


Multi-environment stability of soybean for seed phytic acid and yield

James Ng'ang'a Njoroge, Josephine P. Ouma & Pascal P. Okwiri Ojwang


To cite this article: James Ng'ang'a Njoroge, Josephine P. Ouma & Pascal P. Okwiri Ojwang (2026) Multi-environment stability of soybean for seed phytic acid and yield, Journal of Crop Improvement, 40:1, 71-94, DOI: [10.1080/15427528.2026.2615011](https://doi.org/10.1080/15427528.2026.2615011)


To link to this article: <https://doi.org/10.1080/15427528.2026.2615011>

 View supplementary material 

 Published online: 19 Jan 2026.

 Submit your article to this journal 

 Article views: 97

 View related articles 

 View Crossmark data 

RESEARCH ARTICLE



Multi-environment stability of soybean for seed phytic acid and yield

James Ng'ang'a Njoroge^a, Josephine P. Ouma^b, and Pascal P. Okwiri Ojwang^b

^aOil Crops Program, Food Crops Research Centre Njoro, Kenya Agricultural and Livestock Research Organization, Nairobi, Kenya; ^bDepartment of Crops, Horticulture and Soils, Egerton University, Njoro, Kenya

ABSTRACT

Low phytic acid in soybean [*Glycine max* (L.) Merrill] is a significant attribute to its dietary consumption. The presence of high phytic acid in soybean impacts negatively on the bioavailability of minerals and protein digestion for humans and livestock. Understanding the stability of phytic acid accumulation in soybean varieties is essential for formulating genetic improvement strategies to develop cultivars with reduced phytic acid. The objectives of this study were to determine genotypic variation of soybean genotypes for seed phytic acid content, assess its stability, and seed yield in multi-environments. Forty-eight soybean genotypes were evaluated in an Alpha Lattice design across three locations over two cropping seasons. Genotype was the main determinant of the variation in phytic acid content. However, environmental factors significantly contributed to the phenotype mean value for phytic acid across environments. Commercial genotypes Hill, EAI 3600, DPSB 19, and SC Saga had lower mean phytic acid content of 3.6, 3.5, 3.5, and 3.2 mg g⁻¹, respectively, than the mean (3.8 mg g⁻¹). However, all the commercial genotypes had higher phytic acid content (3.2–4 mg g⁻¹) compared to the mean (1.5 mg g⁻¹) of N6003LP, the check genotype. The mean yield across sites ranged from low (0.3 t ha⁻¹) for N6003LP to 1.5 t ha⁻¹ for genotype NJSB 6. The results provide critical information for planning a breeding strategy for low phytic acid cultivars.

ARTICLE HISTORY




Received 24 June 2025
Accepted 2 January 2026

KEYWORDS

genotype x environment;
soybean meal; stability;
WAASB; seed phytate

Introduction

Soybean [*Glycine max* (L.) Merrill] is an important legume globally due to its economic value and source of protein and minerals for human and livestock (Jansone et al. 2021). The demand for soybean products and animal feed has increased steadily, largely due to the growing population. Equally, change in dietary habits has created the need for inexpensive sources of energy and nutrient dense food alternatives. The global production of soybeans was estimated at 371.3 million (M) metric

CONTACT James Ng'ang'a Njoroge  jamnjoros@gmail.com  Oil Crops Program, Food Crops Research Centre Njoro, Kenya Agricultural and Livestock Research Organization, P.O. Private Bag, Njoro 20107, Kenya
 Supplemental data for this article can be accessed online at <https://doi.org/10.1080/15427528.2026.2615011>.

© 2026 Informa UK Limited, trading as Taylor & Francis Group

tons (MT) in 2020 with a yearly growth rate of 1.8% from 2020 to 2030 (Siamabele 2021). The world's leading producers are Brazil at 152.1 M MT, the United States of America at 113.3 M MT, and Argentina at 25.0 M MT. China was the fourth largest producer with a production of 19.4 M MT. In Africa, South Africa is the leading producer and in the same period produced 2.7 M MT followed by Nigeria with 1.3 M MT and in the third place was Zambia with 0.7 M MT (FAOSTAT 2023). In the eastern Africa region, Kenya's production does not meet its domestic demand estimated at 200,000 MT per annum and thus depends on imports.

Soybeans have a distinctive nutrient profile; hence, it is a suitable option to ensure food and nutritional security. However, the existence of significant amounts of inherent anti-nutritional compounds, specifically inositol hexakisphosphate (phytic acid), is a major drawback to its utilization (Jain et al. 2017). These anti-nutritional compounds reduce the nutrient use of soybean products for food or feed consumption (Thakur, Sharma, and Thakur 2019). Phytic acid ($C_6H_{18}O_{26}P_6$) named 1,2,3,4,5,6 hexakisphosphate is the principal storage of phosphorus (P) and has reactive groups of P that chelate positive cations such iron (Fe), zinc (Zn), and calcium (Ca) thus promoting mineral deficiencies (Prajapati and Shah 2022). This leads to reduced nutrient bioavailability causing mineral deficiencies and micronutrient malnutrition, and hidden hunger (Samtiya, Aluko, and Dhewa 2020). Phytic acid can bond with proteins to form complexes leading to reduced solubility of proteins and enzyme activity (Sarkhel and Roy 2022).

The feed industry has traditionally relied on enzymatic approach to alleviate the effects of phytic acid through the use of exogenous phytase (*myo*-inositol hexaphosphate phosphohydrolase). Phytase is the enzyme incorporated in feeds to hydrolyze the phytate molecule to release phytate P (Sureshkumar et al. 2023). However, soybean cultivars with low phytate content alleviate the need for addition of enzyme phytase in the feeds of livestock and aquatic animals reducing the cost of feed production. Qin et al. (2020) observed that *natto*, a traditional Japanese fermented food prepared from low phytate line, had higher inorganic P and lower phytate levels compared to *natto* prepared from normal phytate soybeans. Although there were no significant differences in macronutrient concentration between the low phytate and normal phytate soybean cultivars, the low phytate prepared *natto* had higher mineral bioavailability, was less sticky, and had a more appealing color. While evaluating poultry feeds, Sens et al. (2021) observed that use of soybean meal of superior quality combined with higher doses of phytase enhanced diet digestibility, utilization of energy, and phytate hydrolysis. Despite the advantage in using low phytate soybean for feed and human consumption, cultivars grown in sub-Saharan Africa largely have significantly high levels of phytate. This is because limited breeding effort has been placed on the development of low phytate soybean, and

instead the major focus has been on yield improvement and, to some extent, protein and oil content.

Yield is an important trait in soybean production, and so are the yield contributing traits. Production of low phytate soybeans would have a positive impact, where the trait would be accompanied by high seed yield. Taliman et al. (2019) observed that growth following germination, yield, and seed attributes were the same in the low and normal phytate cultivars treated with the same level of phosphate fertilizer. Dong et al. (2020) reported that low-phytate soybeans had higher seedling growth and nitrogen (N) fixation capabilities, in addition to expressing higher root phytase and root and nodule phosphatase activity levels than normal-phytate soybean lines. They suggested that these lines would possibly adapt better in low-P environments. Development of low phytic acid genotypes enhances the bioavailability of micronutrients, but in some instances may reduce the germination and yield in crops.

Multi-environment trials are conducted to evaluate crop genotypes for productivity, adaptability, stability, and genotype-by-environment ($G \times E$) interactions (Lee et al. 2023). Low phytate soybean lines with low phytate and different genetic backgrounds treated with different fungicides were tested for seed emergence and yield characters (Averitt et al. 2020). The results indicated that there was no increase in yield for any genotype, but low phytate genotypes with *mips* or *lpa1/lpa2* mutations gave similar results to normal phytate lines under particular soil and environment conditions due to $G \times E$ interactions (Averitt et al. 2020). The composition of soybean seeds drives the demand for soybeans for various industrial uses. The seed composition determines the quality of the product in the market; hence, the need to quantify and determine its stability across environments. Wang et al. (2024) stated that protein and oil content, among other seed quality traits, are regulated by genetic and environmental factors. Furthermore, they evaluated 150 soybean varieties under different environmental conditions to identify superior and stable soybean genotypes in oil and protein content and identified four varieties stable in protein content and six varieties stable in oil content. Employing a different analysis method, Abdelghany et al. (2021) evaluated soybean for seven seed composition traits using the weighted average of absolute scores biplot (WAASB) for the best linear unbiased predictions of the genotype by environment interaction and multi-trait stability index (MTSI) to determine stability of the traits and identified two genotypes for stability in protein, two for stability in oil content, and one each for palmitic, stearic acid, oleic acid, linoleic, and linolenic acid. The use of WAASB and MTSI thus becomes important, powerful and simple tools for identification of superior genotypes in terms of performance and stability in seed quality traits that includes phytic acid. Despite its importance in food security and environmental pollution, there is limited information on phytic acid

variation in soybean genotypes and its stability across environments. Therefore, the objectives of this study were to assess the genetic variability and stability of soybean genotypes for phytic acid and yield in multi-environments. Thorough evaluation of the impact of the environmental conditions on soybean seed nutrient composition is a useful consideration in the identification of the ideal selection environment and subsequent selection of superior lines for future deployment. In addition to understanding the genetic architecture of low phytic acid in soybean, broadening our knowledge on $G \times E$ interactions will aid breeders in planning breeding strategies for developing low-phytate varieties for the formulation of high-value feed.

