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Integrating Combining Ability Analysis and Artificial Neural Networks to Enhance Genetic Improvement and Yield Potential in Little Millet (*Panicum sumatrense*)

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Abstract: Little millet, a highly nutritious grain, is valued for its fiber, protein, and mineral content. Its adaptability across various agro-climates and increasing consumer demand have led to higher market prices and expanded cultivation. This study aimed to improve little millet's yield and resilience by assessing combining ability and heterosis with machine learning. A line × tester design (4 lines × 5 testers) generated 20 hybrids, evaluated in a randomized complete block design. Traits like seed yield per plant were recorded, and genetic effects were partitioned into general combining ability (GCA) and specific combining ability (SCA). Heterosis was estimated based on parental performance. An artificial neural network (ANN) was used to predict outcomes and validated for accuracy. The analysis revealed significant GCA and SCA effects, indicating both additive and non-additive genetic influences. The parents GPUL-2, Nallasama, KOPLAM-53,

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and WV-126 were identified as strong general combiners. The crosses GPUL-4 × OLM-203 and Nallasama × GPUL-2 demonstrated superior performance, showing desirable heterosis and favorable SCA effects for seed yield and other traits. The ANN model achieved ~97% prediction accuracy, confirming genetic consistency. These findings highlight the importance of both additive and non-additive gene actions in improving yield and resilience in little millet.

Keywords: Little millet, combining ability, General Combining Ability (GCA), Specific Combining Ability (SCA), Artificial Neural Network (ANN), hybrid performance.

1. Introduction

Little millet varieties are a distinct, nutrient-rich group valued for their adaptability and fast growth. They thrive in diverse climates, offering high protein, fiber, and essential minerals, making them ideal for sustainable farming and healthy diets. Little millet is mainly grown in Karnataka, Tamil Nadu, Andhra Pradesh, Maharashtra, Odisha, Madhya Pradesh, and Bihar, where conditions favor its cultivation for food security and sustainable farming (ICAR. 2018). In India, most states have unique little millet varieties, yet many traditional types have been lost due to the Green Revolution's focus on high yields over diversity and quality. (Ratnam *et al*., 2025). Little millet cultivation is hindered by low yields, long maturity, lodging risk, limited agro-ecological adaptability, and lack of improved varieties. Additionally, poor market awareness, labor-intensive processing, and weak infrastructure limit its commercial growth despite its nutritional value. Little millet has been cultivated in India since ancient times, especially in tribal and hilly areas. Known for its drought resistance, it spread to nearby regions like Sri Lanka and Nepal, serving as a vital cereal crop for early communities (Kheya *et al*.,2023) . Understanding the genetic makeup of a genotype is crucial for designing effective breeding methodologies. Most important traits are controlled by many genes and strongly influenced by the environment, causing low heritability and making selection difficult. Accounting for environmental variation in complex traits remains a key challenge in prediction and

analysis. Identifying trends in environmental indices and linking them to genetic changes is vital for understanding complex plant traits and predicting future climate impacts (Napier *et al*., 2022). Though empirical breeding has achieved much, new tools like genomics, speed breeding, and gene editing must be adopted to meet future food demands amid climate change and resource challenges (Xiong *et al*., 2022). Crop variety success relies on choosing the right parents and understanding gene activity and environment effects on traits. Combining ability studies provide this key information to plan effective breeding. This method helps identify parents with high general combining ability (GCA) and parent pairs with high specific combining ability (SCA). Combining ability analysis helps identify parents with strong trait transmission (GCA) and specific parent pairs with superior hybrid performance (SCA). It assesses the roles of additive (GCA) and non-additive (SCA) gene actions in trait inheritance to guide breeding strategies (Rajan *et al*., 2022). Selecting parents only by phenotype is insufficient. Hybridization is the best method to increase yield and develop high-yielding varieties. Success depends on choosing parents based on genetic merit, not just appearance (Ali *et al*., 2020). This technique helps estimate additive and nonadditive gene actions, guiding heterosis use and pure line selection. Increasing sustainable agricultural production relies heavily on technological advancements and innovation (Diaz *et al*., 2023). The United Nations Food and Agriculture Organization (FAO) describes this transformative impact as the "Digital Agricultural Revolution (Bellon-Maurel *et al*., 2022). Environmental computing currently supports various services, allowing users to manage regulation, control, and commands. Research is now exploring the development of intelligent controllers using fuzzy logic for enhanced adaptability and decision-making (Prauzek *et al*., 2016). As a consequence, this research used an artificial neural network to analyze gene activity, heterosis, and their complex interactions for developing diverse fragrant rice traits (Farooq *et al*.,2024).

Most important agronomic traits in little millet are influenced by environment, causing low heritability and challenging selection (Nageraja *et al*.,2023). Combining ability studies guide breeding plans. As a consequence, this study used an artificial neural network to analyze gene action, heterosis, and interactions in developing various little millet traits.

2. Materials and Methods

The experiment was conducted during *Kharif*, 2019 at Agricultural Research Station, Perumallapalle, Tirupati situated at an altitude of 182.9 m above mean sea level, 13°N latitude and 79°E longitude.

Experimental material used in the present study comprised of nine parents and twenty cross combinations obtained by crossing four lines (females) *viz*., BL-6, GPUL-4, Nallasama and WV-126 with a set of five testers (male) *viz*., BL-150, DHLTMV-14-1, GPUL-2, KOPLM-53 and OLM-203 in line x tester mating design (kempthorne, 1957). The F_1s were raised in a randomized complete block design (RBD) with two replications along with parents during *kharif*, 2019 at Agricultural Research Station, Perumallapalle. The list of pedigree details of nine parents used in the study are presented in Table 1.

All the 20 crosses were developed by following Line × Tester mating design and sufficient number of hand pollinated seeds were produced during *kharif*, 2018 at Agricultural Research Station, Perumallapalle. Simultaneous hand emasculation and pollination was done between 8 AM to 9 AM. During this time florets opened at a rate that made it possible to emasculate them efficiently. For pollination male parents were rubbed and allowed to open. Opened male florets were placed in a glassine bag, which was inverted over the emasculated panicle. This was left for five days for crossing and to preserve moisture.

Table 1: Details of nine little millet parents used in the present study

S. No.	*Genotypes*	*Pedigree*	*Centre*
LINES			
1	BL-6	Paiyur-1 × OLM-29	Jagdalpur
2	GPUL-4	JK-8 × Peddasame	Banglore
3	Nallasama	Selection from Local	ARS, Perumallapalle
4	WV-126	Local collection from Dangas	Waghai
TESTERS			
5	BL-150	Paiyur-2 × DLM-369	Jagdalpur
6	DHLTMV-14-1	CO-2 × TNAU-110	Hanumanamatti
7	GPUL-2	Pure line selection from Peddasame	Banglore
8	KOPLM-53	Selection from local germplasm	Kolhapur
9	OLM-203	Pure line selection from Lakshmipur local	Berhampur

The nine parents and 20 crosses were tested during *kharif,* 2019 in a Completely Randomized Block Design with two replications.

