

Selection for High-Yielding Peanut Lines Using the Factor Analysis and Genotype-Ideotype Design (FAI-BLUP) Index

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Abstract

Peanut (*Arachis hypogaea* L.) is an important oilseed and food legume, yet its productivity is often constrained by environmental variability and the complex nature of yield-related traits. This study aimed to identify high-yielding peanut genotypes using a multi-trait selection approach. A total of 59 genotypes, comprising 54 breeding lines and 5 check varieties, were evaluated across two dry-season environments in Thailand using a randomized complete block design with three replications. Data were analyzed using mixed linear models to estimate best linear unbiased predictions (BLUPs), and the Factor Analysis and Ideotype-Design BLUP (FAI-BLUP) index was applied to integrate multiple traits and rank genotypes based on their similarity to a predefined ideotype. Significant genetic variation was detected for most traits, and factor analysis grouped the traits into three principal factors associated with yield performance, physiological efficiency, and seed quality. Using a 20% selection intensity, twelve genotypes were identified as superior. Among these, 12BS018, 12BS022, 13W089, and 11231-3 demonstrated the highest yield potential (up to 2278 kg·ha⁻¹) and favorable agronomic attributes, outperforming all check varieties. These results confirm the effectiveness of the FAI-BLUP index for simultaneous improvement of multiple traits without requiring economic weights. The study highlights the utility of multi-trait selection tools in peanut breeding and identifies promising genotypes for development into high-yielding cultivars suitable for dry-season production.

Keywords

Arachis hypogaea, BLUP, FAI-BLUP Index, Multi-Trait Selection,

1. Introduction

Peanut (*Arachis hypogaea* L.) is a major oilseed and legume crop cultivated globally for its edible oil and high-protein seeds. In 2023, global production was estimated at approximately 53 million tons with a harvested area of about 29 million hectares [1]. Asia is the leading production region, contributing nearly 70% of global output and over 60% of total cultivated area, primarily in China, India, and Southeast Asia. Africa accounts for around 25% of the global peanut area, particularly in Nigeria, Sudan, and Senegal, although yields in these regions remain comparatively low due to rainfed farming systems [2] [3]. The Americas, especially the United States, contribute a smaller proportion of the cultivated area but achieve among the highest yields owing to mechanization and improved cultivars [4]. The global average yield is approximately 1.9 t ha⁻¹, while Thailand achieves a slightly higher average yield of 2.0 t ha⁻¹ under rainfed conditions. In contrast, countries such as the United States and China record substantially higher yields of 3.5 - 4.5 t ha⁻¹ due to irrigation, mechanization, and genetic improvement [3] [4]. These differences underscore Thailand's competitive position relative to the global average while highlighting the potential for further productivity gains through advanced agricultural technologies and cultivar improvement. Climate change poses a major threat to peanut productivity worldwide. As a predominantly rainfed crop in Asia and Africa, peanut is highly sensitive to abiotic stresses such as drought, high temperature, and erratic rainfall patterns that negatively affect flowering, pegging, and pod filling stages [5] [6]. Increased temperatures beyond the optimal range of 28°C - 30°C reduce photosynthetic efficiency and impair reproductive development, resulting in significant yield losses [7]. Drought stress during pegging and pod development restricts assimilate partitioning and reduces pod formation, leading to yield declines and inferior seed quality [8]. Furthermore, climate variability increases the incidence of aflatoxin contamination, pest outbreaks, and soil moisture deficits, compounding yield instability in vulnerable regions [9]. To mitigate these adverse impacts, climate-resilient peanut cultivars with improved drought tolerance, heat resilience, and efficient water use must be developed and integrated with climate-smart management practices [10] [11]. Therefore, enhancing peanut resilience to climatic stress is crucial for maintaining yield stability and securing food and nutritional security under changing agroclimatic conditions. Peanut yield is a complex quantitative trait governed by multiple yield components such as pod number per plant, seed weight, and 100-seed weight, which are positively associated with pod yield and can serve as effective selection criteria [12]. Physiological traits such as harvest index, which reflects the proportion of assimilates partitioned to pods, are also valuable indicators for selecting

