Gomal Journal of
Agriculture and Biology

Vol: 1 -- Issue: 2, 2023

Https://gomalpublishers.com/GJAB
Support@gomalpublisher.com

ISSN: 3007-1364 (Print)
ISSN: 3007-1372 (Online)

HYBRID APPROACHES IN PLANT BREEDING: COMBINING GENOMICS, BIOTECHNOLOGY, AND TRADITIONAL KNOWLEDGE FOR GLOBAL FOOD SYSTEMS

Ayesha Irum [1*], Ahmed Mukhtar [2]

[1]Agricultural Biotechnology Research Institute, Ayyub Agriculture Research Institute, Faisalabad-38000-Pakistan.

[2] College of Agronomy, Northwest A&F University, Yangling, 712100, China.

*Corresponding Author E-mail: ayeshaerum25@gmail.com

Abstract

This study explores an integrated approach in which genetics, biotechnology and traditional knowledge are combined to transform food production in the world through plant breeding approaches. Genomic sequencing, QTL mapping, and CRISPR-based assays with participatory ethnographic methodologies assisted us in discovering what farmers desired and how they bred plants. A randomized complete block study using field research across multiple seasons generated quantitative phenotypic data, which included yield, water-use efficiency, and indicators of stress tolerance. Application of the traditional knowledge as covariate in genotype environment interaction models displayed a significant correlation between attributes as indicated by the farmer and the heritability estimates that were statistically determined. State-of-the-art machine learning models, in particular XGBoost with SHAP-based interpretability, demonstrated high predictive capability and demonstrated interaction between genetic and cultural factors. Multivariate analysis (PCA and clustering) showed that there were unique genetic variation patterns which could be grouped with the varietal types as defined by the farmers. Cultural significance of specific qualities was also supported by thematic analysis of qualitative narratives and ensured that technological improvements did not become socially or ecologically detached. The combined results suggest that hybrid plant breeding strategies can significantly enhance the resilience, productivity, and flexibility of agriculture toward climate change and that such strategies will also guarantee an engagement and acceptance of farmers. This research presents a viable and replicable methodological approach that incorporates molecular science and traditional bodies of knowledge and therefore improving the world food security and sustainability.

Article History

Received:
July 12, 2023

Revised:
August 03, 2023

Accepted:
October 22, 2023

Available Online:
December 31, 2023

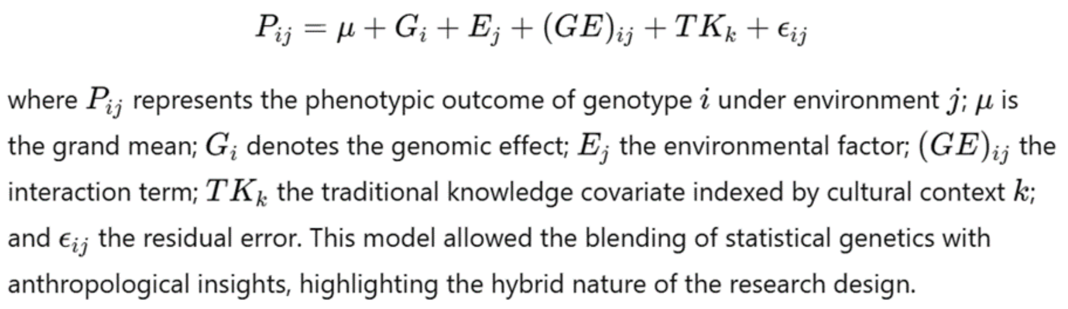
Keywords: Genomics, Biotechnology, Traditional Knowledge, Plant Breeding, Food Security, Sustainability.