2.3. Experimental details

The experiment was conducted at the Agricultural Research Station, Perumallapalle, Tirupati, during the Kharif season of 2019, using a Randomized Block Design (RBD) with two replications. The study involved 20 F1 hybrids and 9 parental entries, with rows of 3 meters and spacing of 22.5 cm × 7.5 cm. Fertilizer applied was 20:20:20 NPK (kg ha^{-1}). Sowing was done by hand dibbling on 27th July 2019. Observations were recorded on five randomly selected plants for most traits, except days to 50% flowering and days to maturity, which were recorded per plot. The values were averaged and reported as the mean for each trait.

2.4. Statistical Methods

In computing the ANOVA for combining ability effects, parents and crosses were treated as fixed variables, whereas replication was treated as a random effect. The individual effects are estimated as follows:

(i) *gca* effects of lines $(g_i) = \frac{x_{i\cdot\cdot}}{tr} - \frac{x\ldots}{ltr}$

(ii) *gca* effects of testers $(g_j) = \frac{x_{\cdot j\cdot}}{lr} - \frac{x\ldots}{ltr}$

(iii) *sca* effects of crosses $(s_{ij}) = \frac{x_{ij\cdot}}{r} - \frac{x_{i\cdot\cdot}}{tr} - \frac{x_{\cdot j\cdot}}{lr} + \frac{x\ldots}{ltr}$

Where,

$x_{i..}$ = Total of i^{th} line over 't' testers and 'r' replications

$x_{.j.}$ = Total of j^{th} tester over 'l' lines and 'r' replications

x… = Total of all cross combinations over all replications

$x_{ij.}$ = Total of the hybrid between 'i^{th}' line and 'j^{th}' tester over 'r' replications.

t = Number of testers

l = Number of lines

r = Number of replications.

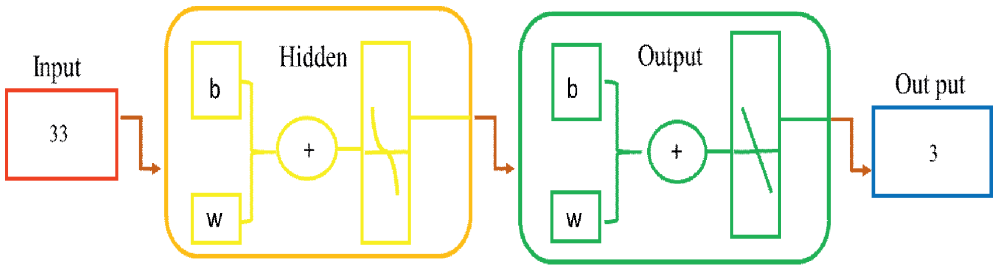

Figure 1: Artificial Neural Network (ANN) Validation Architecture with Input, Hidden, and Output Layers

Artificial neural networks help solve real-world problems such as predicting crop yields under variable environmental conditions, diagnosing plant diseases early, optimizing food processing parameters, forecasting market demand, and managing resources sustainably in agriculture and food industries (Farooq *et al*., 2024). Artificial neural networks are also valuable in other disciplines, including medicine for disease diagnosis, finance for risk assessment and stock prediction, engineering for system optimization, and environmental science for climate modeling and pollution monitoring (Zhang *et al*., 2025). Artificial neural networks are widely used in areas beyond food processing. For example, they support smart vehicle security through facial recognition, automate gender recognition in virtual assistants, and even assist in cryptographic analysis and credit scoring systems within the banking sector (Zhang *et al*., 2025). Artificial neural networks are widely applied in plant breeding for tasks such as predicting crop yield, identifying disease resistance, analyzing phenotypic traits, and accelerating the selection of superior genotypes. They enable efficient handling of complex data, improve selection accuracy, and contribute to the development of resilient, high-yielding crop varieties. AI-driven models optimize storage, transportation, and logistics in agriculture, reducing waste and improving efficiency through data analytics and smart route planning. Artificial neural networks are increasingly used to enhance agricultural production efficiency and farm management by analyzing complex data for better decision-making, as highlighted in scientific articles on ANN applications in agriculture (Castillo *et al*.,2025) Machine learning integration in farming demands robust software to handle vast data generated through the growing season—from sensors, weather stations, and soil tests. These

systems analyze complex data to provide predictive insights on crop health, pest control, irrigation timing, and yield forecasts. Effective data management and AI-driven analysis enable optimized resource use, cost reduction, and enhanced farm productivity (Swami Durai *et al*., 2022). With the growing emphasis on precision farming and digital agriculture, an increasing number of farms are adopting artificial intelligence-driven tools. The structural design of the artificial neural network (ANN) is illustrated in Figure 1 and described below.

A neural network model processes information through multiple layers, beginning with the input layer, which receives data from external sources. This data is then transmitted to one or more hidden layers—networks of interconnected neurons that analyze and transform the information using mathematical operations. While a simple neural network may have a single hidden layer, more complex models can include multiple hidden layers to capture intricate patterns. Finally, the processed data reaches the output layer, which consolidates the computations from previous layers to produce the network's final decision or prediction. The output layer may consist of one or several nodes depending on the complexity and purpose of the model (Attri *et al*., 2023).

Due to advancements in industrial automation and the Internet of Things (IoT), acquiring data for monitoring operations such as food drying, extrusion, and sterilization has become considerably simpler. Artificial Neural Networks (ANNs) have become preferred in food process engineering, excelling at modeling complex, nonlinear relationships and outperforming traditional regression techniques in predicting food quality parameters, safety assessments, and grading systems (Alsaedi *et al*., 2024). Meanwhile, in the broader agricultural landscape, AI-enhanced digital twins—powered by machine learning and fed by real-time data from sensors, drones, and remote sensing platforms—are enabling dynamic virtual representations of farms. These systems facilitate accurate simulation and optimization of farm operations, thereby enhancing efficiency, resilience, and sustainability (Awais *et al*., 2025). Farmers increasingly use IoT sensors—such as for soil moisture, environmental monitoring, and variable-rate irrigation—enabling data-driven management of inputs like water and fertilizers. However, it also highlights significant limitations to

adoption, including costs, communication range, power consumption, and scalability issues across rural areas (Hundal *et al*., 2023).

3. Results and Discussion

The analysis of variance explained substantial differences here between parents (P), F1, and the P vs. F1 interaction (Table 2). This revealed that the treatments had a lot of genetic variability amongst them. For almost all of the characteristics, significant differences due to the P vs. F1 interaction revealed significant differences in SCA among hybrids. The findings highlighted the relevance of combining aptitude studies and suggested that selecting acceptable parents and crosses for the generation of appropriate varieties and hybrids had a decent chance.

