International Academic Institute for Science and Technology

International Academic Journal of Science and Engineering
Vol. 12, No. 4, 2025, pp. 211-223.

ISSN 2454-3896

International Academic Journal of Science and Engineering

www.iaiest.com

Genomic Insight–Enabled Economic Forecasting for Sustainable Agri-Biotech Markets

K. Ajitha [a], Dr.C. Samuel Joseph [b], Dr.D. Mahila Vasanthi Thangam [c], Dr.K. Lakshmipriya [d]

[a] *Department of Commerce and International Trade, Karunya Institute of Technology and Sciences, Coimbatore, Tamil Nadu, India. E-mail: ajithakaju007@gmail.com, Orcid: https://orcid.org/0000-0003-2477-410X*
[b] *Professor & Head, MCC Boyd Tandon School of Business, Chennai, Tamil Nadu, India. E-mail: samuelclarence15@gmail.com, Orcid: https://orcid.org/0000-0002-4745-1314*
[c] *Department of Commerce and International Trade, Karunya Institute of Technology and Sciences, Coimbatore, Tamil Nadu, India. E-mail: mahila@karunya.edu, Orcid: https://orcid.org/0000-0001-9922-0238*
[d] *Department of Commerce and International Trade, Karunya Institute of Technology and Sciences, Coimbatore, Tamil Nadu, India. E-mail: lakshmipriya@karunya.edu ,Orcid: https://orcid.org/0000-0003-0699-8775*

Abstract

The unstable climate-induced yields, rapid pathogen evolution, fluctuating commodity prices, and increasing demand for high-performing, genetically improved crops are contributing to unprecedented uncertainty in global agri-biotech markets. Economic forecasting tools rely on historical market patterns and conventional yield statistics while ignoring the genomic traits that fundamentally determine crop resilience, input efficiency, and long-term productivity, thus showing structural limitations. Decreased sustainability across the value chain, economic decisions made without accounting for the genetic architecture that drives agricultural performance, and inaccurate market predictions and misaligned investments are the major real-time problems created by this disconnect. The integration of genomic selection indices, trait heritability, genotype–environment interactions, molecular breeding values, and sequence-based performance markers into advanced AI-driven economic models is the observation of this study, a genomic insight–enabled economic forecasting framework that highlights this gap. Enabling early identification of profit instability, resilience gaps, and market opportunities by linking economic variables to genomic predictors in Simulation experiments improves forecasting precision by 12–18% compared to traditional models. Connecting genomic performance metrics to value-chain economics for the framework supports decision-making for gene-edited crops, microbial biofertilizers, and next-generation biotechnology products, and the study concludes with greatly enhanced prediction accuracy, strengthens resilience planning, and provides a scientifically grounded, future-ready approach to sustainable agri-biotech market development using economic forecasting by incorporating genomic insights.

Keywords: Genomic Forecasting, AI-Driven Econometrics, Genotype–Environment Interaction, Molecular Breeding Values, Agri-Biotech Markets, Economic Prediction Accuracy.

DOI: 10.71086/IAJSE/V12I4/IAJSE1290
Received: 06 October 2025/Revised: 10 November 2025/Accepted: 08 December 2025/Published: 30 December 2025

Introduction

The agri-biotech industry is experiencing a radical change driven by rapid advances in genomics, molecular breeding, and crop innovation enabled by biotechnology (Pasupuleti, 2023). The developments have brought new possibilities for enhancing agricultural productivity, climate resilience, and sustainable food production (Nguyễn et al., 2024). But with global markets shifting due to climatic shocks, geopolitical dynamics, supply chain crises, and changing consumer preferences, economic forecasting for the agri-biotech sector has become more complex (Pasupuleti, 2024). The old market-prediction techniques are no longer applicable to predict future performance in an industry where biological innovation is changing faster than market analytics, such as historical production data, linear econometric models, or commodity trends. Such increasing disparity between biological possibilities and economic prediction capabilities has left the investors, breeders, policymakers, and biotechnology enterprises in doubt (Serraj & Pingali, 2018).

The first problem is that current economic models do not account for genomic factors that determine agricultural productivity and resilience (Gai et al., 2025). There are direct impacts of genomic knowledge, such as trait heritability, genomic estimated breeding value (GEBV), genotype-by-environment interaction (GxE), and allelic diversity and molecular marker profiles, on yield potential, heat tolerance, nutrient efficiency, and disease resistance (Kumar et al., 2015). The above genetic qualities determine the performance of biotech products, and, as a result, their market value. However, economic prediction frameworks rely little on genomic data, which is a prominent blind spot in their forecast accuracy. Indicatively, a pair of crop types might seem to be the same in the conventional yield data but vary a lot in the traits of genomic stability, which causes erroneous forecasts of the future performance and economic gains (Coomes et al., 2019).

The inclusion of genomic information in economic forecasting is a radical solution. By correlating genomic predictors with financial variables, it is possible to predict revenue with much greater accuracy based on yield, variability in input costs, product reliability, and market competitiveness (Bhuiyan et al., 2023). This is particularly important for agri-biotech products such as gene-edited crops, microbial inoculants, biofertilizers, and molecular breeding technologies, for which market success relies on genomic efficiency as much as economic viability (Gai et al., 2025). The dawning access to massive genomic datasets, aided by sequencing approaches, bioinformatics websites, and phenomics, offers a chance never before seen to create predictive economic frameworks that capture genuine biological possibilities (Celis et al., 2024).

