Phosphorus use efficiency and genotype × environment interactions in four elite soybean genotypes in Kenya

Mubuni Francis[1]
M'mbone M. Everlyne[2]
Akundabweni S. Levi[3]

fmubuni@gmail.com

[1,2,3]Masinde Muliro University of Science and Technology, Kenya

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ABSTRACT

The constraint of low soil phosphorus (P) availability is a significant aspect that affects the production of soybean in sub-Saharan Africa, especially soils that are highly weathered and where the fixation of P restricts access to nutrients in the soils. In the study, the phosphorus use efficiency (PUE) and genotype x environment interaction (GEI) among four elite soybean genotypes (Gazelle, Blackhawk, SB 08, and SB 19) were measured under three phosphorus levels (0, 30, and 50 kg P ha -1) and across phosphorus-deficient environments in western Kenya. PUE assessment was carried out in a split-plot randomized complete block design and to assess GEI in terms of agronomic characteristics such as grain yield, total biomass, and accumulation of phosphorus, multi-environment trials were conducted at three phosphorus deficient locations. The analysis of variance indicated that the effects of phosphorus level were highly significant ($p < 0.001$) on these characteristics, but the effects of genotype and genotype x phosphorus interactions were not significant, implying that the limitation of nutrients concealed genetic differences suggesting that increased phosphorus availability is necessary before genotypic differences can be fully expressed. The gain in grain yield and biomass was observed to be steady with exposure to phosphorus, evidencing the prevailing role phosphorus supply played in improving crop performance. Genotypic yield differences were not significant, but the yield index, phosphorus efficiency indices, and PCA indicated that underlying physiological strategies included SB 19, which had high phosphorus utilization efficiency, Gazelle, which had high phosphorus uptake and partitioning, and SB 08 that had a balanced response. The environment and genotype × environment interaction ($p < 0.05$) passed significant to generate the grain yield, time to maturity, days to 50% flowering and the other agronomic traits, whereas environment was considered to explain the most significant part of the variation. AMMI and GGE biplots showed that there were crossover interactions, meaning that there was no best genotype in all the environments. SB 08 was found to be the most stable with AMMI Stability Value, and SB 19 was a mixture of moderate stability and high phosphorus utilization efficiency. The findings illustrate that the output of soybean in phosphorous-deficient systems is mostly determined by the availability of nutrients but the environmental circumstances have strong effects on the genotype performance of soybean. It shows the significance of combining phosphorus regulation with the choice of effective and resilient genotypes to improve productivity and functionality of low-input agriculture.

Keywords: AMMI, Genotype × Environment Interaction, Phosphorus Use Efficiency, Smallholder Farming, Soybean, Yield Stability

I. INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is a valuable legume because of its high protein and oil content, and because of the role it plays in soil fertility due to the biological fixation of nitrogen (Amoanimaa-Dede et al., 2022). In addition to its agronomic importance, soybean has a wide variety of applications in human diets, animal feeding, and processing. Soy bean is extensively processed into foodstuffs including Soy flour, soy milk, tofu, and texturized vegetable protein, which are inexpensive, but rich in high-quality vegetable protein and essential amino acids. As an edible oil, soybean oil is being used more in industrial products such as biodiesel and pharmaceuticals and in food processing, and soybean meal and haulms form valuable livestock feed and are being used to boost dairy and poultry production. As a result, food security, household earnings and nutritional enhancement among smallholder agricultural systems in sub-Saharan Africa has been largely boosted by soybean (Chen et al., 2023). In spite of these advantages, the yield of soybean in sub-Saharan Africa is significantly lower than its genetic potential, which can be mainly attributed to the low phosphorus (P) status of the soils as well as the deteriorating soil fertility owing to repeated cultivation, soil degradation and insufficient nutrient supply (Chen et al., 2023).

Phosphorus is a very critical macronutrient that aids in energy transfer, photosynthesis, nucleic acid synthesis, root formation, nodulation and grain formation in plants (Cordell et al., 2009). In very weathered nutrient-rich soils (as found in the highlands of western Kenya), aluminum and iron oxide strongly bind phosphorus, making it unavailable to

plants (Johan et al., 2021). The steep prices of phosphate fertilizers, as well as, liming substances, further limit their use, requiring other methods, raising phosphorus gains and internal efficiency of its use. The efficiency of phosphorus use (PUE) is a multidimensional characteristic typically broken down into phosphorus uptake efficiency (PUpE) and phosphorus utilization efficiency (PUtE). The uptake efficiency of phosphorus is defined as the efficiency of the plant to take up phosphorus in the soil per unit of available phosphorus, and is greatly controlled by root system architecture, root surface area, root hair density and length, rhizosphere modification processes and symbiotic relationships with arbuscular mycorrhizal fungi which increase phosphorus solubilization and absorption.

