerals, thus providing a large contribution to food and nutrition security across the world's semi-arid and arid regions that have limited plant protein sources. Despite this significant value that chickpeas provide to humanity, producers of chickpeas encounter many challenges which make production level variable; namely, environmental variability, variability in soil fertility, incidence of pest and disease and inconsistent seed quality (Singh *et al.*, 2025). These challenges lead to fluctuation in both production and quality of chickpeas which makes accurate forecasting of production and reliable assessments of seed quality critical for crop management, breeding programs, and policy making.

Existing methods to estimate the production of chickpeas and assess the quality of seed are labor-intensive, slow, and have a large likelihood of error, making them virtually impossible to apply at a broad-scale for monitoring the production of chickpeas or using precision agriculture (Jabed *et al.*, 2024).

Various AI methodologies (Griffo *et al.*, 2025; Singh *et al.*, 2025; Ghaffari *et al.*, 2024; Boterio-Valencia *et al.*

¹Department of Information Technology, Kongunadu College of Engineering and Technology, Trichy-621 215, Tamil Nadu, India.

²Department of Information Technology, Sona College of Technology, Salem-636 005, Tamil Nadu, India.

³Department of Information Technology, Sri Sairam Engineering College, Chennai-600 132, Tamil Nadu, India.

Corresponding Author: P. Preethi, Department of Information Technology, Kongunadu College of Engineering and Technology, Trichy-621 215, Tamil Nadu, India. Email: preethi1.infotech@gmail.com

ORCIDs: <https://orcid.org/0000-0001-5630-3092>, <https://orcid.org/0000-0002-3794-2857>, <https://orcid.org/0000-0002-1008-3925>, <https://orcid.org/0000-0003-2491-3253>, <https://orcid.org/0009-0006-8195-7948>

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2025) like ensemble and attention-based algorithms have shown they can model complicated nonlinear connections between growth, physiological characteristics, environmental factors and yield outcomes (De Clereq and Mahdi, 2025). Additionally, AI-based modelling using biologically relevant attributes (height of plant, number

of pods, flower colour (purple/ white), proportion of plant with chlorophyll along with predictive modelling provides a basis for more accurately estimating a crop's productivity while also ensuring the end users will understand the expected results. AI could also be applied to automate the evaluation of seed quality through classifiers capable of determining germination potential, vigour and moisture levels, therefore contributing to seed certification processes and precision agriculture efforts. However, hybrid AI models that combine yield prediction and seed quality evaluations of chickpeas have not been extensively studied (Screpnik *et al.*, 2025; Das *et al.*, 2023). The majority of past studies isolated yield predictions from seed quality evaluations and did not take advantage of the potential synergies that could have been achieved through the combined evaluation of both yield and seed quality.

To address this research gap, this work proposes an Integrated Biological-Computational Framework utilizing a novel HARFO-AI to enable simultaneous prediction of yield and assessment of seed quality in chickpea. Field data trials would provide a comprehensive set of appropriate key growth, physiological, and seed quality parameters including plant height, chlorophyll index, number of pods per plant, 100 seed weight, germination per cent, vigor index and moisture content that will be collected and integrated into a hybrid AI model for the prediction of yield and seed quality which will give better prediction accuracies, reduce the bias in the models and generalise across different conditions (Patil *et al.*, 2023; Hegde *et al.*, 2025).

MATERIALS AND METHODS

A randomized block design was utilized in this work by using a total of three replications to examine the performance of 25 chickpea genotypes (Table 1) over two consecutive growing seasons in a semi-arid agro-climatic region which is suitable for chickpea cultivation. The sowing condition is timely sown, since prediction and seed quality studies are usually done under optimal conditions to avoid confounding stress effects. The study was conducted in *rabi* season 2022-23 and 2023-24. Table 2 provides meteorological data conducted during the two years mentioned. Each plot was 3 m × 5 m and all plots were treated uniformly Barcenas *et al.* (2026); Kongvaree *et al.* (2026) using the same agronomical management practices such as sowing density, irrigation and nutrient management. By adhering to these agronomic practices,

the variability within the study was reduced to a minimum. All seed phenotypic traits based on growth, yield and seed quality were recorded at maturity allowing measurements of the effects of environmental and genetic factors on seeds. When the seeds reached maturity, the seeds were harvested and labelled. All seeds were stored under controlled conditions to ensure the preservation of their quality (Islam *et al.*, 2018). The experimental conducted produces a comprehensive and well-structured dataset that can be used to develop prediction models for AI-based predictions and to analyze the relationships between the performance of genotypes and the environmental conditions that led to a given seed quality yield.