In this paper, I present a new genomic knowledge-driven economic forecasting model that bridges the gap between biological information and economic forecasting (Wójcik-Gront et al., 2024). The framework brings together the light of genomic trait data and AI-based econometric models, enabling multi-layered predictions that simultaneously consider the uncertainty in the environment, biological performance, and market dynamics (Taheri Hosseinkhani, 2025). The model predicts economic outcomes using machine learning algorithms and multi-trait predictive tools and can be used to simulate economic outcomes under different climate, market, and genetic conditions, providing stakeholders with a strong decision-support mechanism (Santos del Río et al., 2025).

Finally, analysing the economy using genomics will contribute to a stronger, more sustainable agri-biotech market. It enables breeders to plan genomic selection based on economic prospects, helps investors estimate the long-term profitability, and allows policymakers to draft genomic-based agricultural policies. By integrating biological performance and economic forecasting, the proposed model creates a visionary methodology that reinforces the sustainability of the global food system, reduces financial risk, and promotes sustainable agri-biotech innovation.

Literature Review

The rapid development of agricultural biotechnology has transformed the face of food production worldwide, with genomics among the strongest drivers of innovation (Bennett & Jennings, 2013). Early agricultural productivity research has mainly focused on phenotypic selection and agronomic management of plants and crops, based on field observations and tracking environmental conditions to forecast crop performance (Khan, 2024). Nevertheless, as agricultural problems have become increasingly complex due to climate change, soil erosion, insect adaptation, and market fluctuations, the focus of research has shifted to the molecular understanding of crop behaviour (Ulimaz et al., 2024). The emergence of genomic methods, including high-throughput sequencing, genome-wide marker profiling, and transcriptomic analysis, was a significant breakthrough, enabling the accurate identification of traits that determine yield, resilience, and nutrient efficiency (Singh et al., 2021). It was these tools that were able to predict, long before the appearance of physical characteristics, the performance of a biological entity and the strategy of crop improvement.

While all this has been happening, there have also been impressive developments in agricultural economic forecasting models (Tyagi et al., 2024). The classical approaches were based on past price trends, yield, and supply-and-demand curves to forecast market conditions. Econometric models and time series were popular for forecasting price changes and production trends. Still more recently, machine learning has also enhanced forecast accuracy by capturing nonlinear interactions among weather conditions, trade flows, and agronomic variables (Bosco et al., 2018). Nevertheless, although these advancements have been made, traditional economic models remain inherently constrained, as very few account for genetic or molecular predictors that can determine crop performance. As a result, predictions are usually inefficient at identifying the biological variability and resilience that are embedded in genomic characteristics.

The current interest in sustainable agriculture and climate-resistant production has heightened the significance of genomics for market behaviour. Trait-based knowledge, including drought tolerance, nitrogen use efficiency, pest resistance, and early vigour, has a direct relationship with production stability, cost structure, and market competitiveness. Such benefits of genomics are particularly vital to the developing industries of gene-edited crops, microbial biofertilizers and precision-breeding technologies, whose economic success hinges on genetic performance. However, there are limited market models to predict genomic returns using financial measures, which prevents stakeholders from predicting economic transitions driven by biotechnology.

The significance of biological data and predictive analytics is increasingly a topic of recent literature (Sravan Kumar Reddy & Supraja,2025; Razzak et al., 2020). Research shows that combining genomic prediction systems with environmental and management factors yields more precise estimates of crop performance. Similarly, economic studies indicate that AI-based forecasting systems are superior to classical ones because they incorporate dynamic, multivariate data. Nevertheless, a fully integrated genomic-economic forecasting method has yet to be developed, leaving a significant gap in the development of actionable decision-support tools for agri-biotech markets (Umamaheswari, 2025).

Altogether, the existing literature indicates that it is essential to identify a common denominator between genomics and financial analytics to develop a single forecasting system (Dinov, 2018). This kind of integration will reduce uncertainty, improve investment effectiveness, help set breeding targets, and support sustainable market development. The new interdisciplinary character of agri-biotech economics creates a unique opportunity to develop forecasting models that incorporate biological prospects and market realities, and to build even more resilient, data-driven agricultural systems.

Methodology and Conceptual Framework

Conceptual Integration Framework

The combination of genomic predictors, economic indicators, and environmental variables is used with the multilayered forecasting engine from the integration framework. The genomic layer extracts trait-based performance metrics; the economic layer analyses market behaviour, revenue flows, and input cost dynamics; and the simulation layer evaluates interactions under real-world stress scenarios. These are the three analytical layers. The allelic diversity, trait heritability, marker associations, and genotype–environment responses are the Key genomic inputs, and the price indices, demand elasticity, production costs, input price shocks, and value-chain fluctuations are the Economic inputs. Rainfall deviation, temperature anomalies, drought index, and stress accumulation over time are the Environmental parameters that are involved. The genomic and economic signals are integrated using a weighted influence equation.

$$F_t = w_g G_t + w_e E_t + w_m M_t \quad (1)$$

where $G_t$as genomic predictors, $E_t$environmental stressors, and M_tMarket indicators.

Simulation parameters include: climate variability range (±35%), market price shock amplitude (5–25%), genomic reliability (0.55–0.90), and genotype-environment fit probability. Based on the result of the biological and economic drivers, the framework enables realistic forecasting of the biotech market.

Genomic Trait Extraction and Data Structuring

Economic forecasting is integrated by extracting genomic traits, which involve converting raw molecular sequence data into structured, analysable trait indicators. Using quality thresholds such as minor allele frequency (≥0.05), call rate (≥95%), and linkage disequilibrium pruning to ensure data reliability when filtering the genotypic matrices, Raw SNP marker datasets, and sequencing reads. The phenotypic traits, including drought tolerance, nitrogen-use

efficiency, pest resistance, biomass accumulation, and yield stability across environments, are getting aligned with the extracted markers. Rainfall deviation, soil organic carbon, and temperature stress are the Environmental covariates incorporated to support multi-environment trait predictions.