high-yielding genotypes [13]. Because yield is determined by multiple interrelated traits, plant breeders employ selection index methodologies that combine multiple attributes into a single value to enhance selection efficiency. The concept of index selection was introduced by Smith [14] and Hazel [15] and subsequently refined for crop improvement [16] [17]. These approaches continue to play a central role in modern plant breeding [18] [19]. However, traditional selection indices rely on economic weights, which are often difficult to assign in practice [20]. To address this limitation, Rocha *et al.* [21] developed the Factor Analysis and Ideotype-Design BLUP (FAI-BLUP) index, which integrates factor analysis with best linear unbiased prediction to identify genotypes that most closely resemble the ideotype without requiring predetermined economic weights. This index has been successfully applied in several crops, including wheat, maize, sorghum, and soybean [22] [23] [24] [25]. Therefore, the objective of this study was to identify high-yielding and climate-resilient peanut genotypes by integrating yield components, physiological traits, and agronomic characteristics using the FAI-BLUP index as a multi-trait selection tool.

2. Materials and Methods

2.1. Plant Materials

A total of 59 peanut (*Arachis hypogaea* L.) genotypes were evaluated in this study. These comprised 54 advanced breeding lines developed by the Department of Agronomy, Faculty of Agriculture, Kasetsart University, Thailand, and five standard check varieties recommended by national agricultural agencies. The check varieties were Tainan 9, Khon Kaen 5, Khon Kaen 9, KU Koh Kae 40, and KU ARDA 1, each representing widely cultivated cultivars with known performance for yield and adaptability under Thai agro-climatic conditions.

2.2. Experimental Design and Field Management

Yield trials were conducted during the 2020/21 dry season (December 2020–April 2021) at two research locations in Thailand: Chiang Mai Field Crops Research Center, San Sai District, Chiang Mai Province (18.9047°N, 99.0045°E) and Lopburi Research Station, Khok Charoen District, Lopburi Province (14.7995°N, 100.6534°E). The experiments were arranged in a randomized complete block design (RCBD) with three replications at each location. Each experimental plot consisted of two rows, each measuring 5 m in length, with 0.80 m row spacing and 20 cm plant spacing within rows. Two seeds were sown per hill to ensure proper establishment. Standard agronomic practices for peanut cultivation were followed uniformly across both locations, including land preparation, basal fertilization, pest and weed management, and supplemental irrigation where necessary to avoid moisture stress. The following agronomic and yield-related traits were recorded: pod yield (kg ha⁻¹), shelling percentage (%), harvest index, 100-seed weight (g), number of pods per plant, pod weight per plant (g), number of seeds per plant, seed weight per plant (g), and number of seeds per pod.

2.3. Statistical Analysis and Multi-Trait Selection

Data from the two locations were analyzed using a mixed model as follows:

$$y_{\{ijk\}} = \mu + a_i + \tau_j + (a\tau)_{\{ij\}} + b_{\{jk\}} + \varepsilon_{\{ijk\}} \quad [26]$$

where $y_{\{ijk\}}$ is the observed value of the i^{th} genotype in the k^{th} block at the j^{th} environment; μ is the grand mean; a_i is the random effect of genotype i ; τ_j is the fixed effect of environment j ; $(a\tau)_{\{ij\}}$ is the random genotype $\times$ environment interaction; $b_{\{jk\}}$ is the block effect within environment; and $\varepsilon_{\{ijk\}}$ is the residual error.

Variance components and broad-sense heritability were estimated. Best linear unbiased predictions (BLUPs) were generated using mixed linear models, with genotypes and environments considered as random effects to obtain precise estimates of genetic values across locations.