Materials and methods

Experimental site description

The trials were established at three locations in Kenya: The Food Crops Research Center, Njoro (Njoro) in Nakuru County, Mabanga ATC (Mabanga) in Bungoma County, and the Non-Ruminant Research Institute (Kakamega) in Kakamega County for two cropping seasons. Njoro site ($0^{\circ} 20'S$, $35^{\circ} 56'E$) is located at an altitude of 2185 m above sea level (m.a.s.l.). The area has a mean temperature of $15.9^{\circ}C$ with a daily minimum of $9.1^{\circ}C$ and maximum of $22.6^{\circ}C$ and a mean annual rainfall of 1032 mm with a bimodal rainfall pattern. The main cropping season is from March to August, while the short rain cropping season starts in September and stretches to December. The soils in Njoro are well-drained *vitric Andosols*, moderately deep brown to dark brown, very friable loam to sandy clay. Mabanga ($0^{\circ}37' 24"N$, $34^{\circ} 36' 52" E$) is at an altitude of 1515 m.a.s.l. The soil type is sandy loam, strongly acidic at a pH of 5.22 (Abubakar et al. 2020). The area has a mean temperature of $21.5^{\circ}C$ with a minimum temperature of $14.1^{\circ}C$ and a maximum of $29.1^{\circ}C$ (<https://en.climate-data.org/africa/kenya/bungoma/bungoma-11167/>). The mean monthly rainfall is 1618 mm. The warmest month is March, and the coldest is July. Kakamega ($0^{\circ} 28' 0" N$, $34^{\circ} 45' 0"E$) is at 1585 m.a.s.l. The annual rainfall ranges from 800 to 2000 mm, distributed in two cropping seasons. The agro-ecological zone is classified as the upper midland zone (UM1) with a daily average temperature of $21^{\circ}C$. The temperature ranges from $15^{\circ}C$ to $29.4^{\circ}C$ (<https://en.climate-data.org/africa/kenya/kakamega/kakamega-922/>). The soils are *dystric-mollic Nitisols* and experience two cropping seasons referred to as the long and short rainy seasons. These environments represent the medium maturity (1000–1600 m a.s.l) and late maturity market segments (1600–2200 m.a.s.l) where soybean production is practiced. In the medium altitude

environments, soybean production is done in both seasons, but more pronounced in the short rains.

Soybean genotypes

Forty-eight local and introduced soybean genotypes (Table 1) were sourced from the soybean breeding program at the Food Crops Research Center, Njoro, International Institute of Tropical Agriculture (IITA), Agri SeedCo Ltd, USDA, and Genetic Resources Research Institute (GeRRI). The program Edgar from within Genstat analytical software (<http://www.edgarweb.org.uk/>) was used for randomization and field layout design (Singh and Bhatia 2017).

Soil characteristics

Soil samples were taken before planting at a depth of 30 cm using a soil auger in all the sites. Twelve samples were collected per site and composited, from which a sample of 500 g was sourced for soil nutrient analysis. The sites had varying soil characteristics (Table 2). The locations had medium acidity (pH 5.10–5.97) in all the seasons except for Mabanga, which had strong acid soils (pH 4.67) in the long rains of 2022. The total soil N was adequate in all the

Table 1. Soybean genotypes used in the study.

Genotype	Entry No.	Source	Genotype	Entry No.	Source
NJSB 1	G1	KALRO	NJSB 9	G25	KALRO
Kensoy 009	G2	KALRO	Kensoy 05	G26	KALRO
NJSB 2	G3	KALRO	SB24	G27	IITA
SB93	G4	IITA	916/5/15	G28	KALRO
NJSB 3	G5	KALRO	SB61	G29	IITA
NJSB 4	G6	KALRO	835/5/30	G30	KALRO
DPSB8	G7	KALRO	NJSB 10	G31	KALRO
NJSB 5	G8	KALRO	NJSB 11	G32	KALRO
SBH 3/7/4	G9	KALRO	Kensoy 10	G33	KALRO
N6003LP	G10	USDA	NJSB 12	G34	KALRO
Red Tanner	G11	KALRO	DPSB19	G35	KALRO
NJSB 6	G12	KALRO	NJSB 13	G36	KALRO
929/5/30	G13	KALRO	917/5/16	G37	KALRO
NJSB 7	G14	KALRO	Nyala	G38	KALRO
Flora531	G15	KALRO	Hill	G39	KALRO
Gazelle	G16	KALRO	SB4	G40	IITA
NJSB 8	G17	KALRO	EAI3600	G41	KALRO
SB50	G18	IITA	SC saga	G42	Agri-Seedco
Black Hawk	G19	KALRO	NJSB 14	G43	KALRO
Salama	G20	Agri-Seedco	NJSB 15	G44	KALRO
SB91	G21	IITA	NJSB 16	G45	KALRO
Bossier	G22	KALRO	NJSB 17	G46	KALRO
SBH 7/7/1	G23	KALRO	NJSB 18	G47	KALRO
SBH 5/2/2	G24	KALRO	SB37	G48	KALRO

Abbreviations: IITA-International Institute of Tropical Agriculture; KALRO – Kenya Agricultural & Livestock Research Organization.

Table 2. Soil characteristics of Njoro, Kakamega, and Mabanga in the 2021 short rains and 2022 long rains.

Fertility results	NJA		NJB		KKA		KKB		MABA		MABB	
	Value	Class	Value	Class	Value	Class	Value	Class	Value	Class	Value	Class
Soil pH	5.62	MA	5.97	MA	5.40	MA	5.03	MA	5.10	MA	4.67	SA
Total Nitrogen%	0.24	A	0.26	A	0.23	A	0.23	A	0.12	L	0.14	L
Total Organic Carbon %	2.60	M	2.86	A	2.60	M	2.55	M	1.18	L	1.66	M
Phosphorus ppm	20.5	L	12.9	L	12.7	L	7.4	L	3.3	L	1.1	L
Potassium meq%	1.56	H	1.64	H	0.40	A	0.44	A	0.12	L	0.10	L
Calcium meq %	10.7	A	10.0	A	7.50	A	6.5	A	1.00	L	1.00	L
Magnesium meq%	3.27	H	3.10	H	2.13	A	2.01	A	1.56	A	1.36	A
Manganese meq %	0.66	A	0.50	A	0.74	A	0.40	A	0.17	A	0.12	A
Copper ppm	2.74	A	2.85	A	3.93	A	6.90	A	3.93	A	3.33	A
Iron ppm	95.7	A	103.2	A	27.9	A	31.4	A	36.2	A	37.4	A
Zinc ppm	15.5	A	15.2	A	4.80	L	9.64	A	0.97	L	4.80	L
Sodium meq%	0.34	A	0.20	A	0.34	A	0.26	A	0.18	A	0.18	A

Abbreviations: MA = Medium Acid; SA = Strong Acid; A = Adequate; L = Low; M = Moderate; H = High.

sites across seasons, ranging from 0.23 to 0.26% except for two seasons in Mabanga, where the total N was 0.12% and 0.14%, respectively. The total organic carbon (C) varied across the locations and seasons and was reported as either moderate or adequate except in the short rains of 2021, when low (1.18%) total organic C was recorded in Mabanga. Phosphorus, important for root development, was low in all the soils across the sites. The range was 1.1 ppm in Mabanga in 2022 to 20.5 ppm in Njoro in 2021. Potassium was low (0.12 and 0.44 meq%) in both seasons at Mabanga. Calcium was adequate in all locations except Mabanga, where it was low (1.00meq%) in both seasons. Magnesium was high in Njoro (3.10% and 3.27 meq%) but adequate in all seasons at Kakamega and Mabanga. The micronutrients manganese (Mn), copper (Cu), iron (Fe), and sodium (Na) were adequate in all the sites in all the seasons. Zinc content was low (4.8 meq %) in Kakamega in the short rains of 2021 and in Mabanga (0.97 meq %). The Zn content was adequate in Njoro and in the long rains of 2022 at Kakamega.

Trial establishment and management

The genotypes were planted in an Alpha-Lattice design of double row plots, 2 m long, each spaced at 45 × 10 cm, resulting in a plot area of 1.8 m² replicated three times. The experiment was planted for two seasons in each site, in 2021 and 2022, respectively, giving a total of six environments based on year-location combinations. Planting was done at a seeding rate of 75 kg ha⁻¹ and di-ammonium phosphate (18:46:0) applied as basal fertilizer. Weeds were controlled using metribuzin at a rate of 750 ml ha⁻¹ as a pre-emergence herbicide. Soybean rust (*Phakopsora pachyrhizi*) was controlled using difenoconazole. Other foliar diseases and insect pests were controlled by

application of recommended pesticides. Data were collected on days to maturity as the number of days from sowing to physiological maturity; plant height (cm) measured from the base of the main stem to the apex of the plant, pods plant⁻¹ as the mean number of pods collected from 10 randomly selected plants in a plot, grain yield (t ha⁻¹) calculated as amount of grain harvested in a plot⁻¹, 100 seed weight as the weight of a random 100 seeds harvested in a plot and seed phytic acid content.