3.1. Nature of Gene Action

Estimates of highly significant GCA and SCA variation for every trait showed that both additive and non-additive genes contributed to the characters' expression. A number of quantitative characteristics, including additive and nonadditive gene effects, were inherited in little millet, supporting earlier research by Anuradha *et al*. (2017) and Tejashwini *et al*. (2024). For the majority of the characteristics, the σ2 GCA/σ2 SCA ratio was less than unity, which further suggested that nonadditive genetic variation predominated (Nandaniya *et al*., 2016). Therefore, for this characteristic, heterosis breeding could be beneficial. On the other hand, transgressive breeding is a better choice for these characteristics since days to 50% blooming and days to maturity were mostly regulated by additive gene activity. The conventional pedigree method would leave the unfixable components of genetic variances untapped for grain yield and its associated traits, which were primarily controlled by additive and non-additive gene action. In addition, alternative breeding techniques like biparental mating, reciprocal recurrent selection, or diallel selective mating may be reconstituted.

3.3. GCA Effects and Performance Per Se of Parents

Combining ability analysis identifies suitable parental lines for hybridization. General Combining Ability (GCA) reflects overall parental performance and is influenced by stable traits and additive genetic factors. According

Table 2: Combined analysis of variance for L X T crosses and analysis of variance for combining ability for 10 quantitative traits in the F1 generation

Source of variation	*df.*	*Days to 50% flowering*	*Days to maturity*	*Plant height (cm)*	*Number of productive tillers per plants*	*Panicle length (cm)*	*Main panicle weight per plant (g)*	*1000-seed weight (g)*	*Fodder yield per plant(g)*	*Harvest index (%)*	*SPAD chlorophyll meter reading*	*Specific leaf area(cm2/g)*	*Grain yield per plant (g)*
Replications	1	2.03	2.5	102.72	0.4	2.03	0.154	0.12	20.45	20.25	0.18	452.73	0.03
Croses	19	205.07**	197.47**	283.02**	4.75**	11.93**	3.74**	0.44**	88.65**	97.10**	46.87*	4798.76**	13.57**
Lines	3	958.69**	910.57**	148.23	5.03**	28.26**	4.42**	0.1	79.37**	265.78**	53.69	3645.20**	20.31**
Testers	4	28.79**	31.60**	655.95**	2.71**	4.51*	3.96**	0.28*	152.10**	99.49**	77.27**	1792.83**	15.40**
Lines × Testers	12	75.42**	74.48**	192.40*	5.36**	10.32**	3.50**	0.58**	69.83**	54.13**	35.03	6089.13**	11.27**
Error	19	2.76	5.03	62.05	0.93	1.48	0.33	0.08	9.23	8.6	16.92	398.37	1.87
GCA variance		52.39	51.59	38.85	0.35	1.62	0.42	0.01	11.76	19.38	5.81	244.22	1.79
SCA variance		26.62	33.86	69.99	2.32	4.27	1.55	0.25	29.97	22.97	10.95	2784.07	4.7
GCA/SCA		1.97	1.52	0.56	0.15	0.38	0.27	0.04	0.39	0.84	0.53	0.09	0.38
σ^2A		104.79	103.18	77.7	0.7	3.24	0.84	0.02	23.52	38.76	11.63	488.45	3.58
σ^2D		26.62	33.86	69.99	2.32	4.27	1.55	0.25	29.97	22.97	10.95	2784.07	4.7
Ratio σ^2A: σ^2D		3.93	3.04	1.11	0.3	0.75	0.54	0.1	0.78	1.68	1.06	0.17	0.75

* Significant at 5% level, ** Significant at 1% level

to Renganathan (2017), selecting parents based on GCA is crucial in plant breeding.

Key indicators for evaluating parental lines are mean performance and General Combining Ability (Table 3). According to Mohan *et al*. (2002), Dangariya *et al*. (2009), and Nandaniya et al. (2016), parents excelling in both are considered excellent combiners. Combining mean performance and GCA traits provides a framework for selecting the best parents for hybridization.

Heterosis breeding is beneficial for this trait, while transgressive breeding is better for days to 50% bloom and maturity, controlled by additive genes. Parental lines for hybridization are selected based on combining ability analysis, using GCA or parental line performance. Strong combiners are those with good mean performance and GCA impact.

OLM-203 performed well in terms of plant height, 1000-seed weight, fodder production, SPAD reading, and harvest index, although it had negative GCA impacts. In terms of plant height, panicle length, primary panicle weight, fodder yield, SPAD reading, and seed yield, GPUL-2 performed well and had favourable GCA impacts. Grain yield and important characteristics such as harvest index, panicle weight, and productive tillers were positively impacted by GCA in NALLASAMA. Because additive gene effects affect grain yield, conventional breeding techniques, such as matching suitable donor and restorer parents, are useful for increasing yield.

None of the parental lines showed high general combining ability (GCA) across all traits based on their GCA impacts because character traits are complementary, which is prominent among the component characters. By assigning a score of "+1" for significant GCA effects in a desirable direction, "-1" for major GCA effects in an undesirable direction, and "0" for nonsignificant GCA effects, a scoring system was used to identify the overall best general combiners for each characteristic separately (Table 4). Following this assessment, GPUL-2, NALLASAMA, and GPUL-4 were found to be the best combiners overall. With their increased potential for heterosis, these parents become excellent candidates for additional hybridisation. WV-126 and BL-150, on the other hand, were found to be inadequate combiners.

Table 3: Per se and GCA effects performance of parents for 12 quantitative traits

Genotype	Days to 50% flowering		Days to maturity		Plant height (cm)		Number of productive tillers per plant		Panicle length (cm)		Main panicle weight per plant (g)		1000-seed weight (g)		Fodder yield per plant (g)		Harvest index (%)		SPAD chlorophyll meter reading		Specific leaf area (cm2/g)		Grain yield per plant (g)	
	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	GCA	Per se	SCA
Lines																								
BL-6	53	-2.47	87	-2.45**	104	1.91	4	-0.25	28.2	2.06**	1.9	-0.19	2.8	0.03	8.8	0.03	26.4	-2.33*	38.5	-2.12	97.1	-3.77	3.8	-0.98*
GPUL-4	48	-10.57**	81	-10.35**	107.2	4.18	5	-0.29	27.8	-0.79	0.4	0.83**	2.6	0.03	1.7	3.82**	26.4	-6.13**	39.7	2.71*	100.4	11.95	0.8	-1.14*
Nallasama	47	0.03	84	0.15	109.8	-1.51	5	1.05**	25.9	0.56	4.1	0.68**	2.3	0.09	20.1	-0.96	22.5	4.88**	38.8	1.13	129.3	-25.34**	7	1.95**
WV-126	72	13.02**	106	12.65**	86.4	-4.59	7	-0.51	25.6	-1.82**	0.9	0.342	2.1	-0.15	8.7	-2.89**	29.9	3.59**	39.3	-1.73	79	17.17	4.1	0.17
SE(gi)		0.53		0.71		2.49		0.31		0.38		0.92		0.09		0.96		0.92		1.3		6.31		0.43
Testers																								
BL-150	68	-0.82	87	-0.82	97.8	-6.54*	5	-0.02	25.9	0.04	1.4	-0.73**	2.7	-0.02	8.8	-5.17	28.4	-0.01	34.6	0.04	91	12.52	4.1	-1.79**
DHLTMV - 14-1	59	1.3	92	1.05	109.3	-2.69	5	0.45	30.3	-0.14	2.5	-0.26	2.8	-0.08	11.4	4.28**	28.5	-5.05**	40	-3.25*	126.3	12.74	5.6	-0.77
GPUL-2	74	-0.82	108	-1.08	140.9	12.76**	4	0.5	27.8	1.18*	5.5	1.05**	2.5	0.13	36.4	4.47**	21.3	-0.75	42	3.47*	137.6	3.85	11.3	1.92**
KOPLAM-53	73	2.55	107	2.92**	99.9	5.62*	6	0.01	27.5	-0.19	2.7	0.33	2.2	-0.25**	12.8	-0.27	28.7	1.06	36.5	2.7*	129.3	-6.21	6.3	0.21
OLM-203	73	-2.2	107	-2.08*	102.3	-9.14**	5	-0.94**	28.5	-0.89	1.2	-0.38	2.7	0.22*	9.8	-3.30**	29.4	4.75**	38.7	-2.96*	122.9	-22.89*	4.6	0.43
SE(gj)		0.59		0.79		2.79		0.34		0.43		1.03		0.1		1.07		1.03		1.45		7.05		0.48