Multi-trait selection was carried out using the Factor Analysis and Ideotype-Design BLUP (FAI-BLUP) index, which integrates factor analysis with the BLUP methodology to facilitate simultaneous selection for multiple traits without the need to assign arbitrary economic weights. The FAI-BLUP index was computed according to the procedure described by Rocha *et al.* [21]. Genotypic values obtained from BLUP were first standardized, and factor analysis was employed to reduce data dimensionality and account for correlations among traits. An ideotype representing the optimal trait combination was then constructed based on the most desirable expression for each trait. The Euclidean distance of each genotype from the ideotype was calculated using the formula:

$$P_{ij} = \frac{\frac{1}{d_{ij}}}{\sum_{i=1; j=1}^{i=n; j=m} \frac{1}{d_{ij}}}$$

where P_{ij} is the probability of genotype i matching the desired value j , and d_{ij} is the distance between the observed and desired values. And then, genotypes were ranked according to their proximity to the ideotype, with smaller distances indicating superior performance. A selection intensity of 20% was adopted to identify superior genotypes. All statistical analyses were conducted using R software [27]. The metan package was employed for estimating variance components, BLUPs, and computing the FAI-BLUP index.

3. Results

3.1. Genetic Variability and Heritability Estimates

Analysis of variance using the mixed model method revealed significant ($p < 0.05$ or $p < 0.01$) differences among the 59 peanut genotypes for pod yield (PY), number of pods per plant (PdPt), seed weight per plant (SwPt), and number of seeds per plant (SdPt), indicating substantial genetic variability within the breeding population. Significant genotype $\times$ environment ($G \times E$) interactions were detected for

pod yield, 100-seed weight (SW100), and seed traits, confirming differential genotype performance across environments. Broad-sense heritability (h^2) estimates ranged from low for the number of seeds per pod (0.06) to moderate for 100-seed weight (0.46) and shelling percentage (0.28). Traits with moderate heritability, particularly 100-seed weight, demonstrate a stable genetic component, suggesting that these traits are likely to respond reliably to selection across environments (**Table 1**).

Table 1. Estimate of variance component and genetic parameters for pod yield (PY), shelling percentage (SH), 100-seed weight (SW100), harvest index (HI), number of pod per plant (PdPt), pod weight per plant (PwPt), seed weight per plant (SwPt), number of seed per plant (SdPt), number of seed per pod (SdPd) for 54 peanut lines and 5 standard varieties evaluated across 2 locations in the dry crop season.

Parameter	PY	SH	SW100	HI	PdPt	PwPt	SwPt	SdPt	SdPd
h^2	0.19	0.28	0.46	0.19	0.15	0.12	0.22	0.20	0.06
σ_g^2	1696*	9.45**	34.8**	0.0009**	13.9*	16.6 ^{ns}	6.9**	22.1**	0.002 ^{ns}
σ_{ge}^2	1347*	1.46 ^{ns}	10.2**	0.0003 ^{ns}	17.7**	20.0*	2.3 ^{ns}	8.7 ^{ns}	0.005*
σ_{res}^2	6131	23.0	30.7	0.0035	61.9	103.4	21.8	97.7	0.025
CV (%)	33.13	12.21	16.6	51.33	38.65	50.66	37.49	35.39	22.24

Note: * and **: Significant difference at $p < 0.05$ and $p < 0.01$, respectively; ^{ns}: Non-significance; h^2 : Broad-sense heritability; σ_g^2 : Genetic variance; σ_{ge}^2 : G $\times$ E interaction variance; σ_{res}^2 : Residual error variance; CV: Coefficient of variation.

3.2. Factor Analysis and Trait Grouping

Factor analysis with varimax rotation classified the nine evaluated traits into three principal factors, cumulatively accounting for most of the total genetic variance. Factor 1, which comprised pod yield, number of pods per plant, pod weight per plant, seed weight per plant, and number of seeds per plant, explained the largest proportion of variation, demonstrating that these traits were the primary contributors to yield. Factor 2 was dominated by harvest index, while Factor 3 was associated with seed quality traits such as shelling percentage and 100-seed weight. High communality values (>0.69) for all traits confirmed that the extracted factors reliably captured the underlying structure of genetic variation.

3.3. Multi-Trait Selection and Selection Gains

Application of the FAI-BLUP index under a 20% selection intensity produced positive selection differentials for all evaluated traits (**Table 2**). The highest percentage gains were recorded for seed weight per plant (+15.39%), number of seeds per plant (+12.28%), and harvest index (+6.49%), followed by pod yield (+5.29%). These results demonstrate that the multi-trait selection index effectively captured genetic gains in both productivity-related and physiological traits. This confirms the efficiency of the FAI-BLUP approach in identifying genotypes that simultaneously excel in multiple desirable characteristics.