Phytic acid analysis

Phytic acid content in soybean grain was determined by a colorimetric method as described by Kariithi et al. (2016). Ten grams of soybean seeds were milled using a chrome ball mill (Retsch mill model MM400). The milling component was teflon-coated to prevent contamination of the milling chamber (Kariithi et al. 2016). To initiate the analysis, 0.2 g of soybean flour was transferred into a 7 ml vial tube. Two ml of 0.4 M hydrochloric acid was added and incubated for 12 h at 4°C to extract the phytic acid present in the sample. The sample extracts were then filtered using Whatman 125 mm diameter filter paper, and approximately 100 µl aliquot of each was transferred into a test tube and supplemented with an equal amount (100 µl) of Chen's reagent (1 volume 6N H₂SO₄, 1 volume 2.5% ammonium molybdate, 1 volume 10% ascorbic acid, and 2 volumes H₂O). The assay was then allowed to develop a phospho-molybdate blue coloration for about 2 h at room temperature. The samples were then analyzed using a Shimadzu UV 1900i spectrophotometer at a wavelength of 833 nm.

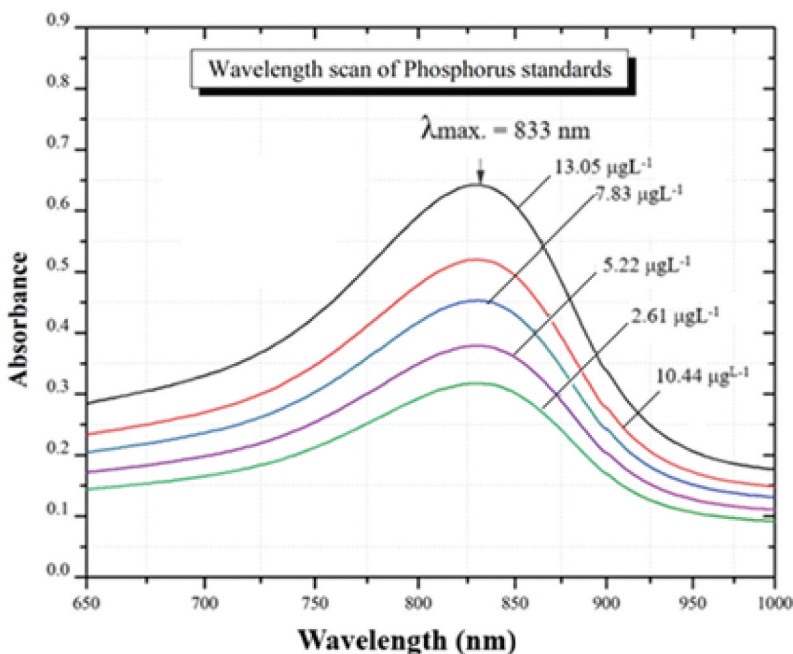
Standard curve development

Standard curves were developed by dissolving 0.174 g of di-potassium hydrogen phosphate (K₂HPO₄) in 1 L of distilled H₂O to give a concentration of 1 Mm K₂HPO₄. Five standards were then prepared in order of increasing concentration by pipetting 15, 30, 45, 60, and 75 µL and supplementing them with 100 µL of Chen's reagent, 10 µL of 0.4 M HCl, and distilled water in order of reducing volumes (Table 3). The different concentrations of the di-potassium hydrogen phosphate were scanned using a double-beam UV-Vis spectrophotometer (K19000) from 190 to 1100 nm. Deionized (DI) H₂O was used as the reagent blank/reference. This was to identify the analyte peak absorption wavelength. Origin Pro graphing software was used for plotting the illustrated spectra (Figure 1).

The analyte peak was identified at 833 nm, which corresponded to the phosphomolybdate compound. The intensity of the blue coloration increased with an increase in the concentration of P. Photometric absorbance measurements were then performed at 833 nm for the varying

Table 3. Concentrations of di-potassium hydrogen phosphate, distilled water, HCL, Chen's reagent, standards, and absorbance in the development of the standard curve.

Standard	μL of 1 mM K_2HPO_4	μL of 0.4 M HCl	mL of dH_2O	μL of Chen's reagent	Standard ($\mu\text{g L}^{-1}$)	Abs.@ 833 nm
1	15	10	2.000	100	2.61	0.353
2	30	10	1.985	100	5.22	0.460
3	45	10	1.970	100	7.83	0.553
4	60	10	1.955	100	10.44	0.695
5	75	10	1.940	100	13.05	0.734

**Figure 1.** Spectra of absorption wavelengths of different concentrations of di-potassium hydrogen phosphate for standard curve development.

concentrations of the standards, and the results were recorded (Table 3) and displayed (Figure 2).

The phytic acid content was calculated using the following formula:

$$\text{Phytic acid content mg g}^{-1} = v \left(\left(\frac{a - 0.2594}{0.00676} \right) \right) / (w \times 100) \quad (1)$$

where v = volume of the acid, a = absorbance, and w = weight of sample.

Data analysis

Multi-environment trial data for all quantitative traits across six environments were based on season-location combinations where each season in

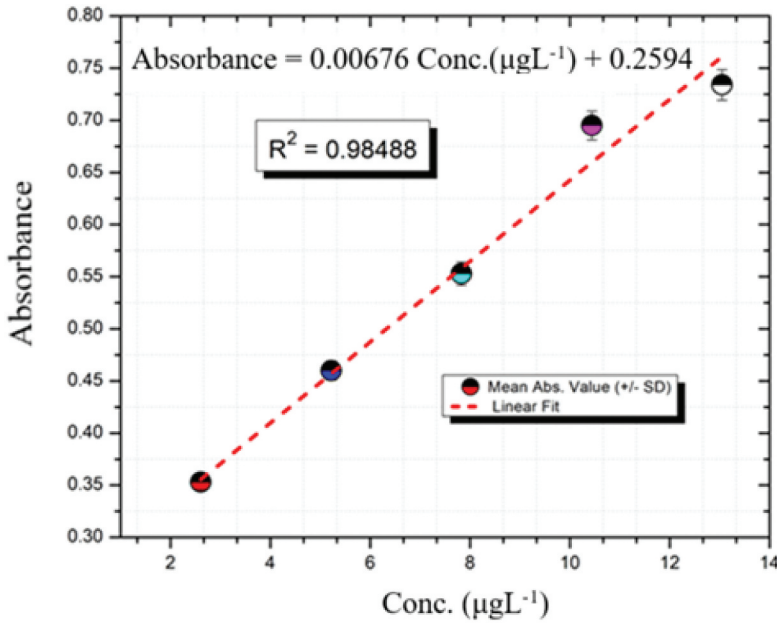


Figure 2. Developed a standard curve for comparison in colorimetric quantification of phytic acid extract. Abbreviations: PHY = Phytic acid; Env = Environment; Gen = Genotype.

every location was considered as a separate environment. Season-location combinations were important for understanding the repeatability and representativeness of the test sites (Yan et al. 2011). Mixed model analysis was fitted across the six environments using Residual Maximum Likelihood (REML) estimates procedure (Mohring, Williams, and Piepho 2015; Patterson and Thompson 1971; Patterson and Williams 1976). The statistical model was fitted using Genstat 15th edition computer software program (VSN International 2012). The statistical model is shown below.

$$Y_{ijkl} = \mu + E_i + R_j + B_{k(j)} + G_l + GE_{li} + \varepsilon_{ijkl}$$

where: Y_{ijkl} is the response of the l^{th} genotype in the k^{th} block of the i^{th} environment, μ is the general mean; E_i is the effect due to the i^{th} Environment; R_j is the effect of the j^{th} replicate in the i^{th} Environment; $B_{k(j)}$ is the effect due to the k^{th} block in the j^{th} replicate; G_l is the effect due to the l^{th} genotype in the k^{th} block; GE_{li} is the effect due to the l^{th} genotype in the i^{th} environment; ε_{ijkl} is the random error due to the l^{th} genotype in the k^{th} block of the i^{th} environment. The genotypes were considered fixed while the environments were considered random.

Genotype plus genotype-by-environment (GGE) interaction analysis was deployed to evaluate the genotype (G) main effects and genotype-by-environment interactions (GEI). To demonstrate the repeatable and non-

repeatable GEI based on season correlations between locations, the location-season combinations were considered as environments (Yan 2019). The GGE analyses revealed which genotypes won where and the discriminative ability and representativeness of the test environments (Kebede et al. 2023; Malosetti, Ribaut, and Van Eeuwijk 2013; Olivoto and Lúcio 2020; Yan and Kang 2002; Yan and Tinker 2006). The model employed was as indicated below

$$Y_{ij} = \mu + e_j + \sum_{k=1}^t \lambda_k \alpha_{ik} l_{jk} + \varepsilon_{ij}$$

where Y_{ij} is the response of genotype i in environment j , μ is the grand mean; e_j is the mean value of environment j ; $j = 1 \dots e$, and $i = 1 \dots g$ with g and e being the numbers of genotypes and environments, respectively; t is the number of principal components (PC) used or retained in the model, with $t \leq \min(e, g - 1)$, λ_k is a scale factor (the single value), α_{ik} is the product of the cultivar score, l_{jk} is an environment score and ε_{ij} is the residual association with genotype in environment j . Genstat® software 15th Edition (VSN International 2012) was employed for analysis. Stability and discriminative analysis for yield and phytic acid were further done using the “metan” package in the R environment (Arminian 2025). There were no missing data.