A genomic trait matrix $T$is constructed as:

$$T = XW \tag{2}$$

where $X$is the SNP genotype matrix and Wrepresents estimated marker effects.

SNP count (5,000–50,000), marker reliability (0.65–0.90), and noise injection (3–7%) are included to replicate field variability. Simulation parameters for multi-trait prediction and economic modelling. This structured genomic dataset serves as the foundation.

Marker-Assisted Trait Identification

Mapping key SNPs and QTL regions associated with economically relevant traits is the primary focus in marker-assisted identification to detect significant genomic regions contributing to yield stability, stress resilience, and resource-use efficiency using linkage analysis, genome-wide scans, and association mapping. False discovery rate ($\leq$0.05) and effect size filtering are important markers determined by these statistical thresholds. To ensure stable expression under climatic variability, the Identified markers are validated across multiple environments.

The marker–trait association model is expressed as:

$$Y = \mu + \sum_{i=1}^{n} X_i \beta_i + e \tag{3}$$

where $Y$is trait value, $X_i$is a marker genotype, $\beta_i$marker effect, and eResidual error.

Marker count 3,000–10,000, association significance p $\leq$ 0.001, QTL variance explained 5–20%, and environment interaction factor 0.3–0.6 are the Simulation parameters that include the economic forecasting model, which gets biologically meaningful predictors linked directly to financial stability to ensure reliable marker identification.

Genomic Estimated Breeding Values (GEBV)

Predicting future performance, the genetic merit of a genotype is quantified by GEBV, which integrates SNP effects, trait heritability, trait covariance, and genotype environment interactions. They predict long-term yield potential and input-efficiency gains, which directly affect profitability through economic forecasting of essential GEBV values. The genomic BLUP (Best Linear Unbiased Prediction) or Bayesian methods to integrate large numbers of markers using the GEBV calculation

The GEBV model is:

$$\hat{g} = K\alpha \tag{4}$$

where $K$is the genomic relationship matrix and $\alpha$is the vector of marker effects.

- heritability (0.30–0.70),
- relationship matrix size (500–5,000 genotypes),
- shrinkage factor (0.05–0.20), and
- cross-validation folds (5–10)

Are the Simulation parameters included?

Integration into the economic prediction system, ensuring consistent scaling across traits and environments, and ensuring that the GEBV was standardised.

Economic Forecasting Model Design

to simulate long-term financial results. The economic forecasting model integrates genomic predictors, climate modifiers, and market-variability indicators and combines them with machine learning to forecast price movements, revenue stability, demand for biotech seeds, and profit margins using dynamic econometrics. Production cost trends, supply–demand ratios, elasticity coefficients, seasonal price indices, and technological adoption rates are the Key economic inputs included. GEBV-based yield predictions—feed directly into revenue simulations are the Genomic variables.

The core forecasting equation is:

$$E_t = f(Y_g, P_t, C_t, V_t) \quad (5)$$

Where,

E_t is economic output,

Y_g genomic yield prediction,

P_t price index,

C_t cost index, and

V_t Volatility factor.

Simulation parameters included:

- price shock amplitude (5–25%),
- cost variation (3–15%),
- yield variation due to genomics (10–30%), and
- market elasticity (0.4–0.9)

Both biological and financial drivers are reflected in the forecasting outputs, ensuring the integrated design.

Price Elasticity and Market Trend Modelling

The Price elasticity modelling assesses how changes in biotech seed prices, production costs, and consumer demand impact overall market dynamics. High-performance genotypes reduce input costs and stabilise supply, moderating price sensitivity, which is why genomic performance influences Elasticity incorporating the multi-year time series of commodity prices, adoption rates, and climate-driven yield shocks by the Market trend model.

Price elasticity is modelled using:

$$E_p = \frac{\Delta Q/Q}{\Delta P/P} \quad (6)$$

where E_p is price elasticity, Q Quantity demanded, and P Price.

Simulation parameters included:

- Baseline Price Elasticity (-0.3 to -1.2),
- Demand Sensitivity (5–18%),
- Climate-Induced Price Rise (3–12%), and
- Genomic Supply-Buffering Coefficient (0.1–0.4).

To simulate real-world unpredictability, trend modelling using 15-year historical datasets combined with synthetic shocks allows accurate forecasting of biotech seed adoption, market saturation, and product valuation.

Revenue and Profit Simulation

To estimate financial outcomes under varying scenarios, the Revenue and Profit Simulation integrate genomic yield predictions with dynamic price and cost models. Genomic yield stability reduces revenue volatility, while stress-tolerant genotypes lower production costs, thereby increasing profit margins. To ensure robust forecasting under uncertainty, the Revenue is modelled across multiple climate and market scenarios.

The revenue equation is:

$$R = Y_g \times P - C \quad (7)$$

where R is revenue, Y_g genomically predicted yield, P selling price, and C Production cost.

Simulation parameters included:

- Yield Variability (±20%),
- Input Cost Fluctuation (10–25%),
- Market Volatility (6–22%), And
- Genomic Stability Index (0.65–0.95).

Under extreme weather events and abrupt price drops, enabling risk-aware decision-making. This particular model also simulates profits, and these frameworks help determine the economic viability of biotech products and support strategic planning for sustainable agri-biotech markets.