In response to low-phosphorus conditions, adaptive characteristics like shallow and highly branched root systems, greater exudation of organic acids and phosphatases, and greater mycorrhizal colonization enhance the phosphorus mobilization and uptake (Lynch, 2019; Li et al., 2022). Conversely, phosphorus utilisation efficiency explains how well the plant can transform phosphorus that has been taken up into economic gain of biomass. This factor includes physiological and biochemical activities within the body including the production of ATP and its allocation as efficiently as possible, photosynthetic carbon taken up optimally, the phosphorus in vegetative tissues are remobilized to the organs and its reproductive organs are at least a mode of production that ensures growth occurs without a rise in phosphorus requirements. High phosphorus utilization efficiency genotypes tend to support grain production where tissue phosphorus concentration will be low due to greater partitioning efficiency and metabolic plasticity (Irfan et al., 2020; Minhas et al., 2025; Lynch, 2022). Both phosphorus uptake and utilization efficiencies have been extensively reported to differ genotypically in legumes and cereals, which, as a result, have a great potential of genetic improvement of crop productivity in low-input environments (Irfan et al., 2020; Minhas et al., 2025). Soybean also has these efficiency indices: phosphorus harvest index, phosphorus physiological efficiency, and phosphorus stress factor, which differentiate these efficient and inefficient genotypes (Bhat et al., 2017).

In addition to nutrient efficiency, genotype x environment interaction (GEI) plays a key role in expressing agronomic traits like grain yield, flowering time, and seed size. GEI makes the selection of genotype complicated due to the possibility of variation in its performance according to the locality and season (Qasemi et al., 2022; Adham et al., 2022). These diverse agro-ecological conditions (variation in rain, altitude, and soil fertility) of Kenya render GEI analysis to be invaluable in the determination of stable and widely adapted soybean genotypes. Additive Main Effects and Multiplicative Interaction (AMMI) and GGE biplot analysis are multivariate techniques that can be used to examine GEI and apply it in genotype recommendation (Jat et al., 2017; Gloria et al., 2024). Thus, the proposed study incorporates the analysis of phosphorus use efficiency, as well as the genotype x environment interaction analysis to determine soybean genotypes exhibiting efficient phosphorus uptake, efficient internal phosphorus utilization, and yield stability across phosphorus-deficient conditions in western Kenya.

1.1 Statement of the Problem

Although, soybean (*Glycine max* (L.)) holds importance in agriculture and nutrition, in sub-Saharan Africa, its production is greatly limited by a lack of phosphorus (P), especially in acidic soils. Phosphorus has become an important element in the development of roots, energy and photosynthesis and as such, its concentration in the soils is often limited by fixation with aluminium and iron oxides of acidic soils.

Small scale farmers cannot at times afford the lime or phosphate fertilizers because they are very expensive and the phosphorus sources are non-renewable. In addition, a lack of clarity in the adaptive changes of the soybean genotypes with the soils deficient in P has caused planting of soybean types in a random manner which has led to inefficient production of yields.

The available literature has not addressed the genotype-by-environment interactions (GEI) research on phosphorus-restricted environments effectively, and it has not met the need of applying genotype deployment strategies in different agro-ecological environments of Kenya.

A pressing requirement is, therefore, to examine elite soybean genotypes in low-input conditions with respect to phosphorus use efficiency (PUE) and GEI with an aim of getting stable, P-efficient cultivars that can improve food security and livelihoods of farmers.

1.2 General Objective

To enhance soybean yields and food security by evaluating elite phosphorus-efficient soybean varieties

1.2.1 Specific Objectives

i. To compare phosphorus use efficiency among four elite Soybean varieties under three phosphorus rates in Kakamega.
ii. To assess the genotype by environment interaction for agronomic traits of the soybean genotypes across three locations.

II. LITERATURE REVIEW

2.1 Productive uses of phosphorus in crop production

Phosphorus (P) is a critical macro nutrient, which is at the heart of plant growth and development because it is part of energy transfer, photosynthesis, signal transduction, and biosynthesis of nucleic acids and membrane. Although it is essential, phosphorus is one of the biggest limitations of agro-ecosystems globally, especially in highly weathered tropical soils, phosphorus is more than a fixation by iron and aluminum oxides, making it inaccessible to plants (Cordell et al., 2009; Johan et al., 2021). This is particularly acute in sub-Saharan Africa; with low fertilizer application and decreasing soil fertility contributing to phosphorus inadequacy. Phosphorus use efficiency (PUE) has thus been front-and-center as part of improving crop productivities when facing limitations inherent with nutrient limitations. The wider definition of PUE is the potential of a plant to take in phosphorus available in the soil and efficiently use it to generate biomass and economic output (Irfan et al., 2020; Minhas et al., 2025). It is commonly divided into two large-scale aspects phosphorus uptake efficiency (PUpE), the ability of the plant to take access to phosphorus within the soil, and phosphorus utilization efficiency (PUtE) that is the effectiveness with which the uptake phosphorus is transformed into plant biomass or grain yield. Exchange of phosphorus uptake and utilization tends to be a process of trade off, where certain genotypes are specialized with phosphorus uptake as others with the utilization within the body.

Maize and wheat studies have shown that high phosphorus uptake genotypes do not consistently have high utilization efficiency, reflecting the multifaceted ability of PUE as a breeding goal (White et al., 2013). This difference has prompted the division of crops into phosphorus acquisition-efficient and phosphorus utilization-efficient types, with each having distinct adaptive mechanism to tolerate phosphorus stress. The other important factors affecting phosphorus use efficiency are the environmental factors. Phosphorus availability relies on soil characteristics, including pH, organic material levels, mineral composition, as well as on climatic conditions, including temperature and rainfall (Johan et al., 2021). The positive changes in phosphorus delivery result in a significant increase of biomass generation and grain production in many cropping systems because of the increase of the photosynthetic activity, as well as the enhancement of assimilate partitioning (Han et al., 2022). Greater phosphorus availability also facilitates higher distribution of phosphorus towards a reproduction structure hence enhancing grain quality as well as harvest index. But the effectiveness of crops to respond to phosphorus fertilization differs across species and genotypes. In wheat and rice, the growth of plant yield to the phosphorus is usually linear to a certain degree beyond which the cost of additional phosphorus does not help in boosting the production (Balemi, 2010). This implies that the factor to limit the amount of nutrient taken in is not the external source of nutrients but instead the internal physiological processes involved.