Results

Variance components

There was variation in how soybean traits under study were influenced by the environment, genotypes and their interactions. There were significant ($p < 0.001$) differences among genotypes for phytic acid content, seed yield, 100 seed weight, plant height, pods plant⁻¹, and maturity (Table 4). The traits were also significantly influenced by the environment, genotype, and their interactions (Table 4).

Phenotypic variation in seed phytic acid content

Genotypes expressed significant variation in phenotypic performance for seed phytic acid content. Moderate to high (3.5–4.6 mg g⁻¹) phytic acid site means were recorded across all the environments except in Mabanga during the short rains of 2021 (MABA) with 2.8 mg g⁻¹ (Table ST1). Evidently, the check genotype (N6003LP) genetically improved for low phytic acid content, had the lowest phytic acid content across locations varying from a low of 1.3 mg g⁻¹ at Njoro in the short rains of 2021 to a high of 1.7 mg g⁻¹ at Mabanga

Table 4. Residual maximum likelihood table of variance components for phytic acid and agronomic traits in the six environments tested.

Phytic acid											
Fixed term	Wald stat	NDF	DDF	F Stat	P	Seed yield				P	
						Fixed term	Wald stat	NDF	DDF	F Stat	
Genotype	197.31	47	814.0	4.20	0.001	Genotype	142.32	47	814.0	3.03	0.001
Random Term ^a	Variance	S.E				Random Term ^a	Variance	S.E			
Environment	0.1601	0.1634			0.0000	Environment	0.3469	0.3486			0.0000
Rep(Env)	0.1155	0.0628				Rep(Env)	0.2601	0.1327			
Blk(Env.Rep)	0.09595	0.0310				Blk(Env.Rep)	0.2282	0.0462			0.0039
Gen. Env	0.04067	0.0779			0.0000	Gen. Env	0.3800	0.0666			
Residual	0.963	0.0479				Residual	0.508	0.0253			
100 Seed Weight											
Genotype	972.69	47	814	20.70	0.001	Genotype	1100.19	47	814.0	23.41	0.001
Random Term ^a	Variance	S.E				Random Term ^a	variance	S.E			0.0000
Environment	0.355	0.374			0.0000	Environment	344.1	344.6			
Rep(Env)	0.320	0.188				Rep(Env)	257.8	129.6			0.0000
Blk (Env.Rep)	0.304	0.134				Blk(Env.Rep)	236.3	41.7			
Gen. Env	0.973	0.264			0.00005	Gen. Env	380.6	57.6			
Residual	5.354	0.266				Residual	135.5	6.7			
Pods Plant⁻¹											
Genotype	141.24	47	814	3.01	0.001	Genotype	4333.08	47	814.0	9.21	0.001
Random Term ^a	Variance	SE				Random Term ^a	Variance	SE			0.0000
Environment	43.8	44.4			0.0000	Environment	1773.3	1773.9			
Rep(Env)	32.7	17.3				Rep(Env)	1331.7	666.7			
Blk(Env.Rep)	32.1	8.1				Blk(Env.Rep)	1210.9	205.7			
Gen.Env	68.0	13.6			0.0000	Gen.Env	1789.2	262.1			0.0006
Residual	173.3	8.6				Residual	171.5	8.5			

P: probability, N.D.F: numerator degree of freedom, D.D.F: Denominator degree of freedom, S.E.: Standard error, Env.: environment; Rep (Env): replicates nested within environments; Blk (Env.Rep): block nested within replicates and environments, Gen.Env: genotype-by-environment interaction.

^aTesting of random effects in the mixed model for environment and genotype by environment interaction was done using likelihood ratio.

in the long rains of 2022. Notably, three genotypes (Kensoy 009, SBH 5/2/2 and 835/5/30) showed low phytic acid of 1.8, 1.8, and 1.9 mg g⁻¹ respectively, in Mabanga in SR 2021 (MABA). However, this was not repeatable in other environments. Genotypes NJSB 12, NJSB 15, SC-Saga, SB 37, NJSB 5, SBH 3/7/4, NJSB 6, NJSB 4, NJSB 14, 929/5/30, DPSB 8, NJSB 2, SB 50, Black Hawk, DPSB 19, NJSB 13, 917/5/16, SB 4, and NJSB 17 expressed moderate phytic acid content of between 2.1 and 2.9 mg g⁻¹ in Mabanga. In Njoro genotypes NJSB 1, NJSB 2, NJSB 4, Red Tanner, NJSB 7, Gazelle, Black Hawk, SB 50, DPSB 8, SB91, Kensoy 05, SB 24, NJSB 13, Hill, EAI 3600, NJSB 6, and NJSB 18 expressed moderate phytic acid content of 2.2 to 2.9 mg g⁻¹ either in the long or short rains of 2021 and 2022. In Kakamega, genotype SB 50, Salama, NJSB 9, SB 24, NJSB 11, SC Saga, SB 93, SBH 7/1/1, and Kensoy 10 similarly expressed moderate phytic acid content ranging from 2.3 to 2.9 mg g⁻¹. Among the commercial genotypes, Kensoy 05 and Salama had the lowest phytic acid content at 2.5 and 2.3 mg g⁻¹ at Njoro and Kakamega, respectively, in the long rains of 2022. In Mabanga, Kensoy 009 had the least phytic acid content of 1.8 mg g⁻¹ among the commercial genotypes (Table ST1) in the short rains of 2021. There were no noticeable differences in the seed phytate content based on the seed source. Among the commercial genotypes, those with lower mean phytic acid content than the mean of 3.8 mg g⁻¹ across the environments (Table ST1) were SC Saga (3.2 mg g⁻¹), EAI 3600 (3.5 mg g⁻¹), DPSB 19 (3.5 mg g⁻¹), and Hill (3.6 mg g⁻¹).

Yield and related agronomic traits

Significant differences in yield were achieved across locations and seasons. The mean yield across sites and seasons ranged from 0.3 t ha⁻¹ to 1.5 t ha⁻¹, achieved by genotype N6003LP and NJSB 6, respectively. The mean yield for all genotypes in the short rains of 2021 was higher in Njoro at 1.5 t ha⁻¹ and lower in Mabanga at 0.6 t ha⁻¹ (Table ST1). In the long rains of 2022, the mean yield was high (2 t ha⁻¹) in Kakamega and low in Mabanga (0.9 t ha⁻¹) (Table ST1). Except for Njoro, genotypes expressed higher mean yields in the long rains of 2022. High mean yields (2.2 t ha⁻¹) were achieved by genotype SBH/5/2/2 in Njoro in the short rains of 2021 and genotype Nyala performed well among the commercial genotypes with a yield of 2.0 t ha⁻¹. In the long rains of 2022, genotypes SB93 and NJSB 5 achieved a comparatively high yield of 2.3 t ha⁻¹ as Kensoy 009, a commercial genotype, performed best at 2.2 t ha⁻¹ in Njoro (Table ST1). In Kakamega, DPSB 8, a commercial genotype, and NJSB 6 achieved high yields of 3.1 t ha⁻¹ and 3.0 t ha⁻¹, respectively, in the long rains of 2022. However, the yields were depressed in the short rains of 2021 in the same environment for the best yielding genotype NJSB 8 achieved 1.4 t ha⁻¹. In Mabanga, SB50 achieved the highest mean yield of 1.5 t ha⁻¹ in the long rains of 2022 while DPSB 8 yielded 1.2

t ha⁻¹ in the short rains of 2021. In Kenya, there are 12 soybean varieties registered for commercial production which were evaluated in this study, specifically Kensoy 009, DPSB 8, Gazelle, Black Hawk, Salama, Kensoy 05, Kensoy 10, DPSB 19, Nyala, Hill, EAI 3600, and SC Saga. In Njoro, Kensoy 009 and Nyala were among the best-performing commercial genotypes (Table ST1). In Kakamega, DPSB 8 was among the best commercial genotypes, yielding 3.1 t ha⁻¹, while in Mabanga, variety EAI 3600 and DPSB 19 were among the top 3 genotypes (1.4 t ha⁻¹). Among the commercial genotypes, the highest yielding genotype across sites was DPSB 8 (1.5 t ha⁻¹). The least mean yield across sites was achieved by N6003LP, an exotic genotype at 0.5 t ha⁻¹ (Table ST1). There were no clear trends in terms of yield associated with the source of germplasm (Table 1).