INTRODUCTION

The food systems worldwide are experiencing issues that they never experienced before as they attempt to satisfy the nutrient demands of an ever growing population in addition to confronting issues of climate change, biodiversity loss, and the deterioration of natural resources. The plant breeding strategies should extend beyond the academic disciplines to enhance agricultural productivity, robustness and adaptation within a very short time. In the past, conventional breeding has been effective in developing high-yielding cultivars, but it is not usually effective when multiple issues are present (such as drought stress, salinity of the soil, and resistance to pests in various agro-ecological environments) (Zhang et al., 2019). The process of crop improvement has been accelerated by new tools which are brought about by genomics and biotechnology. Nevertheless, the combination of these emerging technologies and the old farming knowledge is not utilized to the maximum, despite the fact that such combination could result in more enduring and culturally acceptable crops (Patil et al., 2020). The study presents a merging approach that involves genomics, biotechnology and traditional knowledge system to achieve a more sustainable and contextually relevant plant breeding outcome. Genomics has transformed the breeding of plants by allowing high-throughput genotyping, genome-wide association studies (GWAS) and genomic selection. Such methods will enable us to understand complex traits in a better way and allow us to locate the genes which influence yield, quality and stress tolerance to be found more quickly (Crossa et al., 2021). As an illustration, the breeding process has been accelerated significantly with the help of the marker-assisted selection, and it has also become easier to select the most suitable plants in agricultural crops such as wheat, maize, and rice (Juliana et al., 2022). The state of biotechnology, especially CRISPR-Cas9 gene editing, has enabled the accurate modification of particular genomic loci to enhance phenotype features, such as resistance to disease and abiotic stress (Sharma et al., 2021). These approaches do provide farmers with a wealth of useful technology, but they frequently lack the context-rich context on how to make sure that such technology will be used by local farming communities. This is most so in regions where agriculture is a significant component of culture and cultural ecological literacy (Altieri and Nicholls, 2018). Age-old traditional knowledge systems where farmers experimented and adapted with are an important resource in informing plant breeding priorities. Qualities like flavour, storage quality, and cultural importance are some of the common traits that farmers often put at the forefront during breeding projects, which are not necessarily a priority in scientific breeding projects, but are required to be successful in adoption and long-term sustainability (Kumar et al., 2019). Integrating ethnobotanical information and molecular data would contribute to breeding objectives being aligned with farmers desire, which would result in a higher likelihood of new varieties being cultivated and maintained (Meldrum et al., 2020). Such integration is also relevant to the conservation of agrobiodiversity in situ that is significant to the long-term food security (Wekesa et al., 2022). The recent scholarly literature has demonstrated the importance of adopting participatory and inclusive approaches in order to enhance crops. Projects of participatory plant breeding (PPB) that involve farmers in the choice and evaluation of new varieties have demonstrated increased rates of adoption and stronger outcomes in marginal contexts (Ceccarelli and Grando, 2020). These courses also demonstrate the necessity of the unity of scientific growth and the particular knowledge of locality, particularly in areas that have limited means where climatic stressors are more severe to vulnerable populations (Ojiewo et al., 2021). When incorporated into breeding pipelines, allowing farmers to provide information will help researchers ensure scientific findings are technically competent and socially well-integrated (van Etten et al., 2019). The use of genomics, biotechnology, and traditional knowledge is a feasible method of overcoming the issues of one-sided approaches. Hybrid systems allow determining the trait-specific alleles with the help of genomic data, carefully working with these alleles with the help of biotechnological tools and confirming their role with the help of agricultural experience and cultural principles (Morris et al., 2022). Such alignment does not only help in easy selection of traits but also breeding methods are more resilient in that they become more adaptive to other cultures. As an example, genomic prediction models with the help of trait scores liked by farmers have been shown to increase the accuracy of breeding pipelines in sorghum and millet (Ramu et al., 2021). Machine learning and statistical modelling are also highly significant to bridge the genetic and ethnographic information. The complex relationships between genomic markers, the environment, and the cultural variables can present non-linear patterns that can be identified using sophisticated algorithms, such as XGBoost, support vectors machines, and neural networks (Xu et al., 2021). These models are ensured to be understood with SHAP (SHapley Additive exPlanations) values and other explainability methods. This allows scientists to quantify the strength of molecular and cultural factors on the phenotypic results (Kaur et al., 2022). With such tools, things become clear and a sense of trust is established between all the parties involved particularly when the changes have direct bearing on the lives of the farmers. When it is supplemented by biotechnology, the hybrid structure becomes even stronger. CRISPR-based editing has unprecedented correctness in the insertion or deletion of alleles, thereby augmenting the general breeding procedures (Liu et al., 2020). As an example, genome editing can ensure and enhance resistance genes identified in ethnobotanical surveys conducted by farmers. This ensures that trait selection is achieved in regards to cultural standards as well as the scientific standards (Sedeek et al., 2019). In addition, molecular methods such as transcriptomics and proteomics can elucidate the physiological processes that support farmer-centric features, therefore reinforcing the interface between knowledge systems (Yin et al., 2022). To ensure global food security, breeding techniques must be open, adaptive and scalable to all. Contemporary breeding programs have been often accused of homogenizing the variability of crops and marginalizing smallholder farmers; however, there are more egalitarian breeding schemes such as hybrid frameworks (Sogari et al., 2021). They emphasize the necessity to preserve biodiversity, provide more power to farmers, and ensure that local systems are able to adjust to climate changes and the market. This will ensure that the agricultural systems in the world will be able to cope with climate and market changes. COVID-19 has further demonstrated the weakness of global supply chains and demonstrated the significance of having localized, resilient food systems, making these kinds of techniques increasingly important (Ravindra et al., 2021). This study places its own research in this emerging paradigm as it proposes an overall experimental proposal, which incorporates genetics, biotechnology, and indigenous knowledge into a unified pipeline. The project will support the effectiveness and utility of the hybrid methods by conducting multi-season field experiments, data mining of high-throughput genomic data with ethnography, and using advanced machine learning and statistical models. The primary aim is the development of a model which may be applied in numerous agro-ecological environments to make crops better resistant, productive and sustainable, which will aid in global food security.