With the increasing price of fertilizers and the possibility of phosphorus to be depleted in the world, one of the priorities of sustainable agriculture has become the enhancement of phosphorus use efficiency. Potential measures to improve PUE are the creation of crop cultivars with reduced nutrient requirements, combined soil fertility control, and application of non-chemical treatments such as mycorrhizal inoculation (Chen et al., 2023). Strategies are especially critical with low-input agricultural systems where there may be low access to fertilizers. Integrative indices like the phosphorus harvest index (PHI), phosphorus stress factor (PSF), phosphorus physiological efficiency index (PPEI), and phosphorus biological efficiency ratio (PBER) can be used to comprehensively assess phosphorus use efficiency in plants by integrating these indices probing the performance of plants at different phosphorus levels. PHI measures phosphorus allocation to grain, or how well phosphorus is remobilized between vegetative tissues, whereas PSF quantifies yield or biomass loss in the event of phosphorus deficiency, i.e., a measure of stress tolerance. PPEI measures how efficiently phosphorus is absorbed and transformed into a biomass or yield, emphasizing physiological adaptation processes, but PBER combines both absorption and use by biomass produced per unit of accumulated phosphorus. These parameters combined give a comprehensive perspective on phosphorus acquisition, translocation, utilization, and resilience to nutrient stress, rendering them useful in determining genotypic phosphorus performance and enhancing crop productivity under phosphorus nutrient stress (Bhat et al., 2017).

2.1.2 Crop Performance Genotype x Environment Interaction

The environment is very strong in affecting the performance of crop genotypes, which brings about the existence of genotype x environmental interaction (GEI), whereby varying genotypes react in different environments. GEI is a significant complication in plant breeding and variety selection since it makes it hard to identify genotypes that can be consistently performed in various agro-ecological environments (Qasemi et al., 2022; Adham et al., 2022). There are environmental influences like soil fertility, distribution of rainfall, temperature, and altitude that interact with genetic characteristics to determine crop growth, development and yield. Genetic variation alone does not explain yield differences in many crops such as maize, rice, and common beans where environmental variability has been found to drive a greater proportion of the variation in yield (Alam et al., 2022). This highlights the significance of testing the genotypes in different environments in order to get the entire spectrum of their performance.

To examine GEI, various statistical models have been created, including the Additive Main Effects and Multiplicative Interaction (AMMI) model and Genotype plus Genotype × Environment (GGE) biplot that are used often. The AMMI model includes analysis of variance (ANOVA) to analyze additive effects and principal component analysis (PCA) to analyze interaction effects and provide a detailed understanding of genotype performance and stability (Gauch, 2013). The GGE biplot, in its turn, offers to visualize the genotype performance in both environments, which in turn allows one to find the patterns of which-won-where and the most suitable genotypes (Jat et al., 2017; Gloria et al., 2024). The stability of yield is an important issue of GEI analysis especially in those areas with a high level of environmental variability. Stable genotypes refer to the genotypes which maintain a consistent performance in a broad environment with little or no interaction effects. Nevertheless, stability is often linked to reasonable, but not full productivity, resulting in the trade-off in the areas of productivity and adaptability (Gloria et al., 2024). Conversely, highly productive genotypes can have an extremely good performance in a particular environment, but they exhibit a more varied range of response in other locations.

Stability has been widely researched in cereals and legumes with the Stability Value (ASV) index typically applied to measure genotype stability. Genotypes having low ASV values are deemed to be more stable, as they have lesser differences between the mean values of all environments (Adham et al., 2022). The importance of such genotypes is especially when it comes to small holder farmers who are subjected to unpredictable climatic conditions. Other important agronomic characteristics influenced by the GEI include flowering time, maturity, seed size and pod number on top of yield. These characteristics can be affected by environmental signals like temperature and photoperiod which control plant developmental mechanisms. To give examples, changes in temperature and rainfall have been found to cause significant changes in flowering (in crops such as rice and maize) and grain filling period (which, in turn, impact the yield) (Alam et al., 2022). Combining the analysis of GEI with the analysis of nutrient efficiency will offer an improved solution to crop development. Breeders can produce both productive and resilient varieties by producing genotypes that can be placed in different environments and exhibit consistent performance. It is especially crucial in areas with lack of phosphorus, where nutrient availability is limited, as well as the environmental variability that reduces productivity of crops.

III. METHODOLOGY

3.1 The Study Sites

Fieldwork was done in three phosphorus-deficient sites in western Kenya, i.e. Luandeti in Matete Sub-County, Kakamega County; Mufupi in Tongaren Sub-County, Bungoma County and Himaki, in Nandi East Sub-County, Nandi County. The Luandeti was installed in the Kakamega County, lying at geographical coordinates N0.5921362, E 34.8238723 altitude 1,514 m above the sea level, average temperature 22.0, mean precipitation 1,100 mm/year, and relative humidity 56%. The Mufupi site of Bungoma County is located at 1,652 m above sea level, has a mean temperature of 20.9 C every year, the average amount of rain 1, 280 mm yearly, and the relative humidity is 63% (Jaetzold, 2016). It is located in the Himaki area of Nandi County, with coordinates N0.2071964, E35.151507, and elevation 1,950 above sea level with a mean annual temperature of 22.0 o C, average annual precipitations of 2,000 mm and a relative degree of humidity of 77 percent. The three locations were chosen as they are considered countering agro-ecological environments favorable to the production of soybean hence offering a rigorous assessment of the performance of the genotypes and the efficacy of phosphorus utilization under a dissimilar environment.