The mean 100-seed weight for two seasons was higher in the 2022 season in all the sites at a mean of 15.8 g in Njoro, 17.7 g in Kakamega, and 15.8 g in Mabanga. In Njoro, NJSB 4, NJSB 3, NJSB 12, and NJSB 7 had a mean 100-seed weight of more than 20 g and thus in the large-seeded category, while genotypes Salama, Red tanner, Black Hawk, DPSB 19, Hill, SB4, SB50, SB24, and SBH5/2/2 are small-seeded with less than 13 g. In Kakamega, genotype NJSB3 (22.4 g) was the only genotype that recorded a mean of more than 20 g. In Mabanga, the 100-seed weight was the least with a mean of 15.59 g, where NJSB3 and NJSB4 recorded high seed weights of 21.2 g and 20 g, respectively (Table ST1). The mean 100 seed weight across sites ranged from 10.6 g for SB50 to 21.2 g for NJSB 3 (Table ST1).

Plant height was greater than the mean of 62.8 cm in Njoro (Table ST1) compared to Mabanga and Kakamega in the long rains of 2022. Except for Njoro, plant height was higher in the long rains of 2022 than in the short rains of 2021. The differences in plant height between seasons were higher in Kakamega (19.2 cm) than in Njoro (3.4 cm) and Mabanga (8.2 cm). The mean plant height across sites and seasons ranged from 17.5 cm to 105.3 cm for genotypes N6003LP and NJSB 5, respectively (Table ST1).

Significant ($p < 0.001$) differences within and across locations among evaluated genotypes on days to maturity were observed. Genotypes were late in maturity at the high-altitude site of Njoro, with a mean of 173.5–193.5 days in the two seasons and early at the lower altitude site of Mabanga, with a mean of 104.5–108.5 days in the two seasons (Table ST1). In Kakamega, the genotypes matured at a mean of 111–119 days. Genotypes were late by 20 days in the long rains of 2022 compared to the short rains of 2021 in Njoro, and a similar difference of 8 days was observed in Kakamega. At Mabanga, the number of days to maturity was 4 days earlier in the long rains of 2022 compared to the short rains of 2021. Among the commercial genotypes, DPSB 19 matured earliest in the highland site of Njoro at 139.7–151.9 days. At Kakamega, the days to maturity ranged from 92.2 for Black Hawk to 130.7

for Kensoy 009, while in Mabanga, maturity ranged between 91.4 days for Black Hawk and 111.8 days for DPSB 8 (Table ST1).

Genotypes differed significantly for the number of pods plant⁻¹ across environments (Table ST1). A higher number of pods did not translate to high yield for all genotypes, e.g. genotype NJSB 14 had highest number of pods, yet it could only achieve a low yield of 1.0 t ha⁻¹, just as SB24 with a lower pod load of 25.8 (Table ST1). Genotype N6003LP, the check genotype for phytic acid, had the least number of pods plant⁻¹ (15.7), low plant height (17 cm), and the lowest yield (0.3 t ha⁻¹). There was a wide variation in the number of pods plant⁻¹ for the commercial genotypes, ranging from 23.6 for genotype Kensoy 05 to 37.5 for genotype DPSB 8 (Table ST1).

Phenotypic correlations

Inter-relationships among soybean traits were observed among the genotypes under evaluation. Yield had a strong to moderate positive and significant ($p < 0.01$) correlation with plant height, pods plant⁻¹, 100 seed weight, maturity, and a weak but significant correlation with phytate content. Hundred seed weight was significantly correlated with maturity ($p < 0.05$), plant height ($p < 0.001$), number of pods plant⁻¹ ($p < 0.005$), and yield ($p < 0.001$) (Table 5).

Genotype-by-environment interactions analyses

The need for increased soybean production to meet the domestic demand for soybean meal, oil, and other products has led to the introduction of new germplasm from different sources for adaptability evaluation in varying ecological zones. Yield is the outcome of genotypic potential (G), Environmental influence (E), and their interactions (Yan and Kang 2002). This study evaluated 48 genotypes in three locations for two seasons, making a total of six environments. The first (PC 1) and second (PC 2) principal components accounted for 50.46% of genotype and genotypes plus environment variation for phytic acid in soybean seeds. Environments Njoro in the short rains (NJA) and Kakamega in the long rains (KKB) had a right angle between them, indicating that the two environments were not correlated, and

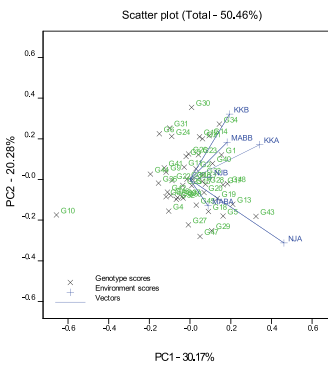
Table 5. Phenotypic correlation coefficient for yield, plant height, pods plant⁻¹, phytic acid content, maturity, and 100 seed weight across six environments of the study in the short rains of 2021 and long rains of 2022.

	100 seed weight	Maturity	Plant Height	Phytic acid content	Pods plant ⁻¹
Maturity	0.0692**				
Plant Height	0.1169***	0.6758***			
Phytic acid content	0.0331 ^{ns}	0.0664 ^{ns}	0.2099***		
Pods plant ⁻¹	0.0728*	0.2950	0.4788***	0.1272***	
Yield	0.3092***	0.2652***	0.5403***	0.1898***	0.5447***

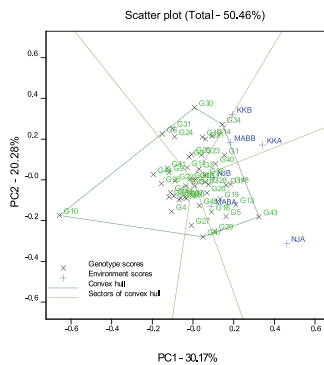
there were no comparisons on the expression of phytic acid content between the two environments (Figure 3a). Acute angles of the vector lines between Kakamega in the long rains of 2022 (KKB) and short rains of 2021 (KKA) and Mabanga in the long rains of 2022 (MABB) presented the environments as correlated. The obtuse angle between environments Kakamega in the long rains (KKB) and Mabanga in the short rains of 2021 suggested crossover events, indicating the impact of the environments on the genotypes (Figure 3a).

The which-won-where biplot presented genotype G10 (N6003LP), the check genotype as having low phytic acid content, while the other genotypes, G34 (NJSB 12), and G43 (NJSB 14) as having high phytic acid content, among genotypes evaluated (Figure 3(b)). Environments MABA, NJB, and KKB in the first quadrant of the Y*WAASB biplot indicated high discriminative ability on phytic acid (Figure 3(c)), and genotypes G10, G47, G23, G31, and G20 achieved low phytic acid but were unstable. Genotypes in

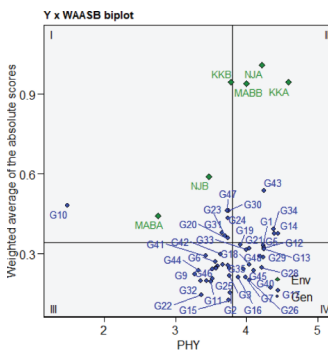
a) Discriminativeness versus representativeness biplot.



b) Which-won-where view of GGE.



c) A Y*WAASB means performance and stability for phytic acid



d) Ranking genotypes with rYWAASB index.

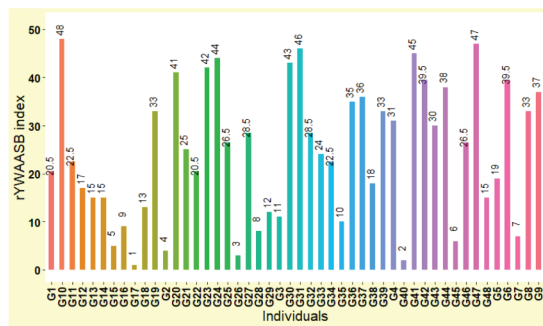
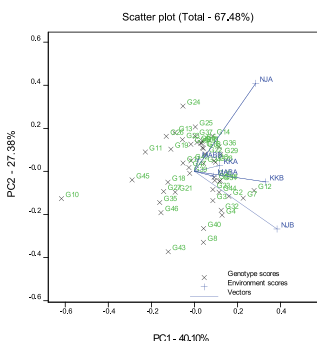


Figure 3. (a) View of the scatter plot for the discriminative versus representativeness of test environments for soybean phytic acid content; (b) which one won where for soybean phytic acid content with a polygon joining genotypes that are furthest from the biplot origin; (c) a Y*WAASB biplot of mean performance and stability for soybean phytic acid content; (d) bar graph ranking genotypes for their phytic acid content by the rYWAASB index. Abbreviations: YLD = yield; Env = Environment; Gen = Genotype.

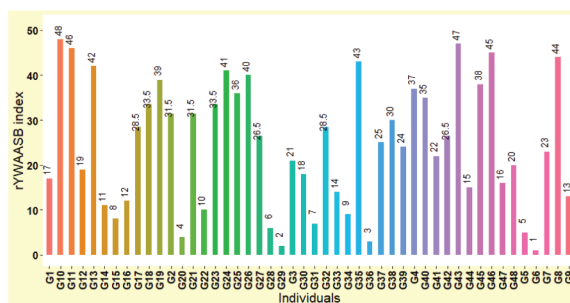
the second quadrant, such as G34 and G43, were unstable but had high phytic acid content. Genotypes in the 3rd quadrant that included G41, G42, G3, and G46 were stable with lower phytic acid content than the mean. Genotypes in the fourth quadrant, among them G33, G13, G18, G16, G26, and G21, were stable with higher phytic acid content above the mean. The rYWAASB bar graph (Figure 3(d)) ranked genotypes indicated as individuals on the x-axis. Genotypes with the highest index had the lowest phytic acid content.