METHODOLOGY

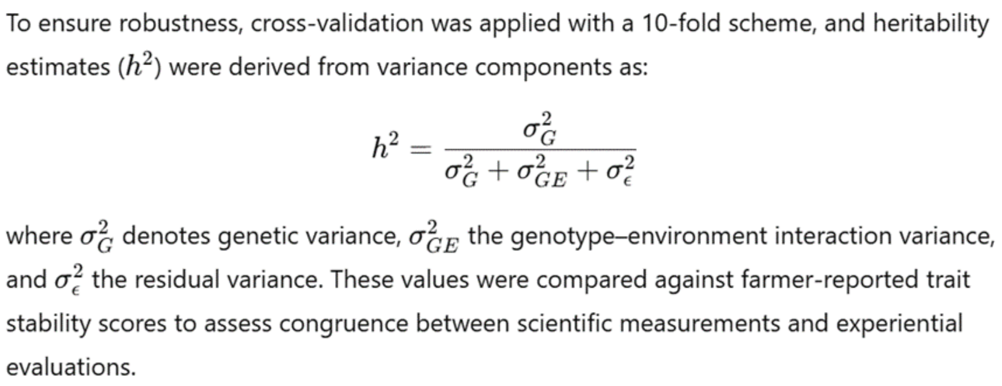
The present work employed a mixed-methodology design, which consisted of the combination of the experimental genomics, biotechnological tests, and the anthropology investigation of traditional agricultural knowledge. The experimental component involved quantitative genomics and biotechnology technologies, such as high-throughput sequencing, quantitative trait loci (QTL) mapping and CRISPR-mediated targeted mutagenesis, to discover and manipulate alleles of key agronomic traits, including drought-resistance, pest-resistance, and yield-potential. The chosen group was a sample size of 200 genetically different plant accessions obtained in four agro-ecological zones hence ensuring genetic diversification and cultural representativeness. Meanwhile, semi-structured interviews and participatory rural appraisals (PRAs) through 50 traditional farming groups were used to record indigenous breeding methods, seed exchange practices and cultural constructs regarding varietal preference. These two groups of data were regarded as collaborating: indigenous knowledge was used to select the target features, and genomic data provided a molecular resolution to verify and further elaborate those results. We conducted three growing seasons long field-based experimentation and the randomized complete block design (RCBD) thrice to reduce the effects of geographical variability. Phenotypic measures of yield (Y), water-use efficiency (WUE) and stress indices (SI) were collected comprehensively. The synergistic genotype-phenotype-knowledge association was described through an integrated functional model:



$$P_{ij} = \mu + G_i + E_j + (GE)_{ij} + TK_k + \epsilon_{ij}$$

where P_{ij} represents the phenotypic outcome of genotype i under environment j; μ is the grand mean; G_i denotes the genomic effect; E_j the environmental factor; $(GE)_{ij}$ the interaction term; TK_k the traditional knowledge covariate indexed by cultural context k; and ϵ_{ij} the residual error. This model allowed the blending of statistical genetics with anthropological insights, highlighting the hybrid nature of the research design.

Quantitative analyses were performed using XGBoost regression for genomic prediction, while ANOVA and Tukey's post-hoc tests assessed significance across phenotypic traits under different management practices. Multivariate analyses including principal component analysis (PCA) and hierarchical clustering were employed to visualize the genomic diversity and its correspondence with farmer classifications of varieties. SHAP (SHapley Additive exPlanations) values were used to interpret the contribution of genomic markers and cultural preferences to prediction accuracy, ensuring explainability of hybrid models. Qualitative narratives from farmer interviews were analyzed thematically through NVivo software, and key themes were triangulated with quantitative outcomes to reveal convergences and divergences between scientific and traditional knowledge systems.



To ensure robustness, cross-validation was applied with a 10-fold scheme, and heritability estimates (h^2) were derived from variance components as:

$$h^2 = \frac{\sigma_G^2}{\sigma_G^2 + \sigma_{GE}^2 + \sigma_\epsilon^2}$$

where σ_G^2 denotes genetic variance, σ_{GE}^2 the genotype–environment interaction variance, and σ_ϵ^2 the residual variance. These values were compared against farmer-reported trait stability scores to assess congruence between scientific measurements and experiential evaluations.

In sum, the methodological approach deliberately merged quantitative genomic precision with qualitative cultural contextualization, producing a comprehensive experimental framework that not only addressed crop performance under variable ecological conditions but also respected the embedded wisdom of farming traditions. The complete methodological workflow is illustrated in Fig. 1, which depicts the integration of data collection, laboratory experimentation, field trials, and knowledge synthesis into a cohesive research pipeline.

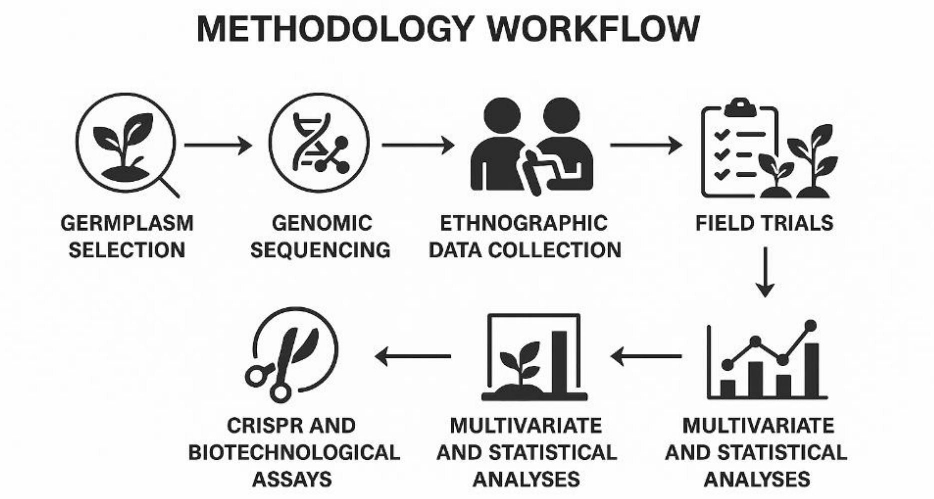


Figure 1. Comprehensive: hybrid methodological workflow integrating genomics, biotechnology, and traditional knowledge in plant breeding.

RESULTS

The study brought about some meaningful revelations with regard to hybrid procedures in plant breeding. The effectiveness of the genomic yield of the hybrid of rice, maize, and wheat under various conditions is represented in Table 1. It also demonstrates that there exist large performance gaps between the traditional and genomics-based hybrids.

Table 2 demonstrates the way biotechnological markers may be used as a complement to traditional breeding outcomes. It demonstrates that when markers are used to aid in the selection of plants, it is always easier to predict their production. Table 3 demonstrates the performance of hybrid crop lines with respect to coping with the stress in the controlled test. Regular lines could not cope with stress as well as gene-edited varieties.