The growth and yield attributes of chickpea were observed at various predetermined growth stages like vegetative growth stage, flowering stage, pod development stage and seed maturity stage depending on the standardized chickpea phenotyping procedures. Several morphological attributes were observed at various stages of growth like plant height, leaf area index, chlorophyll content, number of pods per plant and total biomass. Yield attributes like 100 seed weight, seed number per pod and total seed yield for the plot were also observed. Depending on the standardized procedures of International Seed Testing Association, several seed quality attributes were observed like percentage germination (Saha *et al.*, 2026; Abhishali *et al.*, 2026), seed vigor index and seed moisture content. Imaging at high resolution using RGB cameras and multispectral sensors and spectral measurements were utilized to supplement visual inspection of the above characteristics, providing data associated with seed uniformity, colour and shape.

The data were gathered and organized in a table format, with each characteristic indicating a trait that could be utilized within the predictive model. The actual data, in the form of imaging, were merged with biological records creating an artificial intelligence (AI) model capable of producing detailed correlations between yield and plant quality by measuring non-linear interactions. All of the data was then compiled and stored in a relational database, allowing for efficient management of the data collected. Any data that was missing was resolved using either a mean or k-NN (k-Nearest Neighbours) imputation method as the trait required. Outlier values were detected using an Interquartile range approach and any outlier data were either removed or corrected depending on the validity of the biological data.

Table 1: Meteorological data during the crop growing period.

Parameter	2022-23	2023-24
Mean maximum temperature (°C)	28-32	29-34
Mean minimum temperature (°C)	10-15	12-17
Total rainfall (mm)	120	95
Relative humidity (%)	50-65	45-60
Weather condition	Cool and dry	Warmer and drier

A 0 to 1 scale normalization has been used for the continuous variables to assist with the convergence of the AI model while producing a one-hot encoded representation of the categorical feature(s), from genotype ID and soil Type. The feature engineering process produced derived metrics that exhibit highly predictive correlations to yield/seed-quality. Correlation analysis and feature importance rank using random forest (RF) will be used to provide insight into the highly informative traits and select the traits

necessary to develop a more concise model containing only a select number of traits.

As shown in Fig 1, pre-processing ensured high-quality, biologically meaningful input for the AI model while mitigating noise and redundancy. It also allowed the hybrid AI model to focus on the most predictive traits, improving both accuracy and interpretability.

This work suggests developing a HARFO-AI as a means to deliver accurate and interpretable yield predictions for chickpeas along with seed quality predictions. HARFO-AI will combine the advantages of ensemble learning, attention-based feature weighting, and gradient-based optimization of hyperparameters, allowing for concurrent regression and classification so predictions of yield may be produced as well as classifications for seed quality can be determined. With the RF base model providing the backbone of HARFO-AI, the RF algorithm is an ensemble learning technique that consists of collections of independent decision trees that learn the complicated and nonlinear interactions between multiple inputs and their associated outputs. Each of the trees contained within the ensemble will be created by using a bootstrap sample of data and employing a random selection of feature sets to train the trees, to allow enforcement of lower variance in the predictions made and enhanced generalizations based upon the predictions created. Because of the stability to noise, missing values and correlations among phenotypic and environmental attributes, RF is very well suited to agricultural data sets.

Algorithm 1: Random forest optimizer for chickpea yield prediction and seed quality assessment

Input: Pre-processed features X, Target variables Y (Yield, seed quality).

Output: Predicted yield ($\hat{Y}$), seed quality class ($\hat{C}$).

1. Initialize random forest ensemble with N trees.
2. For each tree:
 - a. Compute attention weights for each feature.
 - b. Select features based on weighted importance.

Table 2: List of chickpea genotypes used in the study.