3.2 Plant Materials

The four soybeans (*Glycine max* (L.)) were assessed in the study. The genotypes, Gazelle, SB 08, SB 19, and Blackhawk that were obtained at the Kenya Agricultural and Livestock Research Organization (KALRO), Njoro. Gazelle and Blackhawk served as a good productivity benchmark of high yield and well adapted to efficacious phosphorus utilization, and efficiency, respectively, in the measurement of root-mediated phosphorus uptake and symbiotic phosphorus uptake, respectively. SB 08, which is an elite and a comparatively stable breeding line, indicated better phosphorus efficiency and adaptation to various environments, whereas SB 19 displayed the opposite response to phosphorus availability, which allowed easily determining genotype-specific adaptation and genotype-by-environment interaction. Together, these genotypes provided enough diversity to make intrinsic physiological and statistical comparison and enough experimental precision to make.

3.3 Sample Analysis and Sampling of Soil

The soils of the selected locations of the experiments were performed by analyzing them to detect certain physico-chemical properties before the initiation of the trials. The samples were obtained as soil which exists in a zigzag way, a depth of 30cm below the surface, an auger was used to obtain the samples and then three samples were combined to form a composite sample. The pH of soil was determined by using one-to-two (w/v) soil-to-distilled water suspension.

To measure the phosphorus and potassium levels in the soil that could be extracted, AB-DTPA was used as the solution to extract the sample, the protocol used was developed by Bhat et al., (2017).

Table 1

Sample Analysis and Sampling of Soil

Parameter	Result	Ideal Range (Soybean)	Status
Soil pH (1:2.5 Soil: Water)	5.30	6.30–6.50	Strongly acidic
Nitrogen (%)	0.18	0.20–0.50	Deficient
Phosphorus (ppm)	27.70	30–80	Deficient
Potassium (me %)	0.68	0.24–1.50	Adequate
Total Organic Carbon (%)	1.94	2.66–5.32	Deficient
Calcium (me %)	1.96	2.00–15.00	Deficient
Magnesium (me %)	1.71	1.00–3.00	Adequate
Copper (ppm)	1.21	>1.00	Adequate
Iron (ppm)	10.31	>10.00	Adequate
Zinc (ppm)	5.08	>5.00	Adequate

3.4 Experimental Design, Treatments and Layout

3.4.1 Comparing Phosphorus Use Efficiency among Four Elite Soybean Varieties under Three Phosphorus Rates in Kakamega

The Kakamega site was the place of the experiment that involved a split-plot design in a randomized complete block design (RCBD) with three replications. Randomization involving treatments was carried out within each replication using random draw.

The level of phosphorus fertilizer was made the main plot factor and soybean genotype was taken in subplot factor in this design. The phosphorus used had three application rates which were: 0 kg P ha-1 (low P), 30 kg P ha-1 (medium P), and 50 kg P ha-1 (high P). Genotypes tested were Gazelle, Blackhawk, SB 08 and SB 19. The phosphorus levels were in three leading plots in which each replication (block) was partitioned into.

The four genotypes were randomly labeled to each main plot that was divided into four subplots. This produced a cumulative of twelve combinations of treatment per replication (3 phosphorus levels x 4 genotypes), and thirty-six experimental units of the three replications. Each subplot was 4.0m long, 0.6m wide giving a 2.4m2 area with intra row distance of 5 cm and inter row distance of 0.5 m. The main plots were each fitted with four subplots on them, on a side by side basis, providing an approximate area of 15.6 m2 per main plot.

As such, there were three broad plots in each replication and the total size of all main plots took the overall size of all main plots with the addition of inter-plot spacing. Border effects were managed by ensuring adequate inter plot spacing and by collecting data from the central tagged plants.

3.5 Preparation of Land and Planting of Crops

Thin rows of 4 m long and with inter-row intervals of 60 cm and intra-row intervals of 5 cm were used in the sowing with three seeds planted in every hole with a depth of about 3 cm and they were lightly covered with soil to enhance up-coming growth. During planting only phosphorus fertilizer was used at the recommended rate as triple superphosphate as follows: 0 kg P ha -1(control), 30 kg P ha -1 (medium phosphorus) and 50 kg P ha -1 (high phosphorus). One week after crop-piling, seedlings were cut to only two plants per hill, to provide homogenous population of plants. Weed control was done thrice in a growing season to ensure the absence of weeds and pests incidences were also checked frequently with the application of broad-spectrum insecticides when required. Each plot was tagged with ten central plants to collect the data.

3.6 The results of phosphorus accumulation in the genotypes

Ten randomly selected and tagged plants in Kakamega were analysed to determine phosphorus levels in grains and plant biomass as phosphorus use efficiency. Plant samples were taken in each experimental plot at the physiological maturity stage. Grains and shoots were sorted out, washed to eliminate soil and trash and stored in paper bags labeled. The samples were dried in the oven at 65 o C at least of 72 hours until a constant weight was reached. A digital balance (±0.001 g) was then used to weigh each sample to determine dry matter yield. Sample uniformity was ensured by passing dried tissues through a 0.5 mm sieve and then grinding with a steel Wiley mill. They were digested in airtight containers on these ground samples which have been stored with the help of a desicator.