* Significant at 5% level, ** Significant at 1% level

Table 4: Scoring of parents based on their rank in GCA effects for 12 quantitative characters in the F_1 generation.

Parents	*Days to 50% flowering*	*Days to maturity*	*Plant height (cm)*	*Number of productive tillers per plant*	*Panicle length (cm)*	*Main panicle weight per plant (g)*	*1000-seed weight (g)*	*Fodder yield per plant (g)*	*Harvest index (%)*	***SPAD chlorophyll meter reading***	***Specific leaf area (cm2/g)***	***Grain yield per plant (g)***	***Total***	***Category***
BL-6	0	1	0	0	1	0	0	0	-1	0	0	-1	0	Low
GPUL-4	1	1	0	0	0	1	0	1	-1	1	0	-1	3	high
Nallasama	0	0	0	1	0	1	0	0	1	0	-1	1	3	High
WV-126	-1	-1	0	0	-1	0	0	-1	1	0	0	0	-3	low
BL-150	0	0	-1	0	0	-1	0	0	0	0	0	-1	-3	Low
DHLTMV-14-1	0	0	0	0	0	0	0	1	-1	-1	0	0	-1	Low
GPUL-2	0	0	1	0	1	1	0	1	0	1	0	1	6	High
KOPLAM-53	0	-1	1	0	0	0	-1	0	0	1	0	0	0	Low
OLM-203	0	1	-1	-1	0	0	1	-1	1	-1	-1	0	-2	Low

3.3. SCA Effects and Performance Per Se of Crosses.

SCA effects are especially useful for evaluating the genetic value of crosses as breeding material since they are thought to represent manifestations of non-additive components of genetic diversity. According to Falconer and Mackay (1996), they have been connected to the presence of linkage during the repulsion phase or the combination of positive, favourable genes from different parents.

Although there were some notable exceptions, favourable, substantial SCA across attributes often corresponded with improved performance in and of itself; as a result, selection should jointly weight both measurements. While Nallasama × GPUL-2 had negative SCA for 1,000-seed weight and productive tillers, it displayed positive SCA for grain yield per plant, main panicle weight, harvest index, and specific leaf area. GPUL-4 × DHLTMV-14-1 matched strong per se performance with positive SCA only for fodder yield, while WV-126 × BL-150 combined high per se performance with positive SCA for productive tillers, fodder yield, and specific leaf area among the six strong particular combiners (Table 5). Strong per se performance was demonstrated by WV-126 × GPUL-2 and GPUL-4 × KOPLM-53, which had ideal SCA for earliness—days to 50% blooming and days to maturity. These trends highlight the necessity of combining SCA and per se performance in order to find better, more balanced hybrids. These crosses can help exploit heterosis for yield and related traits in little millet. The practical strategy is to capture hybrid vigour via hybrids, synthetics, or composites. Many crosses showed desirable SCA for some traits, but none were universal combiners in F_1. Positive SCA often matched strong per se performance, though not always—so selection should use both.

3.4. Heterosis

Negative heterosis is aimed for days to 50% blooming and maturity, but positive heterosis is chosen for yield and its constituent parts (Nagaraja et al., 2024; Amaravel et al., 2024). Only GPUL-4 X OLM-203 shown negative heterosis for days to maturity, whereas the other four crosses—Nallasama X GPUL-2, WV-126 X BL-150, and WV-126 X OLM-203—showed positive heterosis for single-plant yield. To counteract biotic and abiotic stressors, breeders prioritise plants that mature early (Joshi et al., 2023; Gebreyohannes