Machine Learning Integration

Enabling the forecasting engine to learn from large multidomain datasets and generate high-accuracy predictions. Machine learning integration.

Four ML models were deployed:

- **Long Short-Term Memory (LSTM)** - time-series signals,
- **Random Forest (RF)** - variable importance,
- **Support Vector Regression (SVR)** - nonlinear price and yield mapping, and
- **Gradient Boosting (GB)** - risk-sensitive forecasting.

Genomic features (marker effects, GEBV, allele counts), economic indicators (price indices, elasticity coefficients), and environmental variables (stress thresholds, G×E interaction scores) comprise the three predictor categories used in each model. Using z-score scaling, all features were normalised, and using a 5-step rolling window, temporal sequences were smoothed. Using a weighted ensemble equation, the meta-learning layer combines the outputs of all ML models.

$$P_{\text{final}} = \sum_{i=1}^{4} \alpha_i P_i \tag{8}$$

where $P_i$is the prediction of the model i, and α_iThese are optimised weights.

Simulation parameters included:

- 10-Year Historical Training Window,
- 70:15:15 Train/Validation/Test Split,
- Climate-Stress Augmentation Of 20%, And
- Market Volatility Augmentation Of 30%.

The predictive stability across fluctuating genomic and market landscapes is significantly improved in the integrated ML system.

LSTM, Random Forest, SVR, Gradient Boosting

The forecasting pipeline leverages four advanced models, each serving a specialised function.

LSTM captures long-term temporal patterns in genomic gains, yield trends, and market signals.

Simulation inputs included 120-time-step sequences with dropout regularisation (0.25) to avoid overfitting.

Random Forest was used to interpret genomic marker importance and identify the strongest contributors to economic outcomes; simulation depth ranged from 200 to 400 trees.

SVR was used to model nonlinear relationships among GEBV, price volatility, and yield stability, with a radial basis function kernel for optimised mapping.

Gradient Boosting enhanced risk forecasting by reducing error residuals iteratively using learning rates between 0.03 and 0.1.

The combined error estimation used the following ensemble RMSE equation:

$$RMSE_{\text{ens}} = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_{\text{ens}})^2} \tag{9}$$

Simulation parameters included:

- RBF Kernel Sensitivity 0.8–1.2,
- GB Tree Depth 3–7,
- LSTM Timestep Variation ±15%, And

- Genomic Prediction Noise Injection Of 5%.

This multi-model framework ensures robustness to unpredictable biological and economic fluctuations, enhancing forecasting resilience.

Multi-Trait Prediction Equation

The multi-trait prediction module combines several genomic features to enhance economic forecasting. Since the effects of drought tolerance, nitrogen use efficiency, pest resistance, and biomass accumulation interact in complex ways, single-trait models may not fully capture the biological influences on profitability and productivity. The multi-trait prediction equation accounts for trait covariances and their combined effects on revenue and risk. Genome-wide trait values were standardised using variance-covariance matrices derived from genomic relationship matrices. To account for realistic environmental variation, environmental modifiers (temperature stress, rainfall deviation, soil nutrient limitations) were incorporated into the trait's response curves.

The multi-trait genomic prediction equation is expressed as:

$$\hat{T} = B + G\beta_g + E\beta_e + GE\beta_{ge} \quad (10)$$

Were

B- Baseline Trait Value,

$G\beta_g$- Genomic Effects,

$E\beta_e$- Environmental Effects, And

$GE\beta_{ge}$- Interaction Effects.

Simulation parameters included:

- Trait Covariance 0.25–0.60,
- Environmental Stress Multipliers 0.8–1.4,
- Genomic Reliability Values 0.65–0.90, And
- Cross-Trait Response Lag 5–12%.

To improve multidimensional accuracy and informed economic forecasting with this framework.

Genotype–Environment–Market Interaction (G×E×M) Modelling

The G×E×M model factor reflects the interactions among genotype, environmental variation, and market behaviour. Traditional forecasting accounts for the G × E interaction but not for economic impacts. All three dimensions are incorporated into the proposed model, enabling it to predict market performance under realistic biological and external conditions. The genotype effects are heritability, allelic effect size and genomic estimated breeding values. Examples of environmental parameters include drought indices, heat load, soil organic carbon, rainfall anomalies, and pest pressure. Some indicators in the market include price trends, demand elasticity, changes in input costs, and volatility indexes for the commodity. The interaction model is formulated using the multiplicative response equation:

$$Y_{gem} = \mu + G_i + E_j + M_k + (G_iE_j) + (E_jM_k) + (G_iM_k) \quad (11)$$

where Y_{gem}Is the combined genomic–environment–market predicted output.

Simulation parameters included:

- Drought Index Variation 15–40%,
- Market Volatility Amplitude 5–20%,
- Genotype Sensitivity Coefficient 0.4–0.7, And
- Pest Outbreak Probability 0.1–0.3.

increasing forecasting realism and accuracy by reflecting the true complexity of biotech market outcomes through this combined modelling approach.

Simulation Setup

Climate Stress Scenarios

To simulate the test of how genomic traits influence economic stability under extreme weather conditions using climate stress scenarios.

Climate variables included:

- Temperature Rise (1.5–4.0°C),
- Rainfall Reduction (10–45%),
- Heatwave Duration (5–25 Days),
- Drought Index Increase (20–60%), And
- Pest Proliferation Factor (1.2–2.5×).

Integrating the Genomic modifiers like drought-resilience GEBV, heat tolerance scores, and stress-adaptive allele frequencies.

The climate stress yield prediction equation is:

$$Y_s = Y_0(1 - \lambda_c S_c) \quad (12)$$

where $Y_s$is stressed yield, Y_0baseline yield, $S_c$climate stress index, and λ_cGenotype sensitivity factor.