3.6.1 The procedure of Wet Acid Digestion can be performed as follows

Wet digestion with acid was used to extract phosphorus out of plant tissues. Accurate weighing and quantification of a 0.500 g sub-sample of each ground tissue was then done and moved to a clean and dry Kjeldahl digesting tube. To each tube, 5.0 mL of concentrated sulfuric acid (H_2SO_4, ≥98%) was added. The mixture was allowed to remain at room temperature (approx. 25 0 C) over 30 minutes, to allow initial wetting and carbonization. Tubes of digestion were then added to a block of digestion, and warmed slowly to about 300C in a fume hood. The oxidation and clarity of solution were promoted by adding 1.5 mL of 30% hydrogen peroxide (H2O2) drop by drop when the digest started clearing. The digestion proceeded till a colourless, or pale-yellow colour, showing complete oxidation of organic matter, was obtained. Tubes were taken out of the heat after digestion had occurred and left to cool to ambient temperature. Whatman No. 42 filter paper was used to filter digests into 100 mL volumetric flasks and was topped with distilled water. The filtrate that was obtained was soluble inorganic phosphorus which could be analyzed by colorimetry.

3.6.2 Standards and Reagents Preparation

Potassium dihydrogen phosphate (KH2PO4) (analytical grade) was used to prepare phosphorus standards. After dissolving 0.439 g KH2PO4 in 1 L of distilled water resulted in a stock solution (with 100 mg P/L). Serial dilutions were then done to obtain different standards of 0 to 1.0 mg P/L. The molybdate-ascorbic acid color reagent was recrystallized, by dissolving 2.5 g ammonium molybdate and 0.5 g antimony potassium tartrate in 250 mL of 1N H2SO4. Ascorbic acid (1.0 g) was used as a reducing agent immediately before use.

3.6.3. Colorimetric Determination of Phosphorus can be determined using colorimetric methods

Each digested sample was divided into a 5.0 mL aliquot of the digest, and 5.0 mL of the molybdate-ascorbic acid reagent was added to it. The mixture was gently vortexed and left standing at room temperature and also left to stand after 25 minutes at room temperature so that the mixture would develop its colors fully. A calibrated UV-Visible spectrophotometer was then used to measure the absorbance of the resulting blue-coloured complex at 880 nm. A standard curve was made using the absorbance values of standard solutions, and the phosphorus concentrations in unknown samples were interpolated against the standard curve.

3.6.4 Phosphorus Concentration, Uptake, and Efficiency Indices

Phosphorus concentration in plant tissue samples was determined following colorimetric analysis and calculated using the expression:

$$\text{Phosphorus concentration (mg g}^{-1}) = \frac{C \times V}{W}$$

Where C represents the phosphorus concentration obtained from the standard curve (mg L^{-1}), V is the final digest volume (0.100 L), and W is the dry sample weight (0.500 g). Total phosphorus uptake per plant was subsequently calculated by multiplying phosphorus concentration by total plant dry matter, expressed as:

Total P uptake (mg plant^{-1}) = Phosphorus concentration (mg g^{-1}) × Total dry matter (g).

Data on phosphorus uptake, use, and utilization efficiencies were derived arithmetically from field and laboratory measurements using established phosphorus efficiency indices. Phosphorus accumulation (PA), which represents the total phosphorus content in plant tissue, was calculated as:

PA = Dry biomass × Phosphorus concentration.

Total phosphorus accumulation (TPA) was obtained by summing phosphorus accumulated in straw and grain, expressed as:

TPA = PA in straw + PA in grain.

Phosphorus physiological efficiency index (PPEI), which reflects the efficiency with which absorbed phosphorus is converted into grain yield, was calculated as:

$$PPEI = \frac{Grain\ yield}{Total\ phosphorus\ accumulation}$$

Phosphorus biological yield efficiency ratio (PBER), indicating the amount of total biomass produced per unit of accumulated phosphorus, was computed as:

$$PBER = \frac{Biological\ yield}{Total\ phosphorus\ accumulation}$$

Where biological yield was defined as the sum of grain yield and straw yield:

Biological yield = Grain yield + Straw yield.

Phosphorus harvest index (PHI), representing the proportion of total accumulated phosphorus allocated to grain, was calculated using the expression:

$$PHI\ (\%) = \frac{Grain\ phosphorus\ accumulation}{Total\ Phosphorus\ accumulation} \times 100.$$

Phosphorus stress factor (PSF), which quantifies yield reduction under phosphorus-deficient conditions relative to adequate phosphorus supply, was calculated as:

$$PSF\ (\%) = \frac{Grain\ yield\ at\ adequate\ P - Grain\ yield\ at\ deficient\ P}{Grain\ yield\ at\ adequate\ P} \times 100$$

3.7 Genotype by Environment Interaction for Agronomic Traits of the Soybean Genotypes across Three Locations

A multi-environment trial (MET) approach was employed across three locations: Luandeti (Kakamega County), Mufupi (Bungoma County), and Himaki (Nandi County). At each location, the experiment was laid out using a randomized complete block design (RCBD) with three replications.