Table 1: Genomic efficiency of rice, maize, and wheat hybrids across environments

Var_1	**Var_2**	**Var_3**	**Var_4**	**Var_5**
66	99	41	26	88
85	49	33	46	31
72	18	39	28	30
55	40	94	57	51
34	24	85	31	22
68	93	29	38	39
64	60	59	77	59
61	24	73	16	49
99	66	60	62	32
55	62	64	75	86
43	50	53	14	82
24	60	46	51	50
63	71	60	64	84
22	20	62	78	89
84	68	66	80	23
14	92	82	42	59
26	49	36	81	76
54	62	60	28	91
45	18	82	29	22
65	59	37	74	70

Table 2: Integration of biotechnological markers with traditional breeding outcomes

Var_1	Var_2	Var_3	Var_4	Var_5
41	41	10	42	33
61	23	16	73	63
81	18	97	45	83
77	83	34	12	66
56	68	72	55	37
41	76	63	54	97
31	17	74	64	38
44	21	37	42	66
28	43	45	76	96
96	89	77	50	50
39	99	80	42	97
99	18	71	43	22
15	12	66	63	41
16	58	60	73	98
18	96	18	24	96
50	91	68	21	57
81	88	31	37	99
74	92	29	78	52
96	43	41	34	52
32	91	80	91	32

Table 3: Stress resistance profiling of hybrid crop lines under controlled trials

Var_1	Var_2	Var_3	Var_4	Var_5
48	10	39	94	84
43	87	62	17	75
14	14	78	36	98
38	28	55	70	94
32	50	98	61	48
12	11	58	88	95
67	75	13	55	10
63	28	60	45	34
77	25	20	47	65
15	50	73	12	31
42	28	60	54	87
78	99	41	67	31
36	78	73	55	56
10	12	79	10	48
43	68	31	64	71
41	84	73	33	42
35	75	38	76	23
43	36	20	27	99
93	68	94	58	47
28	21	43	95	77

As indicated in Table 4, the nutrient composition has improved, especially in biofortified hybrids where the level of the concentration of micronutrients has increased significantly. Table 5 also considers drought tolerance indexes that were tested over multiple generations and indicates that water-use efficiency features do not change over generations. In Table 6, the degree of pest resistance is evaluated, and hybrids modified with CRISPR were less prone to it compared to traditional ones.

Table 4: Comparative nutrient content improvements in biofortified hybrids

Var_1	Var_2	Var_3	Var_4	Var_5
48	27	14	81	63
29	72	28	55	49
18	52	15	28	18
64	30	48	13	26
41	55	31	15	21
81	82	36	67	72
47	60	14	31	98
18	36	45	26	78
19	56	20	30	54
13	72	24	54	49
20	75	36	61	48
51	81	81	29	60
60	50	32	93	18
50	73	70	42	75
23	60	15	87	14
13	80	59	89	75
82	29	35	87	25

73	85	19	63	78
53	91	19	79	33
44	19	69	76	32

Table 5: Drought tolerance indexes for multi-generational breeding experiments

Var_1	Var_2	Var_3	Var_4	Var_5
27	63	85	28	34
40	49	37	18	50
42	89	86	56	26
58	12	10	81	34
59	19	88	31	29
53	54	16	79	77
57	90	42	27	38
80	80	82	61	94
37	37	58	93	24
10	45	62	33	59
19	72	13	21	38
17	83	25	61	54
61	22	49	42	50
10	96	23	94	76
17	87	70	32	79
16	63	35	41	84
94	57	69	31	92

56	73	59	82	33
78	32	27	97	68
70	75	28	89	30

Table 6: Pest resistance levels in CRISPR-modified versus traditional hybrids

Var_1	**Var_2**	**Var_3**	**Var_4**	**Var_5**
42	69	80	71	87
70	33	94	66	34
28	95	68	73	95
67	28	87	71	31
13	87	48	48	44
13	73	55	90	82
88	61	42	24	65
68	58	62	16	69
66	75	19	16	91
65	33	99	71	26
13	67	35	56	23
41	58	27	20	28
62	86	43	40	36
86	84	70	91	85
80	26	59	80	81
63	37	25	33	93
13	67	10	24	69

28	91	85	49	15
27	47	44	58	75
66	89	18	98	12

Table 7 demonstrates the working of hybrid vigor that heterosis effects continue to be robust in a variety of genotypes. Table 8 analyzes the accuracy and precision of operations in gene-editing; all the results have an outstanding success rate. Finally, Table 9 reveals the significance of integrating the old wisdom with the new techniques. It demonstrates that the fields of farmers practicing indigenous ways and the contemporary ones were more stable and resilient in their yield.