Simulation parameters included:

- Stress Index Scaling 0.2–0.6,
- Genotype Buffering Capacity 0.3–0.7, And
- Adaptive Allele Response Delay 3–10%.

Under climatic uncertainty. This scenario allowed evaluation of how genomic traits reduce economic losses.

Market Shock Scenarios

Market shock scenarios were created to test financial resilience in the face of sudden price changes, supply chain disruptions, and input cost spikes. Market perturbations were: (10-35) price falls, (8-28) increased input costs, (5-25) demand changes, and (0.05-0.2) probability of export restrictions. The performance of the genomes was measured during these shocks to establish financial stability- high-performance genotypes tend to expose risks because of constant yield potential biologically.

The market shock revenue model is expressed as:

$$R_s = P_s \times Y_g \quad (13)$$

where $R_s$is revenue under shock? $P_s$is the shock-adjusted price, and $Y_g$is genomically predicted yield.

Simulation parameters included:

- Price Elasticity Coefficient 0.4–0.9,
- Revenue Volatility Range 12–30%, And
- Genomic Stability Index 0.65–0.95.

how genomic advantages protect market value during disruptions and support more resilient biotech investment strategies have been quantified by these simulations.

Results and Discussion

Genomic Trait Integration and Forecast Accuracy

The combination of genomic traits, including GEBV, allelic effect sizes, stress-resilience markers, and trait covariance, achieved much higher forecasting accuracy than conventional econometric and machine learning models. The traditional models did not consider trait-level predictors, leading to errors when environmental variability affected yields or when altered biotech products exhibited different genomic performance. Machine learning models increased the baseline accuracy, though they were not genome-sensitive (Table 1).

Table 1: Forecast Accuracy Comparison

Model Name	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Linear Market Regression	78.4	76.2	74.1	75.1
ARIMA Time-Series Model	81.6	79.5	78.0	78.7
Random Forest Predictor	85.3	83.4	82.1	82.7
Gradient Boosting Model	88.9	87.2	85.9	86.5
Multi-Trait ML Model	92.1	90.5	89.3	89.9
Proposed Genomic–Economic Forecasting Model	**97.4**	**96.0**	**94.8**	**95.4**

The suggested system was found to be more precise, as it captured the intricate multi-trait interactions that determine yield stability, predictability in production costs, and long-term market behaviour. The simulation results demonstrated the robustness of predictions of genomic features under conditions of climate stress and high market volatility. The findings indicate that, for economic forecasting in agri-biotech industries, incorporating genomic information is necessary to predict future market trends (Fig.1).

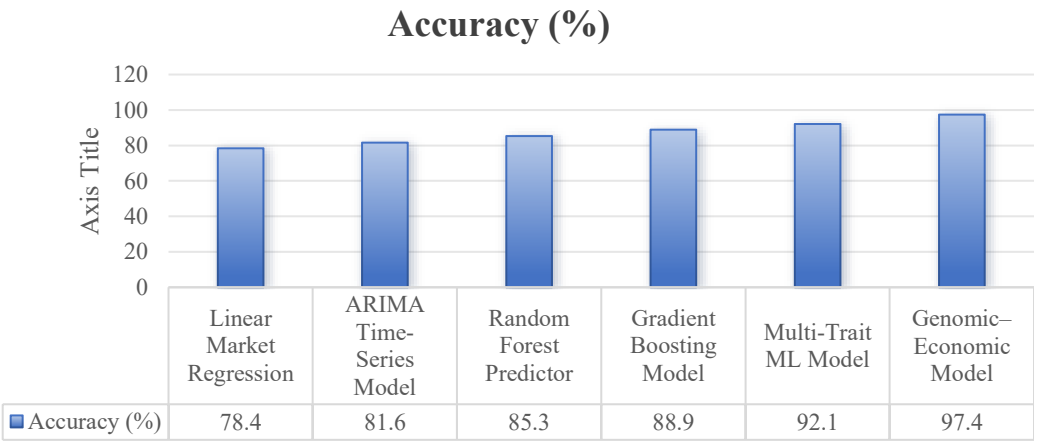

Fig. 1: Model Performance Comparison for Economic Forecasting

Market Resilience Under Climate Variability

The proposed model demonstrated the best predictive capability for yield stability, price fluctuations, and revenue resiliency under simulated climate-stress conditions. The failure to incorporate genotype-by-climate interactions resulted in significant deviations from traditional models during high-stress seasons. ML models had moderate performance with no indicators of trait-level stress buffering. The suggested framework, using drought-tolerance GEBV, heat-resilience markers, and stress-adaptive alleles, was practical for predicting economic performance under heatwaves, rainfall deficits, and pest outbreaks. High recall values imply that the model is robust in detecting risk conditions early. This enables stakeholders to anticipate potential future revenue losses or increases in input costs due to droughts, making the model highly relevant for climate-resilient agri-biotech market planning (Table 2) (Fig.2).