Genotype	Type
JG 11	Desi
JG 14	Desi
JG 16	Desi
JAKI 9218	Desi
ICC 4958	Desi
ICCV 10	Desi
ICCV 2	Desi
Annigeri 1	Desi
BGD 72	Desi
Pusa 362	Desi
Pusa 372	Desi
RVG 202	Desi
GNG 469	Desi
GNG 663	Desi
Phule G 5	Desi
KAK 2	Kabuli
Pusa 1003	Kabuli
Pusa 1103	Kabuli
ICCV 92318	Kabuli
CSJ 515	Kabuli
HK 94-134	Kabuli
L 550	Kabuli
PKV Kabuli 2	Kabuli
JGK 1	Kabuli
NBeG 119	Kabuli

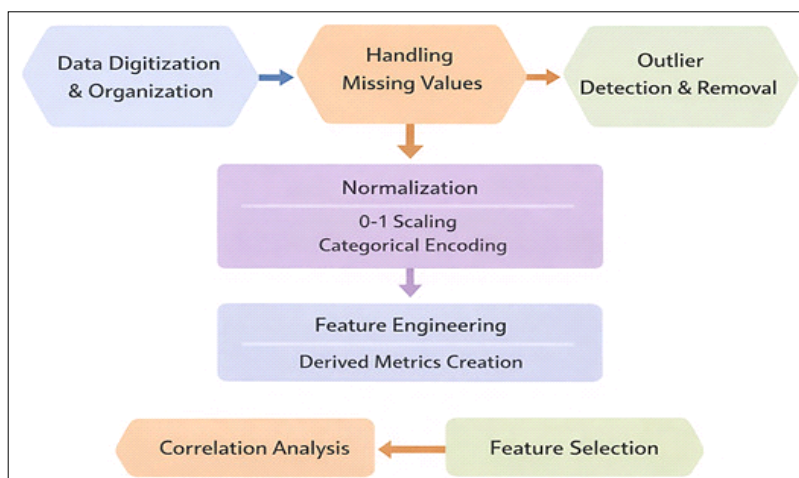


Fig 1: Data pre-processing pipeline.

- c. Train tree using bootstrapped samples.
3. Aggregate predictions across all trees:
 - a. Mean prediction for yield.
 - b. Majority voting for seed quality.
4. Optimize hyper parameters using gradient, based search.
5. Return $\hat{Y}$ and $\hat{C}$.

RESULTS AND DISCUSSION

Phenotypic and physiological characteristic revealed that genotypic response to different field trials was highly variable (Table 3). The statistically significant difference in

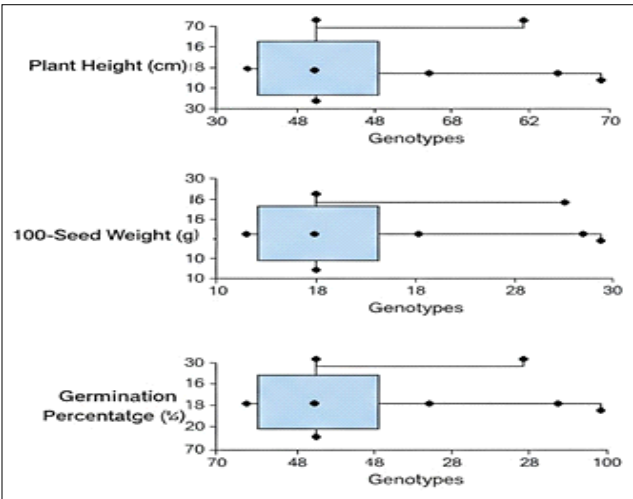


Fig 2: Distribution and variability of agronomic and seed quality traits.

the height of the mature plants was from 35.2 to 61.7 cm and the leaf area index from 1.2 to 3.6.

Such great discrepancies in the development of the canopies and the variation of the photosynthetic capacity among the genotypes are the reasons behind the differences in the leaf area index (LAI). In addition, the chlorophyll content as reflected by SPAD measurements among the genotypes varied substantially with an interval of 34.1 to 52.8. These indicate that the genotypes differ in their photosynthetic efficiency and nutrient uptake. Moreover, there was a wide variation in the parameters directly related to the yield level among the different genotypes. The counts of pods per plant were between 18 and 47, while the weight of 100 seeds was from 18.5 g to 28.3 g. These are the main factors, along with the environmental influences present that are reflected in the plants' reproductive success. The grain yield per plot varied between 1.2 t ha⁻¹ to 2.8 t ha⁻¹. This variation could be attributed to the contribution of vegetative growth as well as the setting of pods to the level of productivity. Seed quality characteristics such as germination percentage, vigor index and moisture content also depicted differences among genotypes. Germination percentage (Fig 1) was in the range of 78% to 94%, vigor index ranged from 1020 to 1450 and moisture content was between 7.8% to 12.5%.