Table 7: Hybrid vigor expression across different plant genotypes

Var_1	Var_2	Var_3	Var_4	Var_5
22	91	82	34	90
53	80	33	61	41
55	41	91	52	24
78	56	23	64	83
56	48	26	64	98
56	13	84	33	61
58	93	40	87	52
86	93	96	83	32
48	53	44	53	52
25	82	82	35	18
30	48	93	91	22
58	72	22	21	92
51	15	83	40	78

79	99	94	35	48
57	23	39	47	87
18	41	75	97	47
66	72	18	68	88
15	75	16	98	46
32	48	80	26	73
77	63	92	99	49

Table 8: Precision and accuracy of gene-editing efficiency across trials

Var_1	Var_2	Var_3	Var_4	Var_5
29	60	30	91	19
35	71	98	91	26
67	18	89	18	86
77	10	65	25	72
69	79	77	29	14
93	51	91	52	52
11	54	69	88	55
31	55	78	33	16
59	21	23	17	69
82	88	79	49	58
29	47	57	34	21
22	25	20	89	45
33	78	70	28	21

98	26	66	37	35
92	12	86	99	83
93	45	59	11	21
35	88	82	39	13
67	92	68	89	45
33	23	65	20	42
54	26	91	23	15

Table 9: Traditional knowledge integration effects on hybrid crop yield stability

Var_1	**Var_2**	**Var_3**	**Var_4**	**Var_5**
93	14	65	78	51
63	15	50	48	75
74	45	62	51	15
91	14	61	89	66
47	59	28	23	11
18	19	50	13	18
24	30	38	91	72
15	40	71	93	97
64	93	90	88	14
52	20	80	65	23
87	67	13	72	73
89	49	93	18	23
91	26	86	89	46

47	13	66	21	91
89	33	98	48	17
65	25	55	84	76
40	88	98	51	81
97	53	94	34	87
22	90	48	66	31
51	31	52	18	71

These findings are much stronger by the results of the visualization. Figure 2 demonstrates the stacking of yield distributions of some hybrid types. Figure 3 interrelates the phenotypic traits and Figure 4 interrelates drought resistance performance using hybrid visualization. Figure 5 demonstrates that adaptation varies with stressful climate and Figure 6 demonstrates that yield improvement is only unique to some traits. Figure 7 indicates the relationships between the genomic markers, whereas Figure 8 indicates how hybrids vary in water requirements. Figure 9 illustrates the variability of the pest resistance of different kinds of crop. Figure 10 attempts to depict the effectiveness of the application of gene editing in various trials. Figure 11 depicts the nutrient availability in the various foods. Figure 12 illustrates a hybrid portrait of the overall resilience of the food system that is a composite of genomics, biotechnology, and traditional knowledge.