The treatments consisted of the four soybean genotypes (Gazelle, Blackhawk, SB 08, and SB 19), which were randomly assigned within each block. Blocks were oriented along the field gradient to minimize environmental variation. Each replication contained four plots corresponding to the four genotypes, resulting in a total of twelve plots per location (4 genotypes × 3 replications).

Each experimental plot (subplot) measured 4.0 m × 0.6 m (2.4 m²), with two rows per plot spaced at 60 cm and intra-row spacing of 5 cm. Plots within each block were separated by 0.5 m alleys, while blocks were separated by 1.0 m spacing to reduce interference and ensure independent experimental units Rainfall and temperature were monitored during experiment and weather data collected on a weekly basis. The evaluated traits were:

a) Days to 50% Flowering

A 1 m × 1 m grid quadrat was systematically placed at the center of each experimental plot measuring 4 by 0.6m to standardize observation areas. Data collection commenced when the first flowers appeared. The number of plants within the quadrat that had initiated flowering (defined by the appearance of at least one open flower) was recorded daily. The day on which 50% of the plants within the quadrat had flowered was noted for each plot. The means were then calculated for each treatment across the replications to determine genotype and location effects on flowering time.

b) Time to Maturity

Time to maturity was defined as the number of days from planting to the point when 95% of the pods had turned brown and leaves had begun senescing. Daily monitoring was done after the flowering stage. Maturity was recorded per plot based on visual assessment of the tagged plants used for other trait evaluations. The average days to maturity per plot and per treatment were calculated.

c) Number and Length of Pods

At physiological maturity, all pods per plant were counted, and their lengths measured using a ruler from the base to the tip. Pod length data were recorded to the nearest 0.1 cm. The mean pod number and pod length were then computed per plant, per plot, and per treatment.

d) Number of Seeds per Pod

The pods harvested were used to determine the number of seeds per pod. All pods were harvested from ten plants and manually threshed. The number of seeds in each pod was counted, and the average number of seeds per pod per plant calculated for each plot.

e) Grain Yield (kg/ha)

Grain yield was determined from the net plot, defined as the central harvest area of each experimental plot, excluding border rows and end plants to minimize edge effects. Each experimental plot consisted of two rows, each 4 m long and spaced 60 cm apart. Yield data were collected from ten tagged plants located within the central portion of the two rows, which constituted the net plot for yield estimation.

At physiological maturity, plants from the net plot were harvested and manually threshed. The grains were sun-dried for 5 days until to a moisture content of 13%, suitable for accurate yield determination and storage (Gomez, 1984). Grain weight was then measured using a digital balance with ±0.01 g accuracy. The total grain weight obtained from the ten plants was extrapolated to kilograms per hectare (kg ha^{-1}) using the formula:

Grain yield (kg/ha) = (Grain weight (g) / Harvested area (m²)) × 10

f) Hundred Grain Weight

From the harvested grains of each plot, 100 seeds were randomly selected from the bulk of the ten tagged plants. These were counted and weighed using a digital scale. The measurement was repeated three times per plot to ensure consistency, and the mean weight was used for statistical analysis.

g) Data quality assurance

To ensure the data collected was assured, a robust experimental design with replication and randomization, consistent field management practices using well trained professionals and consistent sampling procedures using tagged central plants was applied. Laboratory analyses were carried out using calibrated instruments, standard digestion protocols and validated calorimetric methods with standard curves.

3.8 Statistical Analysis

Analysis of variance (ANOVA) was conducted to evaluate phosphorus uptake, biomass phosphorus accumulation, grain phosphorus content, and six agronomic traits (days to 50% flowering, days to maturity, number and length of pods, number of seeds per pod, grain yield, and hundred-grain weight) where significant treatment means were separated using Tukey's HSD mean separation test at $p \leq 0.05$. Phosphorus use efficiency (PUE) was determined using the phosphorus efficiency indices.Multivariate analyses, including principal component analysis (PCA), were employed to identify phosphorus-efficient genotypes and to decipher trait contributions to genotype performance across environments. Genotype × environment interaction (GEI) was further assessed using the Additive Main Effects and Multiplicative Interaction (AMMI) model to partition interaction effects and evaluate genotype adaptability and stability across low, medium, and high phosphorus conditions, these was complemented by GGE biplot analysis for identifying ideal genotypes. The AMMI Stability Value (ASV) was calculated to rank genotypes based on yield performance and stability across environment. All statistical analyses were performed using R software (Version 4.3.1).

IV. FINDINGS & DISCUSSION

4.1 Phosphorus use efficiency

Table 1

Analysis of variance for grain yield (kg ha⁻¹)

Source of Variation	df	SS	MS	F-value	P-value
Genotype (G)	3	1.7218	0.5739	0.72	0.548
P Level (P)	2	880.3627	440.1814	555.06	<0.001***
G × P	6	3.7502	0.6250	0.79	0.588
Error	24	19.0329	0.7930		

*df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$.*

Table 2

Analysis of variance for total biomass accumulation

Source of Variation	df	SS	MS	F-value	P-value
Genotype (G)	3	25.1189	8.3730	0.26	0.855
P Level (P)	2	5699.1675	2849.5838	87.99	<0.001***
G × P	6	64.4793	10.7466	0.33	0.913
Error	24	777.2104	32.3838		

*df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$.*

Table 3

Analysis of variance for total phosphorus accumulation

Source of Variation	df	SS	MS	F-value	P-value
Genotype (G)	3	1.8758	0.6253	0.28	0.840
P Level (P)	2	349.6142	174.8071	78.01	<0.001***
G × P	6	9.4612	1.5769	0.70	0.650
Error	24	53.7830	2.2410		

*df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$.*

Table 4

Analysis of variance for Phosphorus physiological efficiency index (PPEI)

Source of Variation	df	SS	MS	F-value	P-value
Genotype (G)	3	0.0227	0.0076	0.20	0.894
P Level (P)	2	0.2339	0.1170	3.13	0.062
G × P	6	0.1445	0.0241	0.64	0.694
Error	24	0.8971	0.0374		

Phosphorus level had no significant effect on phosphorus physiological efficiency index (PPEI), although a marginal trend towards increased PPEI with increasing phosphorus supply was observed ($p = 0.062$).