Table 5: F_1 hybrid performance and SCA effects across 12 quantitative traits

Genotype	Days to 50% flowering		Days to maturity		Plant height (cm)		Number of productive tillers per plant		Panicle length (cm)		Main panicle weight per plant (g)		1000-seed weight (g)		Fodder yield per plant (g)		Harvest index (%)		SPAD chlorophyll meter reading		Specific leaf area (cm2/g)		Grain yield per plant (g)	
	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA	Per se	SCA
BL-6 X BL-150	57.5	-4.27*	91	-4.17 *	121.6	2.16	5	-0.7	33.2	2.24*	2.6	0.45	2.3	-0.17	14.2	-2.38	27.9	3.63	38.2	1.8	63.2	-64.09**	5.4	0.54
BL-6 X DHLTMV-14-1	60	-3.9	93	-4.05 *	125.5	2.21	7	0.62	27.8	-2.98 **	3.3	0.72	2.3	-0.14	25.7	-0.33	19.9	0.7	31.5	-1.59	110.7	-16.8	6.4	0.5
BL-6 X GPUL-2	58	-3.27*	92	-2.42	131.7	-7.03	6	-0.52	29.8	-2.30 *	4.3	0.36	3.3	0.67**	30.6	4.36	20.6	-2.88	41.3	1.48	136.6	18.01	8	-0.61
BL-6 X KOPLM-53	74	8.85*	107	8.57**	122.6	-9	5	-0.62	30	-0.73	2.8	-0.37	2.4	0.2	15.7	-5.78 *	28.8	3.44	34.3	-4.74	134.6	26.03	6.3	-0.54
BL-6 X OLM-203	63	2.6	96	2.07	128.5	11.66 *	6	1.22	33.8	3.77**	1.3	-1.16*	2.1	-0.56 **	22.6	4.14	24.1	-4.89 *	36.5	3.05	128.7	36.83*	7.2	0.1
GPUL-4 X BL-150	53	-0.67	87	-0.27	116.3	-5.4	4	-1.46 *	26.4	-1.71	2.1	0.56	2.2	-0.31	14.4	-5.96 *	21.6	1.15	40.2	-1.07	145.1	2.11	4	-0.75
GPUL-4 XDHLTMV-14-1	60.5	4.7*	94	4.85*	133.6	8.04	6	-0.43	29.5	1.56	2.7	0.76	2.7	0.28	36.4	6.58**	15.1	-0.33	35.5	-2.42	118.3	-24.93	6.4	0.67
GPUL-4 X GPUL-2	55	1.32	88	0.97	143.1	2.09	6	0.31	31.3	2.03 *	1	-2.29**	2.2	-0.38 *	23.8	-6.21 *	14.3	-5.36*	39.2	-5.50*	110.9	-23.44	4	-4.43**
GPUL-4 X KOPLM-53	50	-7.05 *	84	-7.02**	123.6	-10.22	7	0.91	27.3	-0.59	2.9	0.3	2.3	0.08	29	3.83	22.5	0.98	48.5	4.57	175	50.70 **	8.5	1.74
GPUL-4 X OLM-203	54	1.7	87	1.47	124.6	5.49	5	0.66	25.9	-1.29	2.5	0.66	3	0.33	24	1.76	28.8	3.56	42.7	4.42	103.2	-4.43	9.7	2.76**
Nallasama X BL-150	64	-0.27	97	-0.77	113	-3.01	7	0.4	29.3	-0.15	1.9	-1.14 *	3.5	0.97**	14.6	-0.98	31.5	0.05	37.5	-2.14	51	-54.68**	6.3	-1.55
Nallasama X DHLTMV-14-1	59.5	-6.9*	93	-6.65**	118.3	-1.56	10	2.12**	31.9	2.62*	2.2	-1.27 **	2.6	0.1	24.6	-0.43	26.8	0.4	39.5	3.1	126.6	20.6	9.2	0.33
Nallasama X GPUL-2	72	8.22 *	106	8.47 **	144.1	8.78	5	-2.12 **	30	-0.6	7.6	2.74 **	2.2	-0.50 *	23	-2.23	40.8	10.10**	47.8	4.73	134.8	37.75*	15.9	4.35**
Nallasama X KOPLM-53	69	1.85	103	1.97	139.3	11.12 *	7	0.27	29.8	0.57	3.5	-0.55	2.1	-0.19	26	5.61*	26.3	-6.20 **	39.1	-3.19	76.9	-10.81	9.3	-0.5
Nallasama X OLM-203	60	-2.9	93	-3.02	98.1	-15.31 **	5	-0.67	26.1	-2.43*	3.6	0.23	2.4	-0.38*	15.5	-1.96	31.8	-4.36 *	34.2	-2.49	77.4	7.13	7.4	-2.62*
WV-126 X BL-150	82	5.22*	115	5.22 *	119.2	6.26	7	1.76 **	26.7	-0.37	2.8	0.12	1.8	-0.49 *	23	9.33 **	25.3	-4.84 *	38.2	1.41	264.9	116.60 **	7.8	1.75
WV-126 X DHLTMV-14-1	85	6.1	118	5.85 **	108.1	-8.68	4	-2.31 **	25.7	-1.2	2.9	-0.21	2	-0.24	17.3	-5.81 *	24.3	-0.77	34.4	0.91	169.6	21.13	5.5	-1.5
WV-126 X GPUL-2	71	-6.27*	103	-7.02 **	128.4	-3.83	8	2.33 **	29.1	0.87	3.7	-0.81	2.7	0.21	27.4	4.08	27.6	-1.86	39.5	-0.71	107.2	-32.32	10.4	0.68
WV-126 X KOPLM-5	77	-3.65	110	-3.52*	133.2	8.1	5	-0.56	27.6	0.75	4.4	0.62	2	-0.09	14.9	-3.66	33	1.77	42.8	3.36	63.6	-65.92**	7.3	-0.69
WV-126 X OLM-203	74	-1.4	108	-0.52	108.5	-1.83	3	-1.21	26.1	-0.05	3.3	0.26	3.2	0.61 **	11.6	-3.94	40.6	5.70*	28.8	-4.98	73.3	-39.54 *	8	-0.24
Mean of crosses	65		98.4		124		6		28.9		3.01		2.5		21.7		26.6		38.5		118.5		7.6	
General mean	64.5		97.5		118.6		5.69		28.4		2.8		2.5		19.1		26.6		38.9		116.7		6.9	
C.D. 5%	9.6		5.3		14.9		1.7		2.7		1.3		0.5		6.5		5.9		7.4		47		2.7	
S.E(m)	3.3		1.8		5.1		0.6		0.9		0.4		0.2		2.2		2		2.6		16.1		0.9	
S.E(d)	4.7		2.6		7.2		0.8		1.3		0.6		0.2		3.1		2.8		3.6		22.8		1.3	
C.V.	7.3		2.6		6.1		14.9		4.7		22		10.1		16.5		10.7		9.4		19.6		18.9	

* Significant at 5% level, ** Significant at 1% level

et al., 2024). While Nallasama X DHLTMV-14-1, WV-126 X OLM-203, WV-126 X BL-150, and GPUL-4 X OLM-203 shown negative heterosis for days to maturity, the other four exhibited positive, substantial midparent heterosis for yield. The interplay of its constituent parts causes heterosis in grain yield (Grafius, 1959). Four hybrids showed significant heterosis for key yield traits like panicle length and main panicle weight.

3.5. Heterosis and Combining Ability Effects

The majority of crosses showed considerable midparent heterosis and positive, significant SCA effects in the intended direction, according to the study of heterosis over midparent and SCA effects Table 6. This demonstrated the predominance of non-additive gene activity in the expression of observed heterosis. The heterosis over mid- and better-parent for 10 quantitative features in the F1 generation is compiled in Table 7. Based on the GCA impacts of the related parents, parent grouping revealed high and low GCA parents, and F1 hybrids from these groups showed significant midparent heterosis. Our results are in line with Nandaniya et al. (2016), who discovered superior SCA effects from crosses involving all combinations of general combiners (Table 8): High x High, High x Low, Low x High, and Low x Low. This is in contrast to the expectation that high GCA parents would always produce hybrids with high SCA effects, as suggested by Patel et al. (2016) and Rashitha et al. (2024). High × Low GCA parents had the largest percentage of hybrids exhibiting considerable heterosis (48.57%), followed by High × High (28.57%) and Low × Low (22.85%) GCA parents. High performance resulted from the crosses' notable specific combining ability (SCA) impacts. Due mainly to non-additive genetic factors including dominance and epistasis, crosses with Low × Low GCA parents performed better (Rasitha et al., 2024). The interplay between positive alleles from strong combiners and negative alleles from bad combiners is responsible for the high yield potential of crosses with High SCA involving High × Low combiners. Low × Low general combiners contributed to the high mean grain production and notable SCA impacts of the GPUL-4 × OLM-203 cross combination in the F1 generation.. In segregating generations, this implies the possibility of recovering elite transgressive segregants. The interaction between positive alleles, which are permanent and fixable because of additive

Table 6: Top F_1 hybrids showing high SCA effects and superior per se performance across 12 quantitative traits