The first and second principal components (PC1 and PC2) explained 67.48% of the net difference caused by the genotype and GEI (Figure 4(a)) for seed yield. The Y*WAASB biplot identified environment MABB as having the ability to discriminate genotypes for seed yield (Figure 4(d)). The first quadrant had genotypes such as G10, G11, G24, and G43 that were unstable and achieved lower yields than the mean. The second quadrant had unstable genotypes such as G4, G2, G7, G12, and G38 with yields above the mean, while the third quadrant had genotypes such as G45, G26, G23,

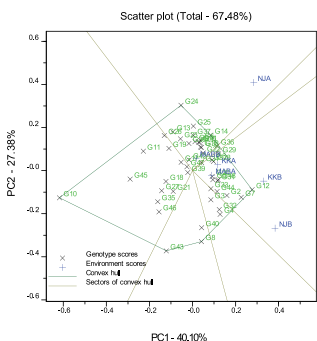
a) Discriminativeness versus representativeness



b) rYWAASB ranking biplot



c) Which won where view of GGE biplot



d) Y*WAASB means performance and stability for yield

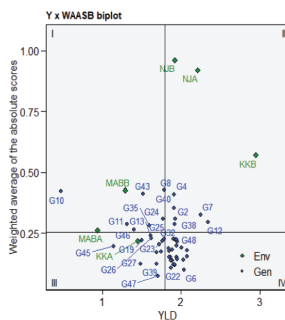


Figure 4. (a) View of the scatter plot of the discriminative versus representativeness of soybean test environments for yield; (b) bar graph ranking genotypes for seed yield by the rYWAASB index; (c) which-one-won where for soybean yield with a polygon joining genotypes that are furthest from the biplot origin; (d) a Y*WAASB biplot of mean performance versus stability for soybean seed yield.

and G39 that were stable but achieved yields lower than the mean. The fourth quadrant had varieties that were stable and high yielding that included G48, G22, and G6. The rYWAASB index bar graph (Figure 4(b)) ranked genotypes indicated as individuals in the x-axis. Genotypes with the highest index had the lowest yield. The which-won-where biplot grouped genotypes into six sectors (Figure 4(c)). The genotypes located at the corners of the polygon are the best or worst in performance in specific locations. While those within the polygon are less responsive (Figure 4(c)). Genotype G12 performed well in Njoro and Kakamega in the long rains of 2022, while G14 performed well at Njoro in the short rains of 2021.

Discussion

The quality of soybeans is defined by their seed composition. Soybean seed composition is controlled by genetic, environmental, and management factors (Assefa et al. 2019). Despite the presence of high-quality protein and oil, soybean seed also contains anti-nutritional factors such as phytic acid that limit its digestibility (Sá, Moreno, and Carciofi 2020) and the bioavailability of key nutrients in the feed and food products. This study aimed to understand the accumulation of phytic acid content among 48 soybean genotypes of different backgrounds, some of which are registered for commercial production. It is of great importance while initiating a low-phytate soybean program to determine the phytic acid content in the breeding program germplasm (Perera et al. 2018). A wide range of genotypic variation exists in soybean phytate-P concentration as observed by Kuerban et al. (2020). The study noted that some of the soybean genotypes had very low seed phytate combined with root traits for efficient P acquisition offering parental material for breeding for low phytate genotypes. The use of such unique parental material combined with marker assisted selection would hasten the availability of low phytate soybean genotypes that would mitigate against malnutrition in Africa, which is high (Wambua et al. 2025). The mean phytic acid content in the genotypes ranged from moderate to high compared to the check genotype N6003LP. Phytic acid accumulation in soybean seeds is genetically controlled but the environment also contributes to the variation, as observed on genotype N6003LP. Kuerban et al. (2020) recorded lower phytic acid contents than what was observed in our results while assessing 256 Chinese genotypes, suggesting that there are wide variations in phytic acid contents among soybean genotypes from different backgrounds. The mean soybean phytic acid content was lower in Mabanga, and this could be attributed to low pH limiting the availability of P and the low P content in the soil as observed in the site soil analysis results (Kamau, Kungu, and Mugendi 2020). Limitation of P availability reduces the enhancement of nodule weight and nitrogenase activity, leading to reduced plant growth

and yield (Sun et al. 2024) as observed in Mabanga. Lowering the phytic acid content may affect the agronomic performance of the generated lines. Punjabi et al. (2018) developed low-phytate soybean lines which had reduced phytic acid by 45%, an increase of inorganic P by 39% and an increase of mineral content of Zn, Fe, and Ca in the seed. The *lpa* transgenic lines had a good response to germination and seedling emergence, suggesting the expectation of normal to higher yields. However, Lin et al. (2024) observed that reducing phytic acid moderately by targeting single *Gmplk1* genes as opposed to multiplex mutagenesis directed toward ultra-low phytic acid content is an ideal approach for low-phytate line development with a negligible drawback in yield performance. Our study established the range of phytic acid concentrations in the breeding program germplasm and further identified environments where variation in phytic acid content can be expressed, making it easier for subsequent related investigations. The set of genotypes evaluated and environments covered is inadequate to make very conclusive statements on phytic acid stability across environments. However, the study has brought to the fore the need to assess phytic acid in soybean germplasm on a wider scale, as is done for quality aspects of protein and oil content. This should be taken into consideration while evaluating soybean genotypes on a regional scale, as in the Pan-African Soybean Variety Trials (Stella et al. 2025) or regional trials executed by the International Institute of Tropical Agriculture.

Genetic diversity of soybean germplasm and testing environments in the study provided a good basis for evaluation and selection of elite genotypes. The first principal components (PC1) and second principal components (PC2) accounted for more than 50% of the variation for phytic acid and yield, suggesting a significant genotype main effect and GEI. This enhances the need for identification of stable genotypes for production in varying agro-ecological zones.

The ideal genotype should be high-yielding and low in phytic acid content. A low but significant correlation was observed between yield and phytic acid. However, the biplots explained 50.46% of phytic acid content, suggesting that other factors contributed to the variation (Yan and Tinker 2006). This will require further investigation in more environments to validate the current information.

Improving yield is a major objective in all breeding programs (Masoudi et al. 2024), and this includes all traits that are of economic importance in the crop under production. There were significant differences in the yield of genotypes under evaluation within and across the locations. Soybean yields are a result of a combination of factors, which include the genetic potential of the genotypes and the environmental factors. The soils in the trial locations varied in terms of mineral content, acidity, and above-ground climatic conditions, and this could have contributed to the yield variance across sites.

Yields were generally low, with a mean of 2.3 t ha⁻¹ across the sites, which was lower than the potential yield of 5 t ha⁻¹ in sub-Saharan Africa (Giller et al. 2011). The yields were low at Mabanga in the short rains of 2022, which could be attributed to low pH, organic C, potassium, and P, as evidenced by the soil analysis results. High acidity decreases the availability of key nutrients, hampering growth and development (Zhang et al. 2023). Among the high-yielding genotypes, four are registered for commercial production, while five are not and can be further evaluated as potential cultivars. However, some genotypes performed well, especially in Kakamega, where genotypes G1 (NJSB2), G7 (DPSB 8), G12 (NJSB 6), G31 (NJSB 10), and G34 (NJSB 12) gave higher yields than the average production in Africa of 1.1 t ha⁻¹, but less than the global average of 2.4 t ha⁻¹ (Khojely et al. 2018). The observed yields were low compared to yields recorded by Mwiinga et al. (2020) where soybean genotypes were evaluated in six environments in South Africa. In a recent study involving 308 genotypes in Uganda, Palange et al. (2025) realized variation in phytate ranging from 14.8 to 6928.8 mg kg⁻¹ and yield that averaged 77.0–1800 g indicating the existence of high yielding low-phytate germplasm that can be used for breeding purposes. The current study identified high-yielding stable genotypes with low phytic acid content.

Conclusions

Genotype and genotype plus environment explained more than 50% of the variation in phytic acid content and seed yield, indicating significant variation in the traits. The study has identified high-yielding stable genotypes which can be further improved by improving their phytate and protein contents, which are key in the preparation of food and feed. There were no genotypes that had lower phytic acid content than the check genotype N6003LP. However, commercial varieties EAI 3600 (G41) and SC Saga (G42) achieved stable low phytate content and can be recommended for production as better varieties are developed. The current study has established the status of phytic acid content of released and promising genotypes in Kenya. This information can be used by breeders to improve the current commercial varieties with high yield and good end-use qualities by crossing them with the low phytic acid genotype N6003LP. Accessing other low-phytate soybean lines with proven end use qualities as parental materials would increase the diversity of low-phytate germplasm. In the short term, molecular markers linked to low phytate can be employed for the precise selection of soybean genotypes with desirable traits. To increase efficiency, gene editing using CRISPR/Cas9 system may be employed targeting *GmlPK1* and *GmMRPS* genes involved in phytate synthesis. Mutation of these genes reduces the phytic acid content, increases P and other mineral bioavailability with minimal

impact on yield and other agronomic traits (Song et al. 2022). Further evaluation of more soybean genotypes in a wider range of environments (acidic, alkaline, irrigated, moisture-stressed) where soybeans are likely to be grown is recommended to increase chances of discovery of low phytate adaptable genotypes and generate more information on the repeatability of genotype by environment interaction on seed composition. There are other anti-nutritional factors in soybeans other than phytic acid, and it would be prudent to determine their levels in the germplasm in order to come up with strategies for improvement of genotypes for commercial utilization in the food and feed industry.