Table 2. Factorial loading after varimax rotation and communalities, overall mean (Xo), selected genotype mean (Xs), selection differential (SD) and percentage of SD (%SD) for the traits based on FAI-BLUP index.

Trait	Factor			Communality	Xo	Xs	SD	%SD	Desirable
	Fac. 1	Fac. 2	Fac. 3						
PY (kg/ha)	-0.08	-0.89	-0.12	0.82	1,868	1,968	100	5.29	Increase
SH	0.06	-0.03	-0.84	0.71	68.27	69.19	0.91	1.34	Increase
SW100 (g)	-0.02	-0.92	0.00	0.85	56.15	58.75	2.59	4.61	Increase
HI	-0.45	-0.75	0.13	0.78	0.291	0.310	0.02	6.49	Increase
PdPt	-0.96	-0.16	0.09	0.96	28.1	30.54	2.43	8.63	Increase
PwPt (g)	-0.89	-0.12	0.33	0.91	28.66	30.67	2.02	7.03	Increase
SwPt (g)	-0.83	-0.44	-0.07	0.89	16.16	18.64	2.49	15.39	Increase
SdPt	-0.98	0.06	-0.10	0.97	34.54	38.78	4.24	12.28	Increase
SdPd	0.04	-0.01	-0.69	0.69	1.353	1.369	0.02	1.13	Increase

3.4. Identification of Superior Genotypes

Based on the FAI-BLUP ranking index, twelve genotypes were selected as superior performers (**Table 3**). Among them, line 12BS018 recorded the highest BLUP-estimated pod yield of 2,278 kg·ha⁻¹, which exceeded the overall population mean (1,868 kg·ha⁻¹) by 410 kg·ha⁻¹. Similarly, lines 12BS022 (2,247 kg·ha⁻¹), 13W089 (2,035 kg·ha⁻¹), and 11231-3 (1,938 kg·ha⁻¹) also demonstrated outstanding yield potential along with favorable values for shelling percentage, hundred-seed weight, and seed weight per plant. Importantly, several selected breeding lines outperformed the highest-yielding check variety, Khonkaen 9, indicating their strong potential for advancement in breeding pipelines and possible varietal release.

Table 3. BLUPs mean for pod yield (PY), shelling percentage (SH), 100-seed weight (SW100), harvest index (HI), number of pods per plant (PdPt), pod weight per plant (PwPt), seed weight per plant (SwPt), number of seeds per plant (SdPt), number of seeds per pod (SdPd) of selected genotypes at selection intensity of 20 % and check varieties.

Genotype	Rank	PY (kg ha ⁻¹)	SH	SW 100 (g)	HI	PdPt	PwPt (g)	SwPt (g)	SdPt	SdPd
11231-3	1	1938	72.8	56.57	0.31	35.1	33.94	22.21	47.8	1.36
12BS018	2	2278	67.6	62.40	0.34	30.7	29.73	18.95	37.8	1.37
13W089	3	2035	69.2	61.57	0.32	32.5	32.17	19.54	38.8	1.35
13W026	4	1918	66.5	57.23	0.33	30.2	33.27	18.49	39.9	1.38
1288-4	5	1897	68.3	56.85	0.31	30.2	29.74	18.05	38.9	1.38
12BS022	6	2247	67.0	64.70	0.33	33.3	34.14	21.02	41.1	1.34
11263-1	7	1782	70.7	55.83	0.31	29.9	29.25	18.53	38.8	1.36
Khonkaen9	8	1938	67.4	62.42	0.30	29.4	30.09	18.82	35.9	1.37
11041-1	9	1893	67.7	54.08	0.27	31.1	31.95	18.81	42.0	1.38
11269-3	10	1706	71.8	57.11	0.32	29.8	27.94	16.97	36.1	1.37