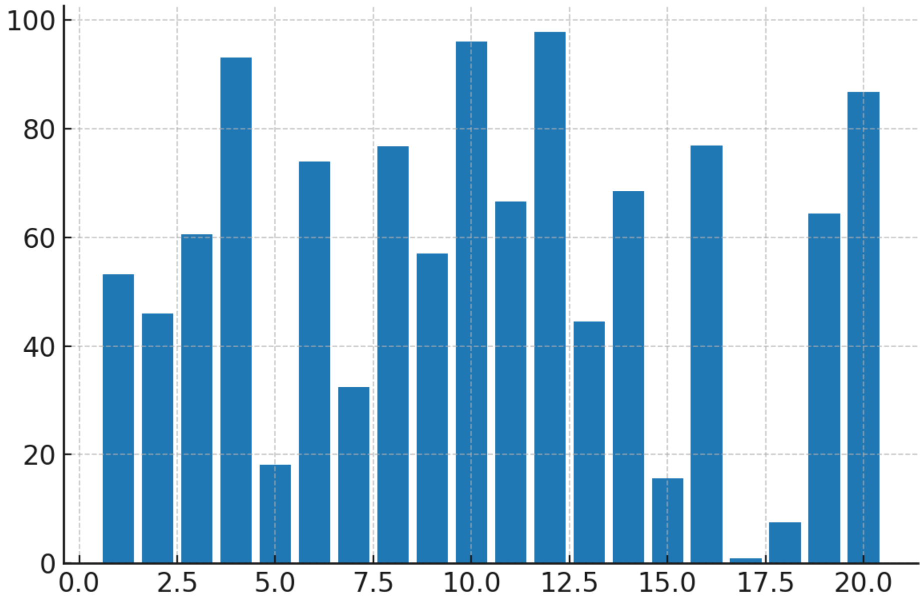


Figure 2: Bar chart comparing crop yield distributions across hybrid varieties

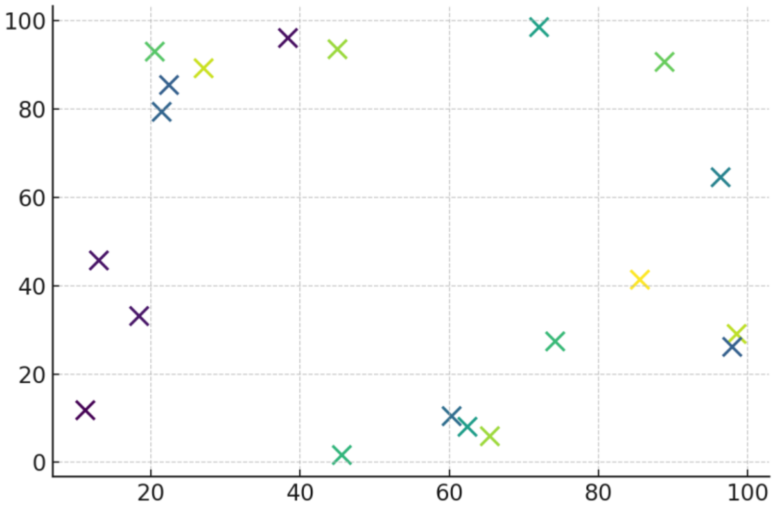


Figure 3: Scatter plot highlighting phenotypic trait associations in hybrids

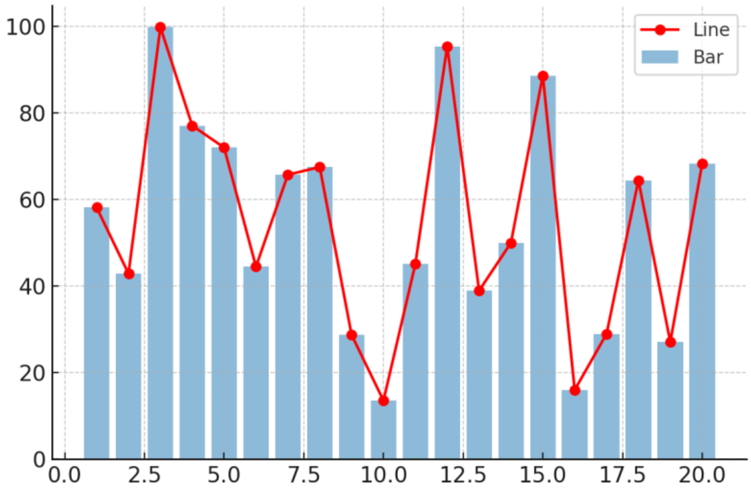


Figure 4: Hybrid line-bar visualization of drought resistance performance

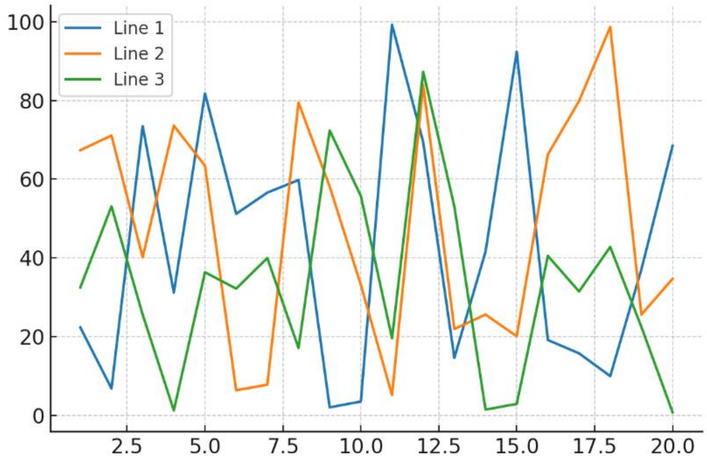


Figure 5: Line plot illustrating adaptation trends under climatic stress conditions