Character	*Hybrids*	*SCA effect*	*Better parent heterosis*	*Per se performance*
Days to 50% flowering	BL-6 X BL-150	-4.27*	-16.06 *	57.5
	BL-6 X GPUL-2	-3.27*	-21.48 **	58
	GPUL-4 X KOPLM-53	-7.05 *	-31.97 **	53
	Nallasama X DHLTMV-14-1	-6.9*	0.85	59.5
	WV-126 X GPUL-2	-6.27*	-4.7	71
Days to maturity	BL-6 X BL-150	-4.17 *	4	91
	BL-6 X DHLTMV-14-1	-4.05 *	1.09	93
	GPUL-4 X KOPLM-53	-7.02**	-21.50 **	84
	Nallasama X DHLTMV-14-1	-6.65**	1.09	93
	WV-126 X GPUL-2	-7.02 **	-5.07 *	103
	WV-126 X KOPLM-5	-3.52*	3.27	110
Plant height (cm)	Nallasama X OLM-203	-15.31 **	-10.66	98.1
Number of productive tillers per plant	Nallasama X DHLTMV-14-1	2.12**	104.26 **	10
	WV-126 X BL-150	1.76 **	8.11	7
	WV-126 X GPUL-2	2.33 **	24.62	8
Panicle length (cm)	BL-6 X BL-150	2.24*	17.90 **	33.2
	BL-6 X OLM-203	3.77**	18.70 **	33.8
	GPUL-4 X GPUL-2	2.03 *	12.43 *	31.3
	Nallasama X DHLTMV-14-1	2.62*	5.37	31.9
Main panicle weight per plant (g)	Nallasama X GPUL-2	2.74 **	38.33 **	7.6
1000-seed weight (g)	BL-6 X GPUL-2	0.67**	17.47	3.3
	Nallasama X BL-150	0.97**	31.95 **	3.5
	WV-126 X OLM-203	0.61 **	16.21	2.4
Fodder yield per plant (g)	GPUL-4 XDHLTMV-14-1	6.58**	217.90 **	36.4
	Nallasama X KOPLM-53	5.61*	29.59	26
	WV-126 X BL-150	9.33 **	159.89 **	23
Harvest index (%)	Nallasama X GPUL-2	10.10**	81.40 **	40.8
	WV-126 X OLM-203	5.70*	36.02 **	40.6
Specific leaf area (cm2/g)	BL-6 X OLM-203	36.83*	4.75	128.7
	GPUL-4 X KOPLM-53	50.70 **	35.37	175
	Nallasama X GPUL-2	37.75*	-2.05	134.8
	WV-126 X BL-150	116.60 **	191.19 **	264.9
Grain yield per plant (g)	GPUL-4 X OLM-203	2.76**	113.17 **	9.7
	Nallasama X GPUL-2	4.35**	39.97 **	15.9

* Significant at 5% level, ** Significant at 1% level

Table 7: Mid- and better-parent heterosis for 12 quantitative traits in F_1 hybrids