Acknowledgements

The authors are grateful to the World Bank-funded Centre of Excellence in Sustainable Agriculture and Agribusiness Management (CESAAM) project for their financial support and the opportunity to carry out the study. Kenya Agricultural and Livestock Organization (KALRO) is greatly acknowledged for granting institutional time for the study. Mabanga Agricultural Training Centre (ATC), KALRO Njoro and KALRO Kakamega are acknowledged for providing sites for the study. The farm managers and staff of the KALRO Centres and Mabanga ATC are appreciated for providing unwavering support.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

The Centre of Excellence in Sustainable Agriculture and Agribusiness Management (CESAAM) project was funded by the World Bank through the International Development Association (IDA) Project Number IDA Credit 5798-KE.

Data availability statement

The datasets collected and analyzed for this study are available upon reasonable request.

Notes on contributors

James Ng'ang'a Njoroge is a senior research scientist at the Kenya Agricultural and Livestock Research Organization, Food Crops Institute. He heads the oil crops breeding program at the Food Crops Research Centre, Njoro. The oil crops include soybean, sunflower, castor and safflower, among others. He has a Master's degree in plant breeding from Egerton University and is pursuing a PhD in plant breeding at the same institution. He is biased towards soybean breeding and seed systems.

Josephine P. Ouma is a graduate of Mississippi State University with a degree in Agronomy and a minor in genetics. Current research interests focused on cereal-legume cropping

systems; fertilizers use; crop propagation methods; agronomy and crop physiology research on a wide range of agronomic crops. She is a proponent of the sustainability of crop production systems with a focus on utilization of organic by-products of agricultural industrial processing in ameliorating soil conditions, hence improving long-term soil fertility and crop productivity.

Pascal P. Okwiri Ojwang is a senior lecturer in the Department of Crops, Horticulture and Soils at Egerton University, Kenya. He has a background in Plant Breeding with an interest in breeding tropical cereals and legumes for resistance to biotic, abiotic stress tolerance, and quality traits. He is a research leader and coordinator of graduate training research projects at Egerton University. Previously, he worked as a dryland legumes breeder at the Kenya Agricultural Research Institute (KARI), currently renamed as the Kenya Agricultural and Livestock Research Organization (KALRO). He has published over 30 research journal articles in peer-reviewed international journals.

References

- Abdelghany, A. M., S. Zhang, M. Azam, A. S. Shaibu, Y. Feng, J. Qi, J. Li, et al. 2021. “Exploring the Phenotypic Stability of Soybean Seed Composition Using Multi-Trait Stability Index Approach.” *Agronomy* 11 (11): 2200. <https://doi.org/10.3390/agronomy11112200>.
- Abubakar, H., J. O. Ochuodho, E. O. Auma, and R. A. Sami. 2020. “Influence of Herbicides on Yield, Weight and Size of Soybean Seed.” *Duste Journal of Pure and Applied Sciences* 6 (1): 2476–8316.
- Arminian, A. 2025. “Simultaneous Selection by Trait and WAASB Index.” https://cran.r-project.org/web/packages/rYWAASB/vignettes/rYWAASB_manual.html.
- Assefa, Y., L. C. Purcell, M. Salmeron, S. Naeve, S. N. Casteel, P. Kovács, S. Archontoulis, et al. 2019. “Assessing Variation in US Soybean Seed Composition (Protein and Oil).” *Frontiers in Plant Science* 10:10. <https://doi.org/10.3389/fpls.2019.00298>.
- Averitt, B. J., E. Gregory, W. X. Li, E. Prenger, J. Qin, and B. Zhang. 2020. “Evaluating Genotypes and Seed Treatments to Increase Field Emergence of Low Phytic Acid Soybeans.” *Agriculture* 10 (11): 516. <https://doi.org/10.3390/agriculture10110516>.
- Dong, Q., K. Echigo, V. Raboy, and H. Saneoka. 2020. “Seedling Growth, Physiological Characteristics, Nitrogen Fixation, and Root and Nodule Phytase and Phosphatase Activity of a Low-Phytate Soybean Line.” *Plant Physiology and Biochemistry* 149:225–232. <https://doi.org/10.1016/j.plaphy.2020.02.015>.
- FAOSTAT. 2023. Accessed March 24, 2025. https://www.fao.org/faostat/en/#rankings/commodities_by_country.
- Giller, K. E., M. S. Murwira, D. K. C. Dhliwayo, P. L. Mafongoya, and S. Mpeperekwi. 2011. “Soyabean and Sustainable Agriculture in Southern Africa.” In *Sustainable Intensification Increasing Productivity in African Food and Agricultural Systems*, edited by J. Pretty, C. Toulmin, and S. William, 9. New York: Routledge.
- Jain, R. K., A. Joshi, H. R. Chaudhary, A. Dashora, and C. L. Khatik. 2017. “Study on Genetic Variability, Heritability and Genetic Advance in Soybean [*Glycine max* (L.) Merrill].” *Legume Research* 41 (4): 532–536. <https://doi.org/10.18805/LR-3874>.
- Jansone, I., V. Sterna, V. Stramkale, A. Stramkalis, A. Justs, and S. Zute. 2021. “Impact of Cultivation Technologies on Soybean Production and Quality. Environment. Technologies. Resources.” *Proceedings of the International Scientific and Practical Conference* 1, 101–107. <https://doi.org/10.17770/etr2021vol1.6605>.

- Kamau, N. N., J. B. Kungu, and D. Mugendi. 2020. "Effects of *Mycorrhizal* and *Rhizobium* Inoculation on Soybean Growth in Acidic Soils of Gatanga, Kenya." *Cell Biology and Development* 4 (1), Article 1. <https://doi.org/10.13057/cellbioldev/v040101>.
- Kariithi, S. N., S. I. Abwao, P. N. Njau, and J. N. Ndung'u. 2016. "Evaluation of Grain Nutritional Quality and Resistant Starch Content in Kenyan Bread Wheat Varieties." *African Crop Science Journal* 24 (4): 417. <https://doi.org/10.4314/acsj.v24i4.8>.
- Kebede, G., W. Worku, H. Jifar, and F. Feyissa. 2023. "GGE Biplot Analysis of Genotype by Environment Interaction and Grain Yield Stability of Oat (*Avena sativa* L.) in Ethiopia." *Agrosystems, Geosciences & Environment* 6 (3): e20410. <https://doi.org/10.1002/agg2.20410>.
- Khojely, D. M., S. E. Ibrahim, E. Sapey, and T. Han. 2018. "History, Current Status, and Prospects of Soybean Production and Research in Sub-Saharan Africa." *The Crop Journal* 6 (3): 226–235. <https://doi.org/10.1016/j.cj.2018.03.006>.
- Kurban, M., W. Jiao, J. Pang, J. Jing, L. J. Qiu, W. Ding, W. F. Cong, F. Zhang, and H. Lambers. 2020. "Targeting Low-Phytate Soybean Genotypes Without Compromising Desirable Phosphorus-Acquisition Traits." *Frontiers in Genetics* 11:11. <https://doi.org/10.3389/fgene.2020.574547>.
- Lee, S. Y., H. S. Lee, C. M. Lee, S. K. Ha, H. M. Park, S. M. Lee, Y. Kwon, J. U. Jeung, and Y. Mo. 2023. "Multi-Environment Trials and Stability Analysis for Yield-Related Traits of Commercial Rice Cultivars." *Agriculture* 13 (2): 256. <https://doi.org/10.3390/agriculture13020256>.
- Lin, W., M. Bai, C. Peng, H. Kuang, F. Kong, and Y. Guan. 2024. "Genome Editing Toward Biofortified Soybean with Minimal Trade-Off Between Low Phytic Acid and Yield." *Abiotech* 5 (2): 196–201. <https://doi.org/10.1007/s42994-024-00158-4>.
- Malosetti, M., J. Ribaut, and F. A. Van Eeuwijk. 2013. "The Statistical Analysis of Multi-Environment Data: Modeling Genotype-by-Environment Interaction and Its Genetic Basis." *Frontiers in Physiology* 4:37433. <https://doi.org/10.3389/fphys.2013.00044>.
- Masoudi, B., A. Gholizadeh, P. Majidian, E. Hezarjaribi, N. Razmi, and F. Shariati. 2024. "A Study on the Genotype \times Environment Interaction in Promising Advanced Genotypes of Soybean Using Graphical GGE-Biplot Analysis." *Journal of Crop Breeding* 16 (4): 77–88. <https://doi.org/10.61186/jcb.16.4.77>.
- Mohring, J., E. Williams, and H. P. Piepho. 2015. "Inter-Block Information: To Recover or Not to Recover It?" *Theory and Applied Genetics* 128 (8): 1541–1554. <https://doi.org/10.1007/s00122-015-2530-0>.
- Mwiinga, B., J. Sibiyi, A. Kondwakwenda, C. Musvosvi, and G. Chigeza. 2020. "Genotype \times Environment Interaction Analysis of Soybean (*Glycine Max* (L.) Merrill) Grain Yield Across Production Environments in Southern Africa." *Field Crops Research* 256:107922. <https://doi.org/10.1016/j.fcr.2020.107922>.
- Olivoto, T., and A. D. Lúcio. 2020. "Metan: An R Package for Multi-Environment Trial Analysis." *Methods in Ecology and Evolution* 11 (6): 783–789. <https://doi.org/10.1111/2041-210X.13384>.
- Palange, N., J. Sserumaga, E. Wembabazi, M. Ochwo, A. Badji, E. Nuwamanya, I. Dramadri, et al. 2025. "Genetic Variability of Anti-Nutritional Factors Among Soybean (*Glycine Max*) Germplasm." *Discover Agriculture* 3. <https://doi.org/10.1007/s44279-025-00199-3>.
- Patterson, H. D., and R. Thompson. 1971. "Recovery of Inter-Block Information When Block Sizes Are Unequal." *Biometrika* 58 (3): 545–554. <https://doi.org/10.1093/biomet/58.3.545>.
- Patterson, H. D., and E. R. Williams. 1976. "A New Class of Resolvable Incomplete Block Designs." *Biometrika* 63 (1): 83–92. <https://doi.org/10.1093/biomet/63.1.83>.
- Perera, I., A. Fukushima, M. Arai, K. Yamada, S. Nagasaka, S. Seneweera, and N. Hirotsu. 2018. "Identification of Low Phytic Acid and High Zn Bioavailable Rice (*Oryza Sativa* L.)