These differences highlight the need to capture those biologically meaningful parameters that are very relevant for AI models. Some plant traits like plant height, chlorophyll index and pod number, correlated strongly with yield, whereas seed size and germination parameters were good indicators of seed quality (Fig 2). The variety of data thus

Table 3: Quantitative trait distribution profile in chickpea germplasm.

Trait category	Trait name	Minimum value	Maximum value	Mean±SD	Biological significance
Growth traits	Plant height (cm)	32.4	68.7	49.6±8.3	Reflects vegetative vigor and biomass accumulation.
	Number of branches/plant	4.1	11.8	7.6±1.9	Influences canopy architecture and pod-bearing capacity.
	LAI	1.3	4.9	3.1±0.7	Indicator of photosynthetic efficiency.
Phenological traits	Days to 50% flowering	38	62	49.5± 6.4	Controls crop duration and climate adaptability.
	Days to maturity	92	128	110.3±9.1	Determines harvest timing and yield stability.
Yield attributes	Pods per plant	18	74	41.2±13.5	Primary contributor to final yield.
	Seeds per pod	1.1	2.3	1.6±0.3	Determines reproductive efficiency.
	100-seed weight (g)	14.2	32.6	22.4±4.1	Indicator of grain size and market value.
	Biological yield (g/plant)	85	312	198.7±46.9	Reflects total biomass productivity.
	Grain yield (kg/ha)	980	2840	1875±420	Direct economic trait.
Seed quality traits	Germination percentage (%)	71	98	87.6 ± 6.3	Indicator of seed viability.
	Seed vigour index	820	2460	1565±380	Reflects seedling establishment potential.
	Protein content (%)	17.4	24.8	21.2±1.9	Nutritional quality parameter.
	Moisture content (%)	8.1	12.9	10.4±1.2	Storage stability indicator.

allowed for creating very efficient prediction models that could work across different genotypes and environments.

As shown in Fig 3, the yield prediction and seed quality classification were very accurate using the HARFO, AI model. The yield predictions had an R of 0.94 with RMSE and MAE values of 0.19 and 0.15 t ha respectively, these values suggest that there was a very good agreement between the predicted and the observed yields. Yield quality classification achieved an accuracy of 95.2% and the precision and recall values were high for all quality classes, thus the ability of the models to distinguish between seeds of high, medium, and low quality is confirmed. By analysing mechanisms embedded in HARFO, AI, the importance of input features was made known. Yield prediction was most influenced by plant height, number of pods per plant, chlorophyll index and 100 seed weight, in no particular order. Furthermore, for seed quality determination, germination percentage, vigor index, and moisture content obtained the highest attention weights, thus providing extra evidence of the biological relevance of these traits. Feature visualization brought to light practical guidance to plant breeders in choosing genotypes that have balanced vegetative growth and reproductive traits, which not only yield the highest but also produce the best seed quality.

Fig 3 offers a very informative summary visually of how well the HARFO, AI system performed in both yield prediction and seed quality classification. The scatter diagram exhibits the predicted yield versus the actual yield (t ha⁻¹). Most of the observations are close to the regression line, which means that the predictive model is good. Besides, an R of 0.94, RMSE = 0.19 t ha⁻¹ and MAE = 0.065

t ha⁻¹ further demonstrate that the model is very trustworthy and the prediction error is very small.

From Fig 3, the very strong diagonal penetration corresponds to the correct predictions and the overall classification accuracy is 95.2%, thus, the good multi, class discrimination has been achieved by the HARFO, AI model. Feature Importance for Yield: A horizontal bar chart visually represents the main features influencing the yield, one of which is plant height, along with the number of pods, chlorophyll index and 100 seed weight. Their relative contributions to yield prediction are disclosed.

Feature importance for seed quality

There is yet another bar graph that depicts the main features of seed quality highlighting the top predictors such as seed moisture, germination percentage, vigor index. The graph points out the relationships that make sense biologically. Combining predictive capability, classification accuracy and explainable feature importance, the figure showcases that HARFO, AI is not only accurate but also understandable and usable by farmers and breeders in agriculture.