Genotype	*Days to 50% flowering*		*Days to maturity*		*Plant height (cm)*		*Number of productive tillers per plant*		*Panicle length (cm)*		*Main panicle weight per plant (g)*		*1000-seed weight (g)*		*Fodder yield per plant (g)*		*Harvest index (%)*		*SPAD chlorophyll meter reading*		*Specific leaf area (cm2/g)*		*Grain yield per plant (g)*	
	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB	RH	HB
BL-6 X BL-150	-5.74	-16.06 *	4.3	4	20.53 **	16.95 *	5.54	-1.48	22.77 **	17.90 **	55.46	36.13	-15.83	-18	61.27	60.45	1.78	-1.76	4.68	-0.6	-32.81	-34.94	38.12	33.37
BL-6 X DHLTMV-14-1	6.67	1.69	3.62	1.09	17.69 **	14.82 *	50.69 **	47.03 *	-4.85	-8.18	50.45	32.02	-18.35 *	-19.07 *	154.33 **	124.45 **	-27.49 **	-30.18 **	-19.61 *	-21.15 *	-0.92	-12.38	36.64	14.78
BL-6 X GPUL-2	-8.59	-21.48 **	-5.61 *	-14.75 **	7.56	-6.53	29.55	29.55	6.55	5.82	16.61	-21.32	23.87 **	17.47	35.52 **	-15.93	-13.57	-21.93	2.78	-1.5	16.41	-0.72	5.42	-29.66 *
BL-6 X KOPLM-53	16.54 *	0.68	10.54 **	0.47	20.27 **	17.91 *	1.04	-10.45	7.84	6.53	22.55	4.22	-3.08	-13.01	45.47	22.42	4.37	0.21	-8.41	-10.73	18.91	4.13	26.21	1.36
BL-6 X OLM-203	-0.4	-13.70 *	-1.29	-10.28 **	24.57 **	23.58 **	21.21	9.09	19.36 **	18.70 **	-12.95	-30.16	-22.28 *	-23.53 *	143.86 **	131.20 **	-13.64	-18.08	-5.48	-5.81	17.01	4.75	72.57 *	58.18
GPUL-4 X BL-150	-9.4	-22.63 **	3.57	0	13.47 *	8.51	-14.76	-17.24	-1.79	-5.17	128.10 *	44.25	-18.45 *	-18.98	171.70 **	62.71	-21.18 *	-23.93 *	8.18	1.21	51.65 *	44.52	64.43	-2.45
GPUL-4 XDHLTMV-14-1	12.56	2.54	8.67 **	2.17	23.43 **	22.23 **	21.21	19.25	1.52	-2.56	88.32 *	8.3	0	-2.36	451.52 **	217.90 **	-45.12 **	-47.15 **	-10.83	-11.16	4.33	-6.38	102.37 *	14.96
GPUL-4 X GPUL-2	-10.57	-26.17 **	-7.12**	-18.89 **	15.37 **	1.56	41.61 *	35.98	12.56 **	12.43 *	-65.68 **	-81.65 **	-13.23	-15.05	24.77	-34.62 **	-39.90 **	-45.71 **	-4.04	-6.62	-6.83	-19.43	-33.91	-64.74 **
GPUL-4 X KOPLM-53	-18.03 *	-31.97 **	-10.64 **	-21.50 **	19.42 **	15.37 *	26.01	15.89	-1.3	-1.94	85.19 *	5.5	-4.63	-11.81	299.31 **	126.90 **	-18.37	-21.62 *	27.21 **	22.10 *	52.37 **	35.37	141.31 **	35.3
GPUL-4 X OLM-203	-11.11	-26.03 **	-6.91 **	-18.22 **	18.95 **	16.25 *	5.06	-1.82	-8.02	-9.04	228.08 **	118.01 *	14.04	12.15	316.49 **	145.52 **	3.04	-2.26	8.83	7.5	-7.6	-16.04	265.38 **	113.17 **
Nallasama X BL-150	10.34	-6.57	13.12 **	11.49 **	8.86	2.91	51.41 **	45.81 *	13.03 **	13.02 *	-31.57	-53.75 **	40.54 **	31.95 **	0.72	-27.51	23.84 *	11.01	2.33	-3.2	-53.65 **	-60.52 **	12.74	-10.95
Nallasama X DHLTMV-14-1	11.74	0.85	5.38 *	1.09	7.99	7.74	105.90 **	104.26 **	13.53 **	5.37	-32.77	-45.54 **	1.18	-6.53	55.75 **	22.14	5.15	-5.94	0.25	-1.29	-0.99	-2.12	45.36 *	30.37
Nallasama X GPUL-2	18.85 *	-2.68	9.84 **	-2.3	14.96 **	2.27	18.68	14.89	11.74 *	8.01	58.41 **	38.33 **	-10.31	-13.52	-18.64	-36.81 **	86.37 **	81.40 **	18.48 *	13.98	1.01	-2.05	72.84 **	39.97 **
Nallasama X KOPLM-53	14.88 *	-5.44	8.09 **	-3.27	32.86 **	26.87 **	40.45 **	28.18	11.61 *	8.44	4.34	-12.99	-7.78	-9.85	58.35 **	29.59	2.78	-8.31	3.96	0.93	-41.07 *	-41.08 *	40.18 *	32.5
Nallasama X OLM-203	-0.41	-17.81 *	-2.35	-12.62 **	-7.51	-10.66	5.88	-1.82	-4.04	-8.34	37.92	-11.52	-5.15	-11.79	3.63	-23.04	22.67 *	8.22	-11.79	-11.83	-38.57 *	-40.10 *	27.84	5.33
WV-126 X BL-150	17.44 **	14.58 *	19.69 **	8.96 **	29.40 **	21.88 **	22.71	8.11	3.56	2.99	135.15 **	95.82 *	-25.62 *	-32.33 **	162.41 **	159.89 **	-13.05	-15.22	3.56	-2.6	211.67 **	191.19 **	90.93 **	90.70 *
WV-126 X DHLTMV-14-1	30.53 **	18.75 **	19.19 **	11.32 **	10.45	-1.1	-36.20 *	-45.95 **	-8.07	-15.11 **	68.90 *	16.32	-19.15 *	-27.59 **	71.88 *	51.09	-16.57	-18.46	-13.1	-13.91	65.15 **	34.21	14.74	-0.63
WV-126 X GPUL-2	-3.07	-4.7	-3.96	-5.07 *	12.96 *	-8.87	50.09 **	24.62	8.96	4.77	14.02	-33.03 **	13.31	5.77	21.56	-24.73 **	7.72	-7.73	-2.65	-5.79	-1.01	-22.09	35.13 *	-8.11
WV-126 X KOPLM-5	5.84	4.76	3.76	3.27	42.96 **	33.33 **	-20.68	-26.43	3.92	0.44	138.04 **	60.73 *	-10.66	-11.66	38.57	16.18	12.73	10.51	13.06	9.12	-38.95	-50.82 **	41.81	17.17
WV-126 X OLM-203	2.76	2.05	1.88	1.4	14.96 *	6.03	-45.72 **	-50.45 **	-3.54	-8.34	212.80 **	185.71 **	28.91 **	16.21	25.71	18.67	37.03 **	36.02 **	-26.04 **	-26.53 **	-27.41	-40.37 *	85.30 **	75.74 *
Maximum	-18.03	-31.97	-10.64	-21.5	-7.51	-10.66	-45.72	-50.45	-8.59	-15.11	-65.68	-81.65	-25.62	-32.33	-18.64	-36.81	-45.12	-47.15	-26.04	-26.53	-53.65	-60.52	-33.91	-64.74
Minimum	30.53	18.75	19.69	11.49	42.96	33.33	51.41	104.26	22.77	18.7	228.08	185.71	40.54	31.95	451.52	217.9	86.37	81.4	27.21	22.1	211.67	191.19	265.38	113.17
Average	4.04	-7.47	3.71	-3.08	17.46	11.65	7.61	11.35	5.27	2.29	60.07	17.77	-2.63	-7.558	106.21	51.32	-0.07	-6.05	-0.43	-3.39	9.43	-1.74	59.27	22.32
Number of crosses with positive heterosis	11 (5)	8 (2)	13 (8)	10 (3)	19 (15)	16 (10)	16 (6)	12 (3)	13 (7)	12 (4)	16 (9)	12 (5)	6 (4)	5 (1)	19 (11)	14 (6)	11 (4)	6 (2)	11(2)	6(1)	9(4)	6(1)	19(10)	14(5)
Number of crosses with negeitive heterosis	9 (1)	12 (8)	7 (4)	9 (7)	1 (0)	4 (0)	4 (2)	8 (2)	7 (0)	8 (1)	4 (1)	8 (4)	13 (5)	15 (4)	1 (0)	6 (3)	9 (4)	14 (5)	9(2)	14(2)	11(3)	14(5)	1(0)	6(2)

* Significant at 5% level, ** Significant at 1% level

gene activities, was linked to high SCA effects, according to the Nallasama × KOPLAM 53 cross, which had High × High GCA parents. Therefore, if there is no repulsion phase connection, superior segregants might be identified from this cross. Using the pedigree technique of selection, it is anticipated that these segregants will be useful in following generations. These results demonstrate how important parental variety is in influencing the observed heterosis, especially GCA effects.

Table 8: Cross frequency based on parental GCA effects for yield and related traits

Characters	*Number of significant heterotic (mp) hybrids and GCA effects of the parents involved*			
	High x High	*High x Low*	*Low x Low*	*Total*
Days to 50% flowering	0	0	0	0
Days to maturity	1	2	0	3
Plant height (cm)	0	0	0	0
Number of productive tillers per plant	0	0	0	0
Panicle length (cm)	0	0	0	0
Main panicle weight per plant (g)	2	1	0	3
1000-seed weight (g)	0	0	0	0
Fodder yield per plant (g)	2	3	1	6
Harvest index	2	6	4	12
SPAD chlorophyll meter reading	2	2	0	4
Specific leaf area (cm2/g)	0	0	1	1
Grain yield per plant (g)	1	3	2	6
Total	10	17	8	35
Percentage	28.57	48.57	22.85	100

4. Validation of Results Using ANN

In order to investigate the effective use of machine learning techniques, particularly Artificial Neural Networks (ANN), in construction management, the study takes into account both internal and external aspects. Although assessing various techniques for data performance may be useful, the main goal of this study is to determine how ANN might be applied in this domain. The study is organised as follows: the ANN model is shown once the suggested characteristics have been justified. The accessible database is analysed in the third step, and the findings are then reviewed

and contrasted with those of earlier research. An advanced technique for confirming and validating experimental results is artificial neural networks (ANNs). Tables 3-7 provide specifics for the inputs, including plant height, panicle length, and other factors. Ten neurones made up the hidden layer of the neural network used in the testing, which used 75% of the data for training, 15% for validation, and 15% for testing. With a value of 881.28, the performance indices based on these input parameters exhibit optimal performance at epoch 6, as shown in Figure 2. In a similar vein, Figure 3 shows the fitting curve with 96.4% accuracy. Finally, the error histogram is shown in Figure 4.