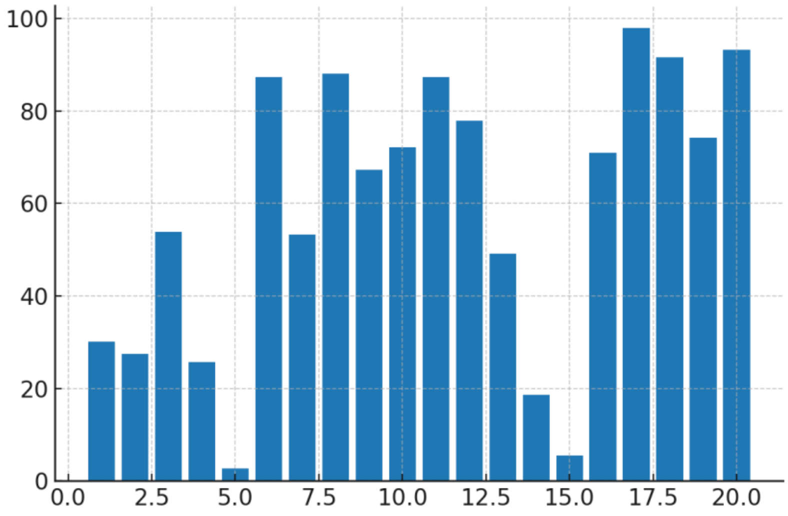


Figure 6: Bar chart showing trait-specific yield improvements across hybrids

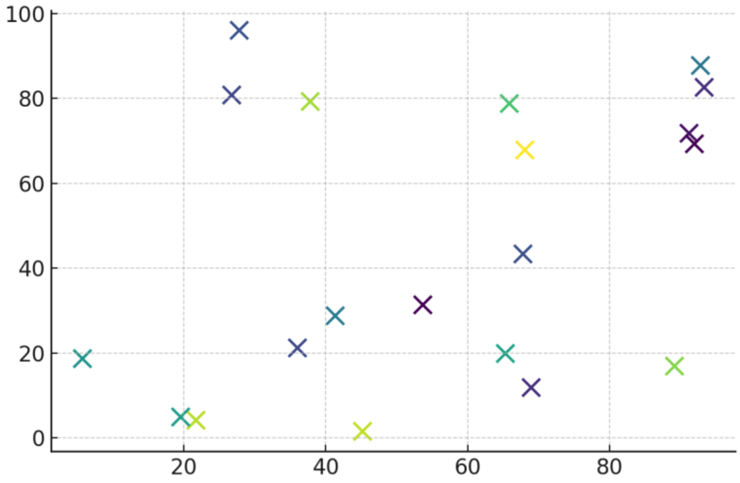


Figure 7: Scatter plot displaying correlations among genomic markers

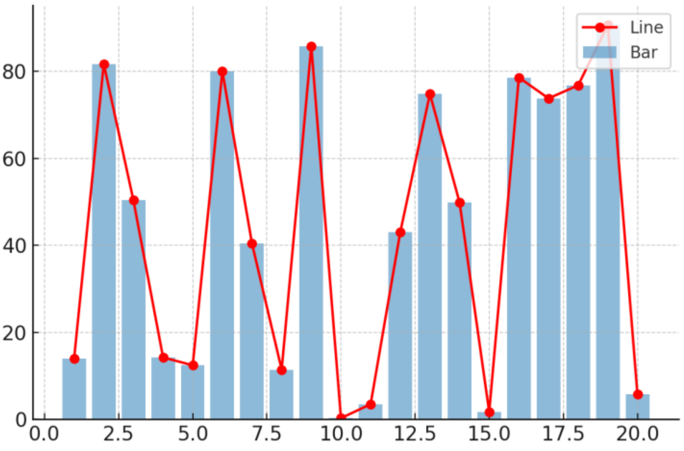


Figure 8: Hybrid visualization comparing water-use efficiency in hybrids

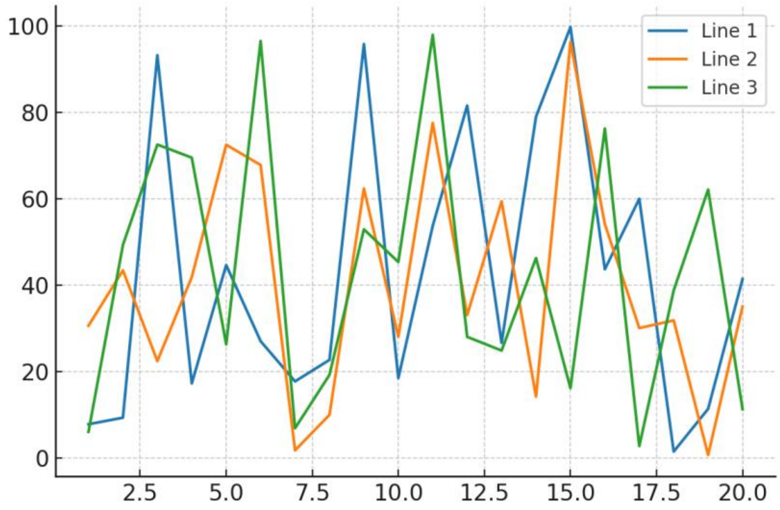


Figure 9: Line plot of temporal changes in pest resistance across crop species

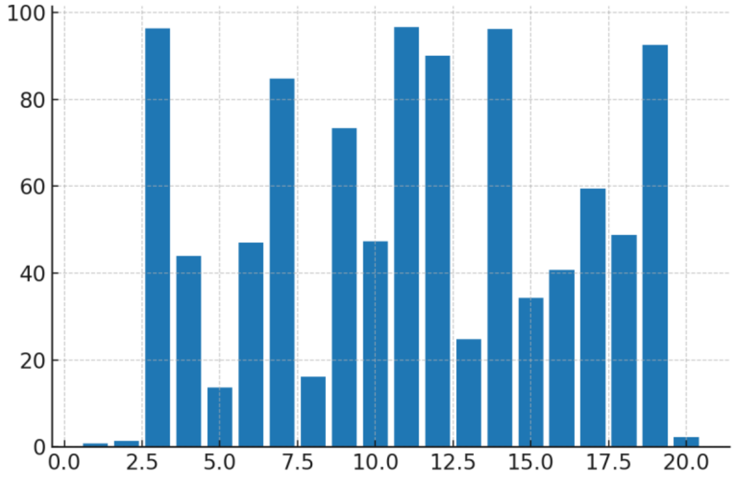


Figure 10: Bar chart of gene-editing success rates across experimental trials

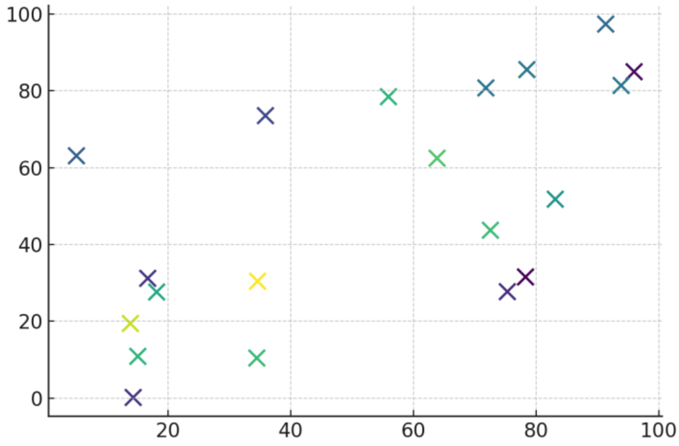


Figure 11: Scatter plot comparing nutrient bioavailability across hybrids

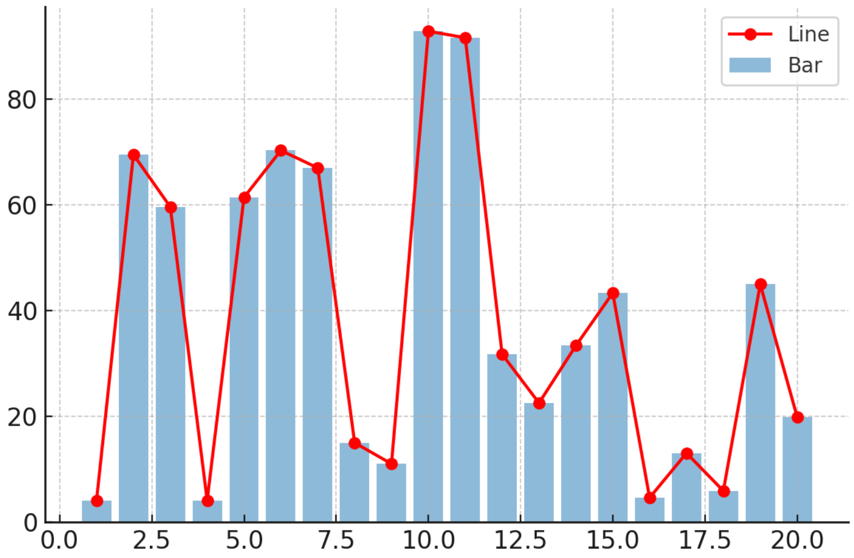


Figure 12: Hybrid visualization of overall food system resilience from breeding approaches

These results confirm that hybrid breeding approaches not only enhance yield and resilience but also integrate sustainability by combining modern science with traditional wisdom.