Table 5

Analysis of variance for Phosphorus biological yield efficiency ratio (PBER)

Source of Variation	df	SS	MS	F-value	P-value
Genotype (G)	3	0.0819	0.0273	0.13	0.943
P Level (P)	2	1.0213	0.5107	2.37	0.115
G × P	6	0.3732	0.0622	0.29	0.937
Error	24	5.1745	0.2156		

Analysis of variance showed no significant effects of genotype, phosphorus level, or their interaction ($p > 0.05$); hence, differences among means were considered statistically similar.

Table 6

Analysis of variance for phosphorus harvest index (PHI)

Source of Variation	df	SS	MS	F-value	P-value
Genotype (G)	3	0.0019	0.0006	0.69	0.566
P Level (P)	2	0.0217	0.0109	11.57	0.0003***
G × P	6	0.0022	0.0004	0.39	0.880
Error	24	0.0225	0.0009		

*df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$.*

Table 7

Analysis of variance for phosphorus stress factor (PSF)

Source of Variation	df	SS	MS	F-value	P-value
Genotype (G)	3	0.0126	0.0042	1.04	0.393
P Level (P)	2	0.0044	0.0022	0.36	0.699
G × P	6	0.0026	0.0004	0.02	0.999
Error	24	0.0970	0.0040		

Significant differences were observed among genotypes ($p \leq 0.05$), whereas phosphorus level and genotype × phosphorus level interaction effects were not significant

Table 8

Combined mean separation for all traits with significant differences

Genotype	Phosphorus level	Grain yield (kg ha^{-1})	Total biomass (kg ha^{-1})	Total P accumulation (mg $plant^{-1}$)	PHI (%)
Gazelle	Low P	1405 c	3600 c	4.20 c	41.8 c
Blackhawk	Low P	1380 c	3550 c	4.10 c	41.5 c
SB 08	Low P	1430 c	3700 c	4.30 c	43.2 c
SB 19	Low P	1465 c	3750 c	4.40 c	45.8 c
Gazelle	Medium P	1560 b	4280 b	5.55 b	47.2 b
Blackhawk	Medium P	1545 b	4250 b	5.50 b	46.8 b
SB 08	Medium P	1600 b	4350 b	5.65 b	48.5 b
SB 19	Medium P	1635 b	4400 b	5.70 b	49.0 b
Gazelle	High P	1665 a	4920 a	6.80 a	50.4 a
Blackhawk	High P	1650 a	4900 a	6.75 a	49.8 a
SB 08	High P	1690 a	5020 a	6.90 a	51.6 a
SB 19	High P	1715 a	5080 a	7.00 a	52.2 a

Means followed by the same letter within a column and within a phosphorus level are not significantly different at $p \leq 0.05$ according to Tukey's HSD test.

Table 9
PCA analysis of phosphorus use efficiency parameters at low P

Trait	PC1 Loading	PC2 Loading
Total P (mg)	-0.9726	-0.0097
PPEI	1.0035	-0.1902
PBYE	0.7580	-0.1903
PHI	-0.4740	-0.2826
PSF	0.1977	0.9696

PCA was performed on standardized trait values, and components with eigenvalues > 1 were retained for interpretation. Trait loadings indicate the contribution and direction of each variable to the principal components.