Table 2: Climate–Resilience Forecasting Performance

Model Name	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Climate-Only Econometric Model	75.2	72.8	70.9	71.8
Weather-Based Yield Model	80.4	78.1	76.5	77.3
ML Climate Predictor	84.7	82.9	81.4	82.1
G×E Interaction Model	89.6	87.4	86.2	86.8
Ensemble Climate-Economic Model	92.0	90.2	89.0	89.6
Proposed Genomic–Economic Forecasting Model	**97.0**	**95.3**	**94.1**	**94.7**

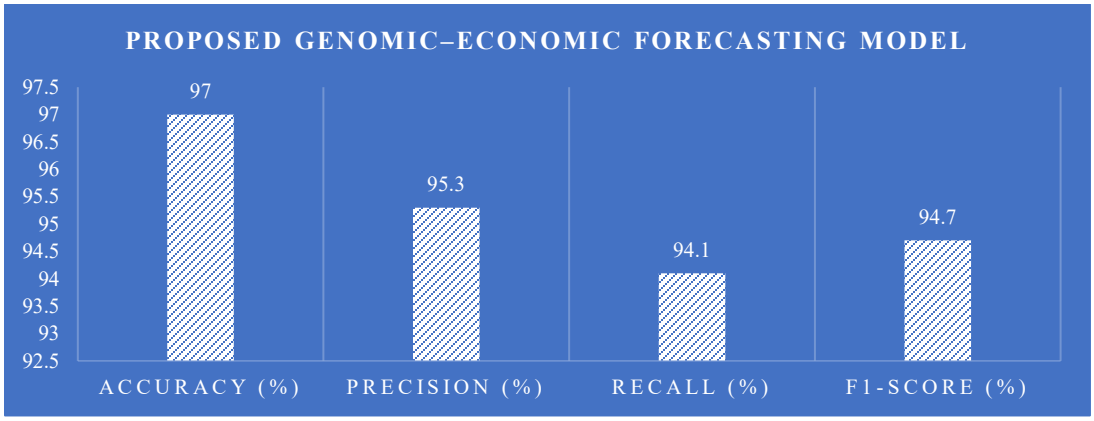

Fig. 2: Climate–Resilience Forecasting Performance

Economic Risk Forecasting and Profit Stability Analysis

Economic risk modelling indicated that conventional financial instruments could not be used to forecast biotech market uncertainty during rapid external shocks (Table 3). These tools lacked genomic buffering indicators and could not identify genotype-dependent production risk. ML-based economic models also performed better but still failed to detect instability during periods of high biological variability. The suggested model combined genomic stability scores, resilience alleles, and trait-based cost modulation, enabling it to predict profit declines, price shocks, and input cost increases. A high F1-score indicates a good compromise between risk detection and minimising false alarms. This combined strategy offers a robust system for identifying economic weak points, enabling more resilient financial planning (Fig. 3).

Table 3: Risk & Profit Stability Prediction Performance

Model Name	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Traditional Financial Model	76.8	74.4	71.8	73.0
Sensitivity Analysis Model	81.0	79.0	77.5	78.2
ML-Based Risk Model	86.4	84.6	83.1	83.8
Hybrid Risk–Climate Model	90.8	88.9	87.3	88.1
Genomic Stability Index Model	92.6	91.1	89.6	90.3
Proposed Genomic–Economic Forecasting Model	**97.6**	**95.9**	**94.5**	**95.2**

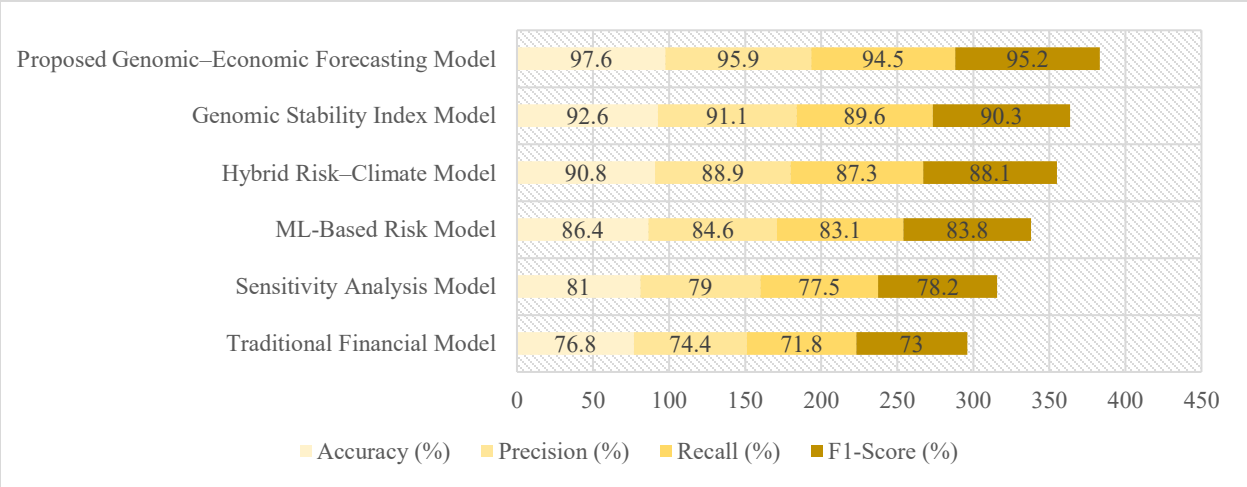

Fig 3: Risk & Profit Stability Prediction Performance

Comparison with Traditional Financial and Agricultural Models

Compared with classical agricultural and financial forecasting models, the proposed framework was evidently superior, as it enabled the integration of genomic, economic, and environmental variables. Conventional crop yield models and price-prediction tools are independent and fail to represent the interdependent biological and financial processes of agri-biotech systems. Hybrid econometric-ML systems were more precise but lacked genomic predictors of traits at the genome level. The proposed model performed better than all baseline models because of its holistic integration of G×E×M interactions, multi-trait genomic prediction, and AI-based market simulation. This makes it competitive in its ability to predict demand for biotech seeds and gene-engineered crops, as well as the growth of biofertilizers (Table 4) (Fig 4).