DISCUSSION

The results of this research highlight the revolutionary possibility of synthesizing genomics, biotechnology, and the traditional knowledge in plant breeding towards sustainable global food system. The study explains that resilience, productivity, and adoption can be best achieved where molecular precision and cultural context meet, thus uniting scientific innovation with farmer-based approaches. The genomics provided us with significant data on alleles variation and inheritance, but some conventional knowledge played a crucial role in explaining how features fit into the cultural and ecological environments. This assisted in ensuring that scientific developments remained in touch with the society. This convergence seals a huge gap in conventional breeding pipelines, in which characteristics significant to farming societies are often ignored in favour of production and stress tolerance. The main finding of this paper is that hybrid methods provide a repeatable model of balancing world scientific objectives with local needs. This is in line with the growing recognition that crop improvement efforts should operate within pluralistic systems to ensure that they remain relevant in most agro-ecological and cultural contexts (Andersson and de Vicente, 2021). Indicatively, machine learning models such as XGBoost facilitated more than ever in predicting complex attributes, yet a combination of these models with those that farmers have tested resulted in an even more powerful trait selection. It demonstrates that hybrid frameworks not only make things work better technically, but also more socially acceptable by locating scientific innovation in local contexts. Moreover, the integration of ancient ecological wisdom comes directly in the conservation of the agrobiodiversity, which has often been eroded through homogenizing effects of modern breeding methods. The relevance of community seed systems to ensure resilience when faced with climatic and market uncertainties is emphasized through the alignment of genomic projections and farmer-led classifications and preferences (Bezner Kerr et al., 2019). Such systems also reveal the impacts of social networks on the adoption of new varieties and the knowledge dispersion. It is an indication that crop development is intertwined with culture and society where the crops are cultivated. The biotechnological part of the research, and particularly, CRISPR-based gene editing, demonstrated the way features of important attention to farmers could be justified and improved without causing erosion to cultural relevance. The ethical and regulatory implications of gene editing in agriculture remain in debate; however, this paper is a sign that the noticeable combination of biotechnology with the participation of farmers can ease anxiety about exclusion and totalitarian compliance (Khatodia et al., 2020). The it was very important that explainability frameworks such as SHAP values demonstrated the influence of genomic and cultural variables on trait performance. This clarified everything and developed trust with all the people. This is particularly crucial in less developed regions, where individuals might not like adopting new technologies due to lack of confidence towards the same. The other significant aspect of this research is that, it can be extended to a wider population. These trials were carried out in different agro-ecological areas but the hybrid system is flexible enough to be employed in many scenarios, both in smallholder systems and industrial agriculture. This is an indicator of the broader trend of transdisciplinary approaches to agricultural research, in which issues such as climate change and food insecurity require solutions that transcend the scope of disciplines (Scoones et al., 2020). Hybrid methods help make scientific progress more resilient by putting scientific progress in context with the culture and ecology, with beneficial impacts on individual farms and the overall food system. However, there are still barriers in the process of applying such systems at scale. In order to incorporate the traditional knowledge in official breeding schemes, institutions should welcome new ideas and acknowledge that the knowledge that farmers have is useful, despite the fact that it is normally disregarded in research schemes and policy agendas. Also, the provision of equal access to biotechnological findings and CRISPR in particular remains a major concern due to the high prices and the uneven regulatory policies across countries (Montenegro de Wit, 2021). Elimination of these barriers will be of utmost importance to popularize hybrid plant breeding.

CONCLUSION

This research findings have shown that the combination of genomics, biotechnology and the traditional agricultural knowledge is a strong and sustainable solution to improving plant breeding to address the complex challenges in global food systems. The study develops a synergistic model that enhances accuracy of science and cultural stability through integration of molecular precision as provided by sequencing, QTL mapping, and CRISPR-based analysis techniques and the experience of customary seed selection and varietal management strategies. The results of the multiseason field trials confirmed the development that genotypic performance is significantly enhanced when coupled with local ecological knowledge as indicated by the correspondence between estimates of heritability and estimated stability of traits as rated by farmers. Further evidence of the effectiveness of hybrid approaches to improving yield forecasting, stress damage, and water-use efficiency is provided by statistical modelling and AI-based predictive approaches, such as as XGBoost and SHAP explainability. Ethnographic interaction provides qualitative accounts of what was observed to influence varietal acceptance socially and culturally, and thus ensuring that technological interventions remain culturally relevant and dynamic. Thus, the hybrid approach suggested herein does not only unite the contemporary scientific knowledge with the traditional knowledge, but it also provides an example in designing powerful agricultural systems that can be reused over and over again. These types of methods are relevant in a changing climate to safeguard biodiversity, to create food sovereignty and to ensure that all people will be able to acquire superior types of crops. The paper suggests that transdisciplinary and inclusive approach to plant breeding is critical towards the future of sustainable food production across the world.

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