- from 69 Accessions of the World Rice Core Collection.” *Journal of Cereal Science* 85:206–213. <https://doi.org/10.1016/j.jcs.2018.12.010>.
- Prajapati, M., and H. Shah. 2022. “Impacts and Industrial Applications of Phytic and Phytate.” *Journal of Pure and Applied Microbiology* 7786 (4): 2292–2302. <https://doi.org/10.22207/JPAM.16.4.6>.
- Punjabi, M., N. Bharadvaja, M. Jolly, A. Dahuja, and A. Sachdev. 2018. “Development and Evaluation of Low Phytic Acid Soybean by siRNA Triggered Seed Specific Silencing of Inositol Polyphosphate 6-/3-/5-Kinase Gene.” *Frontiers in Plant Science* 9 9. <https://doi.org/10.3389/fpls.2018.00804>.
- Qin, D., Y. Hara, V. Raboy, and H. Saneoka. 2020. “Characteristics and Quality of Japanese Traditional Fermented Soybean (Natto) from a Low-Phytate Line.” *Plant Foods for Human Nutrition (Dordrecht, Netherlands)* 75 (4): 651–655. <https://doi.org/10.1007/s11130-020-00865-5>.
- Sá, A. G. A., Y. M. F. Moreno, and B. A. M. Carciofi. 2020. “Food Processing for the Improvement of Plant Proteins Digestibility.” *Critical Reviews in Food Science and Nutrition* 60 (20): 3367–3386. <https://doi.org/10.1080/10408398.2019.1688249>.
- Samtiya, M., R. F. Aluko, and T. Dhewa. 2020. “Plant Food Anti-Nutritional Factors and Their Reduction Strategies: An Overview.” *Food Production, Processing and Nutrition* 2 (1): 6. <https://doi.org/10.1186/s43014-020-0020-5>.
- Sarkhel, S., and A. Roy. 2022. “Phytic Acid Reduction in Pulse Matrix: Structure-Function Relationship Owing to Bioavailability Enhancement of Micronutrients.” *Journal of Food Process Engineering* 34 (5): e14030. <https://doi.org/10.1111/jfpe.14030>.
- Sens, R. F., L. S. Bassi, L. M. Almeida, D. F. Rosso, L. V. Teixeira, and A. Maiorka. 2021. “Effect of Different Doses of Phytase and Protein Content of Soybean Meal on Growth Performance, Nutrient Digestibility, and Bone Characteristics of Broilers.” *Poultry Science* 100 (3): 100917. <https://doi.org/10.1016/j.psj.2020.12.015>.
- Siamabele, B. 2021. “The Significance of Soybean Production in the Face of Changing Climates in Africa.” *Cogent Food & Agriculture* 7 (1): 1933745. <https://doi.org/10.1080/23311932.2021.1933745>.
- Singh, P., and D. Bhatia. 2017. “Incomplete Block Designs for Plant Breeding Experiments.” *Agricultural Research Journal* 54 (4): 607. <https://doi.org/10.5958/2395-146X.2017.00119.3>.
- Song, J. H., G. Shin, H. J. Kim, S. B. Lee, J. Y. Moon, J. C. Jeong, H. K. Choi, et al. 2022. “Mutation of *GmIpk1* Gene Using CRISPR/Cas9 Reduced Phytic Acid Content in Soybean Seeds.” *International Journal of Molecular Sciences* 23 (18): 10583. <https://doi.org/10.3390/ijms231810583>.
- Stella, A. A., J. P. S. Pavan, M. S. Araújo, F. Bruno, V. U. Innocent, P. L. Erica, F. S. Michelle, et al. 2025. “Soybean Selection in Kenya Enhanced by Multi-Trait and Genotype-by-Environment Interaction Modeling.” *Scientific Reports* 15 (1): 27575. <https://doi.org/10.1038/s41598-025-10654-2>.
- Sun, X., H. Zhang, Z. Yang, X. Xing, Z. Fu, X. Li, Y. Kong, W. Li, H. Du, and C. Zhang. 2024. “Overexpression of GMPAP4 Enhances Symbiotic Nitrogen Fixation and Seed Yield in Soybean Under Phosphorus Deficient Condition.” *International Journal of Molecular Sciences* 25 (7): 3469. <https://doi.org/10.3390/ijms25073649>.
- Sureshkumar, S., J. Song, V. Sampath, and I. Kim. 2023. “Exogenous Enzymes as Zoo Technical Additives in Monogastric Animal Feed: A Review.” *Agriculture* 13 (12): 2195. <https://doi.org/10.3390/agriculture13122195>.
- Taliman, N. A., Q. Dong, K. Echigo, V. Raboy, and H. Saneoka. 2019. “Effect of Phosphorus Fertilization on the Growth, Photosynthesis, Nitrogen Fixation, Mineral Accumulation, Seed Yield, and Seed Quality of a Soybean Low-Phytate Line.” *Plants* 8 (5): Article 5. 119. <https://doi.org/10.3390/plants8050119>.

- Thakur, A., V. Sharma, and A. Thakur. 2019. "An Overview of Anti-Nutritional Factors in Food." *International Journal of Chemical Studies* 7 (1): 2472–2479.
- VSN International. 2012. *Genstat for Windows*. Fifteenth ed. Oxford: VSN International Ltd.
- Wambua, J., A. Ali, J. B. Ukwizabigira, and P. Kuodi. 2025. "Prevalence and Risk Factors of Under-Five Mortality Due to Severe Acute Malnutrition in Africa: A Systematic Review and Meta-Analysis." *Systematic Reviews* 14 (1): 29. <https://doi.org/10.1186/s13643-024-02740-9>.
- Wang, J., H. Huong, X. Yan, J. Uan, O. Lu, Y. Gu, and L. Qiu. 2024. "Stability Evaluation for Main Quality Traits of Soybean in the North East and Hyang-Huai-Hai Regions." *Agronomy* 14 (4): 872. <https://doi.org/10.3390/agronomy14040872>.
- Yan, W. 2019. "LG Biplot: A Graphical Method for Mega-Environment Investigation Using Existing Crop Variety Trial Data." *Scientific Reports* 9 (1): 1–8. <https://doi.org/10.1038/s41598-019-43683-9>.
- Yan, W., and M. S. Kang. 2002. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. Boca Raton: CRC Press. <https://doi.org/10.1201/9781420040371>.
- Yan, W., D. Pageau, J. F. Reid, and J. Durand. 2011. "Assessing the Representativeness and Repeatability of Test Locations for Genotype Evaluation." *Crop Science* 51 (4): 1603–1610. <https://doi.org/10.2135/cropsci2011.01.0016>.
- Yan, W., and N. A. Tinker. 2006. "Biplot Analysis of Multi-Environment Trial Data: Principles and Applications." *Canadian Journal of Plant Science* 86 (3): 623–645. <https://doi.org/10.4141/P05-169>.
- Zhang, S., Q. Zhu, W. de Vries, G. H. Ros, X. Chen, M. A. Muneer, F. Zhang, and L. Wu. 2023. "Effects of Soil Amendments on Soil Acidity and Crop Yields in Acidic Soils: A World-Wide Meta-Analysis." *Journal of Environmental Management* 345:118531. <https://doi.org/10.1016/j.jenvman.2023.118531>.