Continued

11S1-1	11	1945	70.3	57.36	0.30	26.2	26.53	15.47	34.4	1.41
11005-1	12	2029	71.1	58.87	0.30	28.0	29.31	16.86	33.9	1.36
Check Varieties										
Tainan9	15	1739	70.2	51.90	0.29	31.69	32.55	18.12	41.3	1.35
Khonkaen5	20	1762	70.4	55.97	0.29	30.51	29.42	17.18	37.7	1.33
KU Kohkae40	31	1619	69.7	52.71	0.29	29.61	28.80	16.31	37.0	1.34
KU ARDA1	30	2039	66.3	57.09	0.30	28.3	29.26	15.95	33.1	1.36
Mean		1868	68.3	56.16	0.29	28.1	28.66	16.16	34.5	1.35

3.5. BLUP Distribution and Ideotype-Based Ranking

Narrative interpretation of BLUP values (**Figure 1**) revealed a wide distribution of pod yield across genotypes, reflecting strong genetic divergence and the presence of high-yielding genotypes within the breeding population. Several breeding lines surpassed the overall mean as well as the majority of the check varieties, confirming the presence of superior genetic potential for yield improvement. The dispersion pattern further highlighted the importance of BLUP in accurately estimating genotypic performance under multi-environment conditions.

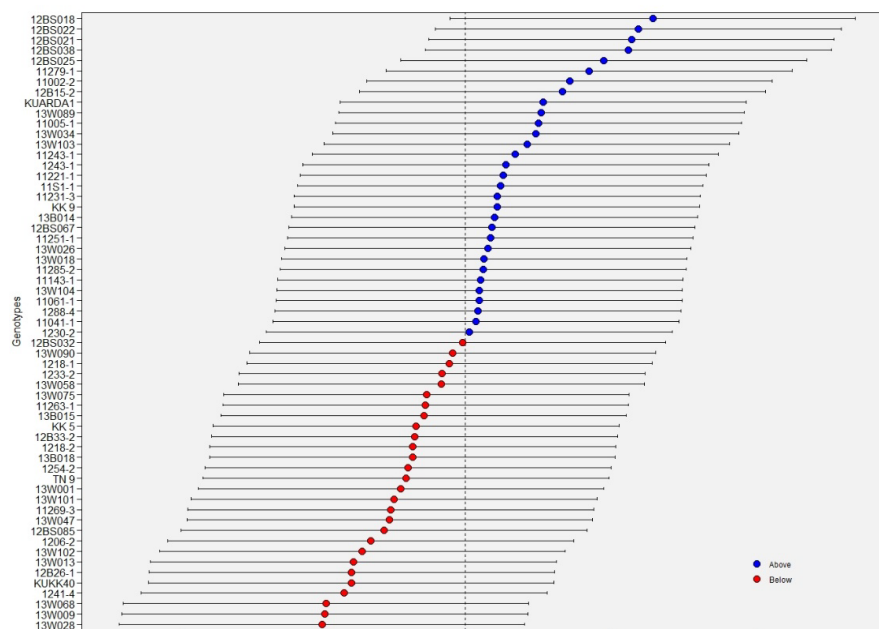


Figure 1. Best linear unbiased prediction for pod yield (PY) of 59 peanut genotypes.

The ranking of all genotypes based on the FAI-BLUP index is presented in **Figure 2**. The index clearly discriminated the superior group of genotypes from the remainder of the population. Twelve genotypes were identified under a 20% se-

lection intensity, each showing a higher probability of similarity to the ideotype compared with checks and the population mean. Among these, lines 12BS018, 12BS022, 13W089, and 11231-3 consistently ranked in the top positions, reflecting their strong alignment with the predefined ideotype. In contrast, several check varieties, such as Tainan 9 and KU Koh Kae 40, clustered in the lower ranks, indicating limited conformity to the ideotype. These results highlight the usefulness of the FAI-BLUP index as an effective tool for ranking and selecting peanut genotypes with superior multi-trait performance.