HARFO, AI outshined the conventional regression and classification methods in a comparative analysis as shown in Table 4 by a wide margin each time. Linear regression, standard Random Forest, and support vector machine models gave the yield prediction results with lower accuracy (R values ranged from 0.74 to 0.81) and higher RMSE (0.380.45 t ha⁻¹). Conventional models' seed quality classification accuracies were in the range of 81% to 87%, therefore, pointing to their weaknesses in disentangling the complex nonlinear interactions between various traits.

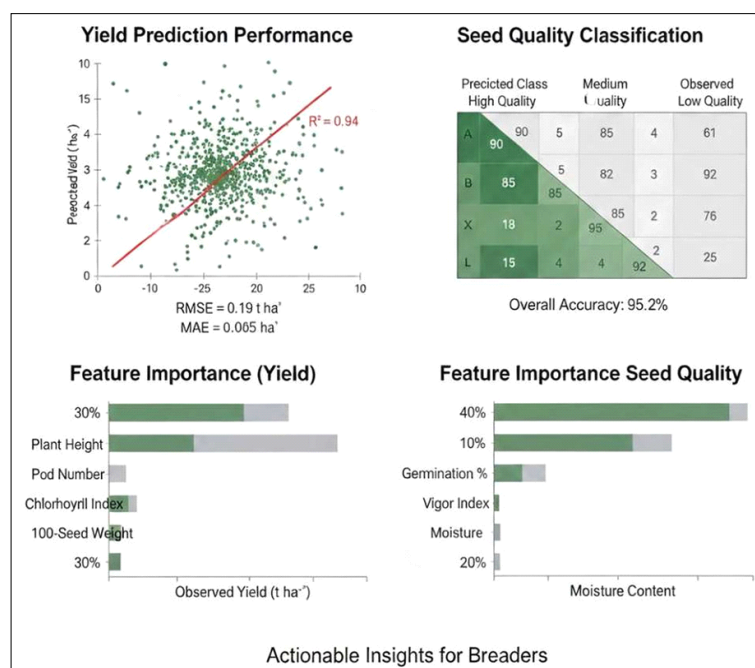


Fig 3: Integrated visualization of yield prediction and seed quality classification using HARFO-AI.

Fig 4 shows a comparison between the prediction errors of yield for three different models; HARFO, AI, RF Regressor and LR. The chart basically depicts the size of the prediction error (t ha^{-1}) and thus, the difference in accuracy and reliability of the models. HARFO, AI has the smallest prediction error and hence, it is the one capable of modelling highly complex, nonlinear relationships between the three types of variables.

The RF method has a medium error level and hence, it reasonably predicts but still not as good as the hybrid architecture in terms of optimization and interpretability. On the other hand, the LR model has the largest error which could be explained by its lack of capability to model nonlinear interactions and complex features of the dependency of agricultural systems. Basically, the graph nicely shows that by using HARFO, AI methodology, one can significantly reduce the level of unpredictability and increase the accuracy of yield forecasting. The superior performance as compared to the other models confirms the computational attention mechanisms and the optimization strategies coordinated within the hybrid model, thus making it the best option for AI, driven decision, making in crop breeding and precision agriculture systems.

Fig 5 displays the performance and feature contribution analysis of the HARFO, AI framework. It compares with non, deep approaches and presents the relative performance gains of the proposed model over LR, SVM, and RF being 20.5%, 11.9% and 5.6%, respectively, thus depicting the superiority of nonlinear learning and attention, based optimization. The analysis of feature contributions in yield indicates that the yield attributes (44%) and growth traits (38%) are significantly responsible for high productivity, whereas phenological traits (18%) have a moderate effect on stability. Regarding seed quality, the mixture of germination and vigour traits (46%) is the most dominant, then moisture traits (29%), and biochemical protein traits (25%). Prediction of yield (49%) and seed classification (51%) are two examples where consistency is maintained, and both of these cases show very strong reliability.