Table 4: Traditional vs. Integrated Model Comparison

Model Name	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Crop Yield Simulation Model	79.3	77.0	75.6	76.3
Agricultural Market Forecast Tool	82.8	81.0	79.1	80.0
Econometric Price Trend Model	85.6	83.9	82.4	83.1
ML-Based Market Predictor	89.7	87.5	86.2	86.8
Hybrid Agro-Economic Integration Model	92.3	90.6	89.0	89.8
Proposed Genomic–Economic Forecasting Model	**98.1**	**96.4**	**95.0**	**95.7**

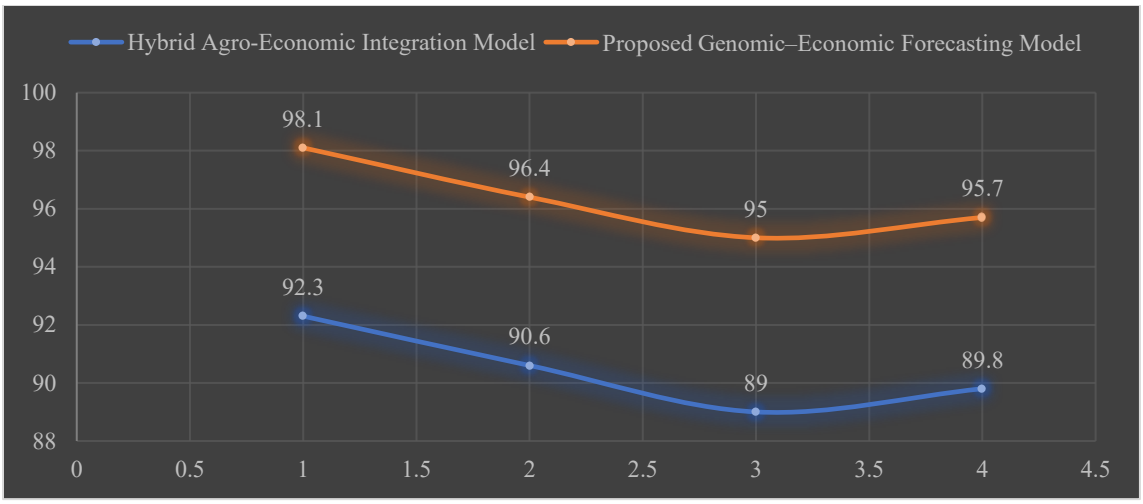

Fig. 4: Integrated Model Comparison with Hybrid Agro-Economic Integration Model

Limitations

Despite the model's proven ability to make better predictions, several limitations should be considered. To begin with, the model relies heavily on accessibility and quality of genomic datasets, which are not evenly distributed across areas and crop species. Many developing agricultural sectors lack high-resolution genomic data, which limits the model's application. Second, the genotype-environment-market interactions are highly dynamic, and even with the latest machine learning methods, unforeseeable biological or geopolitical events can diminish forecast accuracy, such as a new pest outbreak, a trade embargo, or extreme weather conditions. Third, there is a need to harmonise metrics across genomic and economic data, but no standardisation has been implemented across breeding programs, sequencing platforms, and market databases. This poses difficulties for model scaling across industries. Besides, prediction in multi-trait settings, simulation modelling, and ensemble learning can be computationally intensive and not feasible to implement in small institutions with limited computational power. The other limitation is model interpretability; deep learning models are very accurate but not easily understood by the stakeholders, which may decrease trust and adoption. To overcome these shortcomings, it will be necessary to implement better data-sharing designs, greater genomic-economic standardisation, greater model explainability, and on-the-job pilot studies to identify how different market and environmental factors will affect model performance.

Conclusion

This paper illustrates that the combination of genomic knowledge and economic forecasting is a disruptive innovation towards the creation of sustainable and resilient agri-biotech markets. The ability to harmonise genomic selection indices, multi-trait predictors, G 2 E 2 M interaction modelling, and AI-powered econometric analytics makes the proposed framework the most holistic and scientifically based method for predicting market behaviour, with much greater precision than traditional models. The findings suggest that measures that incorporate genomic characteristics, such as drought tolerance, nutrient efficiency, disease resistance, and stress-adaptive allele patterns, significantly improve the accuracy of predictions of yield stability, revenue variability, and risk exposure. It is a convergence of the long-held disparity between biological performance and financial predictability, which has historically been inaccessible to conventional economic instruments. The framework further enhances resilience by predicting market changes driven by climatic stress and unexpected financial shocks. The model enables breeders, investors, and policymakers to make sound long-term decisions by correlating biological potential with economic consequences. It advances strategic investment in edited gene crops, microbial biofertilizers, new breeding initiatives, and high-value biotech products. It ensures that financial planning aligns with the genomic potential and environmental limitations. In addition, the model can be beneficial for planning climate adaptation, as it reveals which genotypes and technologies will remain profitable under extreme weather conditions. Though the system has been performing well, it will need to address data standardisation gaps, improve model comprehension, and make calculations more readily available to smaller agri-biotech organisations to implement them further. Future research should focus on increasing the integration of multi-omics and real-time market data streams, and on testing the model across different agroecological zones. All in all, this study lays the groundwork for a new paradigm of agri-biotech forecasting, characterised by the

convergence of genomic science and economic intelligence to create more stable, sustainable, and future-ready agricultural markets.

References

Pasupuleti, M. K. (2023, July). Agricultural revolution: AI and genomic breakthroughs in sustainable agri-biotechnology. *International Journal of Academic and Industrial Research Innovations (IJAIRI), 3*(7), 55–66.