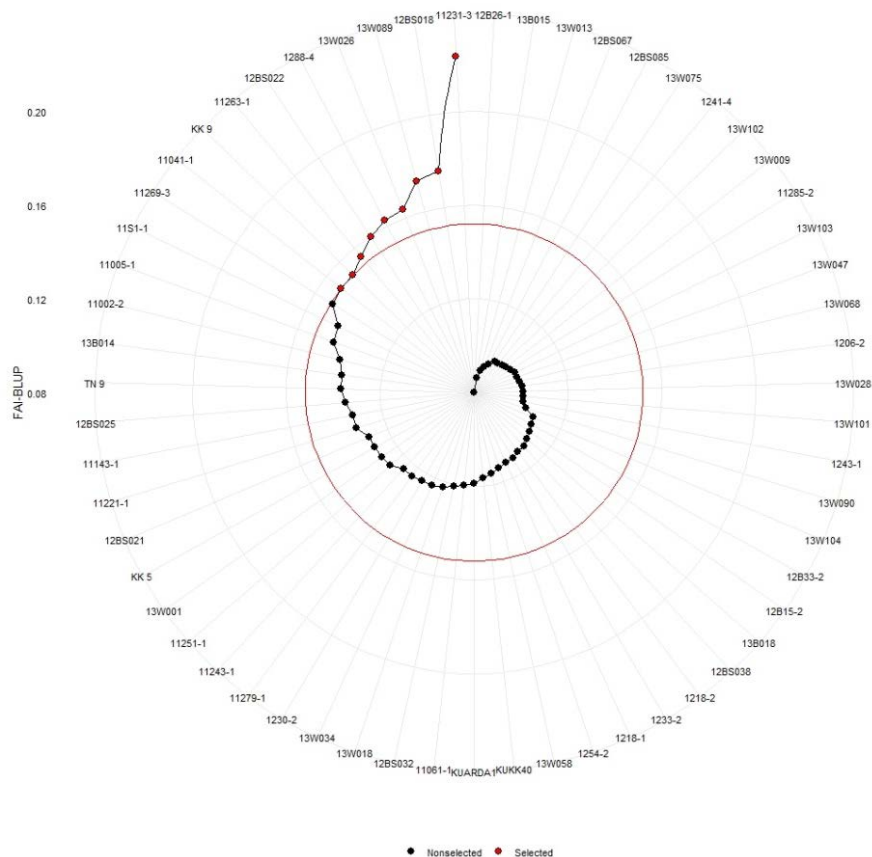


Figure 2. Peanut genotypes ranking and selected genotypes using the FAI-BLUP index.

4. Discussion

4.1. Genetic Variability and Heritability

The significant genotypic variation observed among the 59 peanut genotypes across two environments confirms a broad genetic base suitable for selection and improvement. Traits such as pod yield, seed weight per plant, and pod number showed highly significant genotypic effects, supporting their use as primary selection targets. The detected genotype $\times$ environment ($G \times E$) interaction indicates differential responses across environments. The findings highlight the need to select superior genotypes from diverse germplasm and confirm their stability through multi-environment evaluation [13] [28] [29]. Heritability estimates ranged from low to

moderate, suggesting variable genetic control among traits. Moderate heritability for 100-seed weight and shelling percentage indicates that these traits can be improved via phenotypic selection, whereas low heritability for harvest index and seeds per pod highlights environmental sensitivity and the value of mixed-model BLUP approaches for accurate genetic value estimation [13] [20] [26].

4.2. Trait Associations and Factor Analysis

Factor analysis efficiently grouped correlated traits into three principal components, simplifying interpretation and enhancing selection accuracy. Factor 1 encompassed yield and yield-related traits (pod yield, pod number, seed weight, and seeds per plant), confirming that these jointly define yield potential and can be improved simultaneously. Factor 2 was dominated by harvest index (assimilate partitioning), and Factor 3 captured seed quality traits (shelling percentage and 100-seed weight). This pattern aligns with prior applications of multi-trait indices and factor analysis in cereals and legumes, which reduce dimensionality and mitigate redundancy among correlated traits [24] [25]. High communality values (>0.69) across traits further indicate that the retained components adequately captured underlying variability, validating factor analysis for multi-trait selection frameworks [24] [25] [28].