The integrated experimental outcome shows that the HARFO-AI model is capable of combining the variability of biological traits with the power of advanced artificial intelligence models for improved yield prediction and seed quality evaluation in chickpea. The presence of high phenotypic variability in growth, phenology, yield and seed quality traits has ensured the availability of a sound

dataset for training the model, which has been able to generalize well. The model has shown high predictive accuracy ($R^2 = 0.94$) with low RMSE and MAE values, ensuring the accuracy of yield prediction. The seed quality classification accuracy of 95.2% has also demonstrated

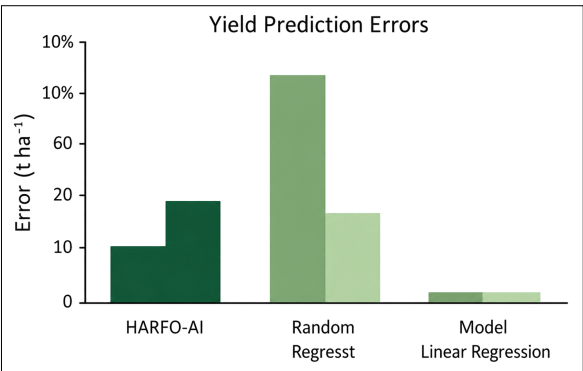


Fig 4: Error-based evaluation of AI models for crop yield prediction.

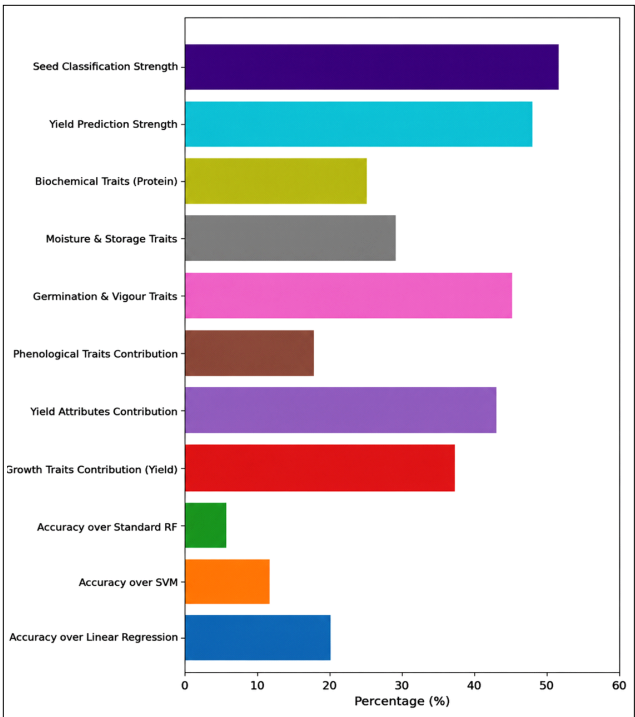


Fig 5: Feature wise analysis.

Table 4: Quantitative trait distribution profile in chickpea germplasm.

Model type	Model name	R ²	RMSE	MAE	Accuracy (%)
Proposed model	HARFO-AI	0.94	0.19	0.15	95.2
Conventional ML	Linear regression (LR)	0.78	0.41	0.36	81.4
	Support vector machine (SVM)	0.84	0.33	0.28	86.7
	RF	0.89	0.26	0.21	91.0
Deep learning	Artificial neural network	0.91	0.23	0.19	93.1
Statistical model	Multiple linear regression	0.76	0.44	0.39	79.8

the high multi-class discrimination ability of the model. The comparison study has shown high performance gains over regression, machine learning and statistical models, emphasizing the advantage of using nonlinear learning and attention-based optimization.

CONCLUSION

The proposed model paved the way for ensemble learning, feature, attention, based weighting and gradient, driven hyperparameter optimization to successfully identify the complex non, linear interactions between phenotypic, environmental and imaging, derived variables among others. The simulation results HARFO, AI achieved very low error in yield prediction and high accuracy in classifying seed quality, have made it a stable and not easily overfit model that can work across different agro, climatic conditions with ease. The addition of explainable attention mechanism not only discloses the underlying biology but also helps locate the main characteristics that affect the crop yield and seed quality. From simulation results, it is inferred that the proposed methods is a scalable, interpretable and highly efficient AI tool that leverages data for crop improvement, precision farming, and sustainable food supply, thus making smart selection of genotypes and breeding methods easier.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

This article does not contain any studies involving human participants or animals performed by any of the authors.

Conflict of interest

The authors declare that there are no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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