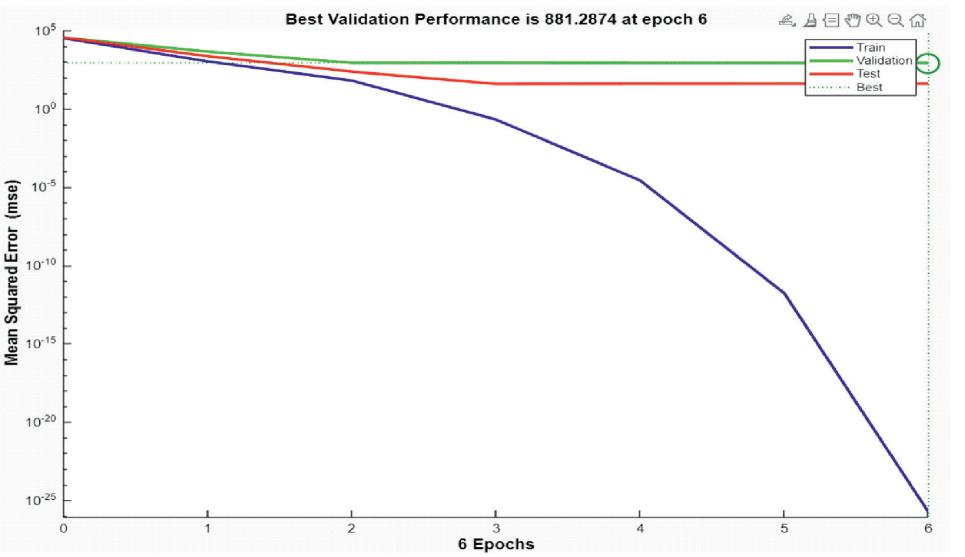

Figure 2: ANN Performance Curve (Best Validation at Epoch 6)

This analysis underscores the efficiency of ANN in providing high-accuracy models for construction management and highlights its potential for further exploration in future studies.

5. Conclusion

The remarkable per se performance, positive heterosis, and notable specific combining ability (SCA) impacts on seed production per plant and other important yield features make the crosses GPUL-4 X OLM-203 and Nallasama X GPUL-2 stand out. These hybrids were excellent prospects for

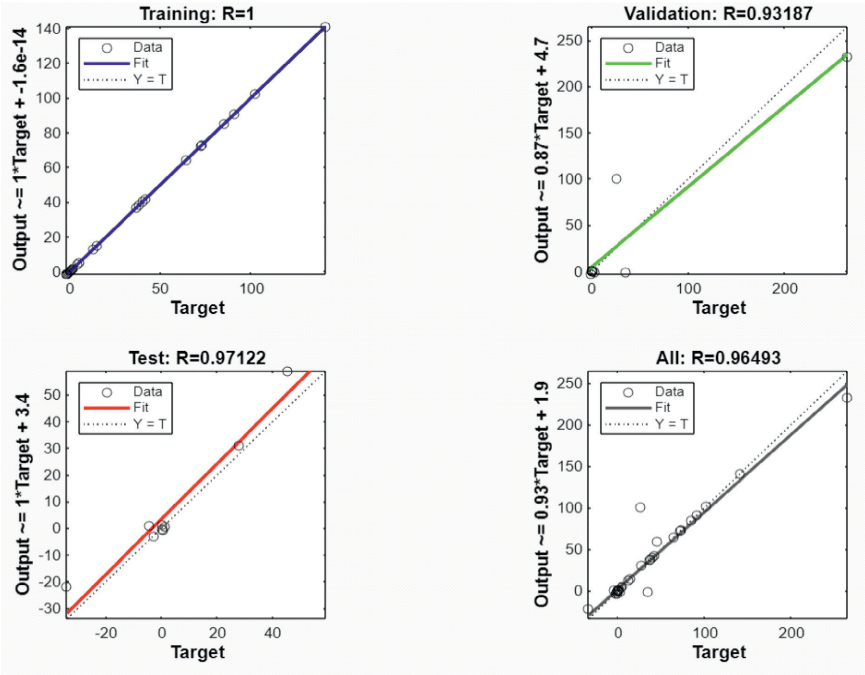

Figure 3: Regression Analysis of ANN Model Output Versus Target for Training, Validation, Testing, and Overall Performance

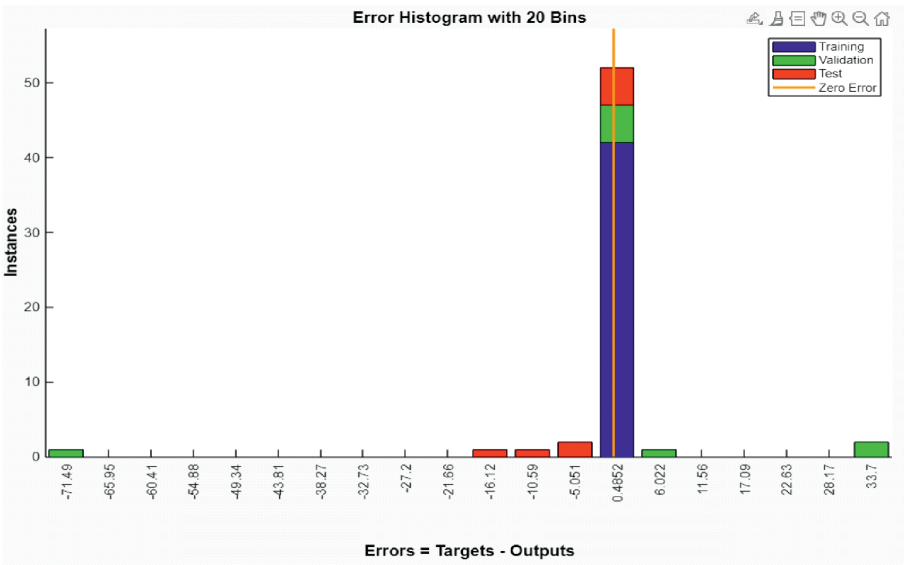

Figure 4: Error Histogram of ANN Model Predictions for Training, Validation, and Testing Datasets

further breeding initiatives because to their high grain production and good heterosis. By fixing the additive genetic variation components in advanced segregating generations, it is possible to create high-yielding lines from these cross combinations. With the potential to recombine beneficial traits like shortened days to maturity, longer panicles, increased main panicle weight, and improved harvest index, GPUL-4 X OLM-203, which was highlighted in this study, offers significant integration opportunities into hybridisation programs.

Heterosis is probably the cause of these choices' higher performance, which calls for more research into separating generations through rigorous testing and screening. An Artificial Neural Network (ANN) model was created and trained using experimental data to enable a more effective validation procedure. With 10 hidden layers, two output parameters, and six input variables, this model showed great promise for understanding the intricate interactions among the many qualities. Future yield prediction and analysis in crop improvement initiatives benefit greatly from the ANN model, which provides a quick and efficient validation tool.

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