4.3. Efficiency of FAI-BLUP for Multi-Trait Selection

The FAI-BLUP index provided consistent, positive selection differentials across all traits under a 20% selection intensity, with the largest predicted gains for seed weight per plant (+15.39%), seeds per plant (+12.28%), and harvest index (+6.49%). By integrating factor analysis and ideotype design with BLUP, FAI-BLUP avoids subjective economic weights and improves selection precision [21] [22]. Similar advantages have been reported in maize, wheat, and sorghum, where FAI-BLUP outperformed traditional indices by balancing gains across correlated traits and enhancing selection response [22] [23] [24]. The present results, therefore, confirm the suitability of FAI-BLUP for peanut breeding, especially when improvement targets multiple yield-determining traits under variable environments [21] [23] [24] [28].

4.4. Identification of Superior Peanut Genotypes

Integrating BLUP with FAI-BLUP identified twelve elite lines with consistent superiority across environments. In particular, 12BS018, 12BS022, 13W089, and 11231-3 ranked among the top positions and combined high pod yield with favorable values for seed and physiological traits. Line 12BS018 recorded the highest BLUP-estimated pod yield ($2,278 \text{ kg}\cdot\text{ha}^{-1}$), exceeding the population mean by $\sim 22\%$. Several selected lines outperformed the best check (Khonkaen 9), indicating tangible breeding progress and strong potential for advancement to regional trials and potential release. Comparable successes using multi-trait indices and BLUP-based rankings have been reported in peanut and other crops, reinforcing the robustness

of this integrated approach for discriminating high-potential genotypes [13] [21] [23] [24] [26].

4.5. Implications for Breeding Cultivars

The presence of high-yielding lines that also exhibited a favorable harvest index under dry-season testing suggests that these genotypes possess intrinsic physiological traits that enhance their adaptation to the dry-season environment. Breeding for drought and heat resilience is essential for sustaining peanut productivity in Southeast Asia's variable rainfall regimes, and the present results align with reports emphasizing physiological efficiency and stress adaptation as core breeding targets [10] [12]. Combining BLUP with FAI-BLUP strengthens prediction under $G \times E$ and provides a rigorous framework for simultaneous improvement in yield and physiological traits. Looking ahead, integrating genomic information and high-throughput phenotyping with FAI-BLUP could further accelerate breeding progress and improve the accuracy of selecting elite lines. Genomic selection enables early prediction of breeding values using genome-wide markers, reducing the need for multi-year field evaluations. This approach is especially advantageous for complex, low-to-moderate heritability traits influenced by climate stress. Together, these tools offer an efficient, modern framework for developing climate-resilient peanut cultivars [28] [30].

5. Conclusion

This study demonstrated the effectiveness of integrating Best Linear Unbiased Prediction (BLUP) with Factor Analysis and Ideotype-Design Index (FAI-BLUP) as a robust framework for multi-trait selection in peanut breeding. Significant genetic variability and moderate heritability estimates for key yield-related traits indicated strong potential for genetic improvement within the evaluated population. The application of the FAI-BLUP index enabled the identification of twelve superior peanut genotypes that exhibited high pod yield, favorable seed characteristics, and desirable physiological traits across multiple environments. Among these, genotypes 12BS018, 12BS022, 13W089, and 11231-3 consistently ranked highest in their resemblance to the ideotype, outperforming standard check varieties including Khonkaen 9. The positive selection gains observed for all measured traits confirm the efficiency of the FAI-BLUP approach for simultaneous improvement of complex, interrelated traits without the need for subjective economic weights. These findings highlight the strong potential of the selected lines for advancement to regional trials and potential release as new cultivars adapted to dry-season environments. Furthermore, the integration of multi-trait selection tools with mixed-model analysis represents a powerful strategy for enhancing breeding efficiency and accelerating genetic gains in peanut improvement programs. Overall, this study provides compelling evidence that the combined use of BLUP and FAI-BLUP can support the development of high-yielding, climate-resilient peanut cultivars. Future work should incorporate genomic selection and high-throughput

phenotyping to further enhance prediction accuracy and support the rapid development of cultivars suited to emerging climatic challenges and production demands.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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