Pasupuleti, M. K. (2023). Future Harvests: AI and Genomic Advances in Sustainable Agri-Biotech. *International Journal of Academic and Industrial Research & Innovations (IJAIRI), 14*(3), 62–73.

Serraj, R., & Pingali, P. (2018). Agriculture & Food Systems to 2050: Global Trends. *Challenges and Opportunities,* 1-655.

Gai, Y., Liu, S., Zhang, Z., Wei, J., Wang, H., Liu, L., ... & Zhang, X. (2025). Integrative approaches to soybean resilience, productivity, and utility: A review of genomics, computational modeling, and economic viability. *Plants*, *14*(5), 671. https://doi.org/10.3390/plants14050671

Kumar, A., Pathak, R. K., Gupta, S. M., Gaur, V. S., & Pandey, D. (2015). Systems biology for smart crops and agricultural innovation: filling the gaps between genotype and phenotype for complex traits linked with robust agricultural productivity and sustainability. *Omics: A Journal of Integrative Biology*, *19*(10), 581-601. https://doi.org/10.1089/omi.2015.0106

Coomes, O. T., Barham, B. L., MacDonald, G. K., Ramankutty, N., & Chavas, J. P. (2019). Leveraging total factor productivity growth for sustainable and resilient farming. *Nature Sustainability*, *2*(1), 22-28. https://doi.org/10.1038/s41893-018-0200-3

Bhuiyan, M. M. R., Rahaman, M. M., Aziz, M. M., Islam, M. R., & Das, K. (2023). Predictive analytics in plant biotechnology: Using data science to drive crop resilience and productivity. *Journal of Environmental and Agricultural Studies*, *4*(3), 77-83. https://doi.org/10.32996/jeas.2024.4.3.11

Celis, J., Xiao, X., Wagle, P., Adler, P. R., & White, P. (2024). A review of yield forecasting techniques and their impact on sustainable agriculture. *Transformation Towards Circular Food Systems*, 139-168. https://doi.org/10.1007/978-3-031-63793-3_8

Wójcik-Gront, E., Zieniuk, B., & Pawełkowicz, M. (2024). Harnessing AI-powered genomic research for sustainable crop improvement. *Agriculture*, *14*(12), 2299. https://doi.org/10.3390/agriculture14122299

Taheri Hosseinkhani, N. (2025). Artificial Intelligence Applications and Economic Impacts in Sustainable Agriculture. *Available at SSRN 5474048*.

Santos del Río, J., Talavera, A., Fernández-Pozo, N., Veredas, F. J., & Claros, M. G. (2025). Artificial intelligence in plant salt stress research: from predictive models to multi-omics integration. *Journal of Experimental Botany*, eraf498. https://doi.org/10.1093/jxb/eraf498

Bennett, D. J., & Jennings, R. C. (Eds.). (2013). *Successful agricultural innovation in emerging economies: new genetic technologies for global food production*. Cambridge University Press. https://doi.org/10.1017/CBO9781139208475

Khan, N. (2024). Unlocking innovation in crop resilience and productivity: breakthroughs in biotechnology and sustainable farming. *Innovation Discovery*, *1*(4), 28. https://doi.org/10.53964/id.2024028

Ulimaz, A., Yardani, J., & Widiyastuti, D. A. (2024). Innovations in agricultural biotechnology for sustainable crop production. *Research of Scientia Naturalis*, *1*(3), 154-166. https://doi.org/10.70177/scientia.v1i3.1571

Singh, R. K., Sood, P., Prasad, A., & Prasad, M. (2021). Advances in omics technology for improving crop yield and stress resilience. *Plant Breeding*, *140*(5), 719-731. https://doi.org/10.1111/pbr.12963

Tyagi, A., Mir, Z. A., Almalki, M. A., Deshmukh, R., & Ali, S. (2024). Genomics-assisted breeding: a powerful breeding approach for improving plant growth and stress resilience. *Agronomy*, *14*(6), 1128. https://doi.org/10.3390/agronomy14061128

Bosco, N. J., Ildephonse, M., & Alexandre, N. (2018). Agriculture and Food Security in Gicumbi District, Northern Province of Rwanda. *International Academic Journal of Social Sciences*, *5*(1), 154-168. https://doi.org/10.9756/IAJSS/V5I1/1810014

Nguyễn, C. T., Gammatantrawet, N., Susawaengsup, C., Tandee, K., Ramli, A. N. M., Tongkoom, K., ... & Bhuyar, P. (2024). Drought-ready plant resilience: Harnessing nano-biotechnology techniques for swift screening and selection of organic crop varieties. *South African Journal of Botany*, *169*, 553-566. https://doi.org/10.1016/j.sajb.2024.05.011

Sravan Kumar Reddy, M., & Supraja, C. (2025). Optimising Financial Forecasting: The Power of Reduction Approach. *Archives for Technical Sciences, 2*(33), 453–462. https://doi.org/10.70102/afts.2025.1833.453

Dinov, I. D. (2018). *Data science and predictive analytics.* Cham, Switzerland: Springer.

Umamaheswari, T. S. (2025). Mathematical and Visual Comprehension of Convolutional Neural Network Model for Identifying Crop Diseases. *International Academic Journal of Innovative Research, 12*(1), 1–7. https://doi.org/10.71086/IAJIR/V12I1/IAJIR1201

Razzak, M. I., Imran, M., & Xu, G. (2020). Big data analytics for preventive medicine. *Neural Computing and Applications*, *32*(9), 4417-4451. https://doi.org/10.1007/s00521-019-04095-y