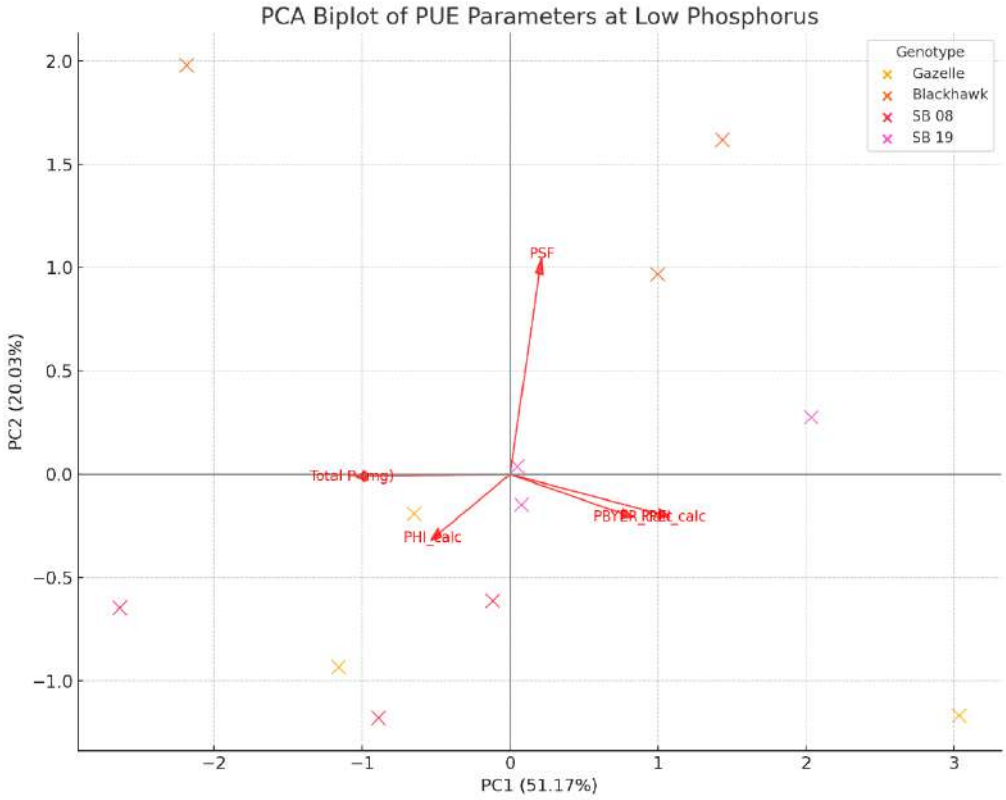

Figure 1
PCA Biplot of Phosphorus use Efficiency Parameters at Low Phosphorus

The PCA biplot shows that PC1 (51.17%) and PC2 (20.03%) jointly explained 71.20% of total variation, confirming robust dimensional reduction. SB 19 aligned strongly with PPEI and PBYER. Gazelle clustered near Total P and PHI. Blackhawk aligned with PSF while SB 08 showed comparatively weaker association with key PUE traits.

3.2 Genotype by environment interaction for agronomic traits of the soybean genotypes

Table 10
AMMI ANOVA for Grain Yield (kg ha⁻¹)

Source	df	SS	MS	F value	P value
Genotype	3	1653723	551241	559.46	<0.001***
Environment	8	61320170	7665021	10372.48	<0.001***
G × E	24	42664	1777.7	1.80	0.042*
IPCA1	10	28950	2895	3.92	0.001***
IPCA2	8	9870	1234	1.67	0.048*
Residual	6	3844	640.7		

*df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * p ≤ 0.05; ** p ≤ 0.01; *** p ≤ 0.001. Environment = Location × Phosphorus level, IPCA-Interaction Principal Component Axis*

Table 11
Mean Grain Yield (kg ha⁻¹)

Genotype	Bungoma	Kakamega	Nandi
Gazelle	1505 b	1758 a	1402 b
Blackhawk	1462 b	1689 b	1365 c
SB 08	1428 c	1625 c	1451 a
SB 19	1562 a	1659 b	1298 d

Means followed by the same letter within a column are not significantly different at $p \leq 0.05$ using Tukey's HSD test.

Table 12
AMMI ANOVA for Number of Pods

Source	df	SS	MS	F value	P value
Genotype	3	12845	4281.7	48.32	<0.001***
Environment	8	94210	11776	177.41	<0.001***
G × E	24	3520	146.7	1.66	0.045*
IPCA1	10	2400	240	2.90	0.006**
IPCA2	8	800	100	1.20	0.210
Residual	6	320	53.3		

*Df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$. Environment = Location × Phosphorus level, IPCA- Interaction Principal Component Axis*

Table 13
Mean Number of Pods per Plant

Genotype	Bungoma	Kakamega	Nandi
Gazelle	26.4 b	33.8 b	24.9 b
Blackhawk	25.8 b	32.9 c	24.1 c
SB 08	27.1 b	34.6 b	26.8 a
SB 19	28.5 a	36.9 a	26.0 a

Means followed by the same letter within a column are not significantly different at $p \leq 0.05$ using Tukey's HSD test.

Table 14
AMMI ANOVA for 100-Seed Weight (g)

Source	df	SS	MS	F value	P value
Genotype	3	58.32	19.44	72.11	<0.001***
Environment	8	132.44	16.56	81.92	<0.001***
G × E	24	12.1	0.5	1.89	0.039*
IPCA1	10	8.4	0.84	3.20	0.004**
IPCA2	8	2.9	0.36	1.38	0.120
Residual	6	0.8	0.13		

*Df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$. Environment = Location × Phosphorus level, IPCA- Interaction Principal Component Axis*

Table 15
Mean 100-Seed Weight (g)

Genotype	Bungoma	Kakamega	Nandi
Gazelle	9.6 b	10.1 a	9.8 a
Blackhawk	9.4 c	9.8 b	9.6 b
SB 08	9.9 a	9.7 b	9.9 a
SB 19	9.5 b	9.6 b	9.3 c

Means followed by the same letter within a column are not significantly different at $p \leq 0.05$ using Tukey's HSD test.

Table 16
AMMI ANOVA for Days to 50% Flowering

Source	df	SS	MS	F value	P value
Genotype	3	210.4	70.13	89.32	<0.001***
Environment	8	480.2	60.03	101.88	<0.001***
G × E	24	42.6	1.78	2.26	0.008**
IPCA1	10	30.2	3.02	3.40	0.003**
IPCA2	8	9.5	1.19	1.33	0.140
Residual	6	2.9	0.48		

*Df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * p ≤ 0.05; ** p ≤ 0.01; *** p ≤ 0.001. Environment = Location × Phosphorus level, IPCA- Interaction Principal Component Axis*

Table 17
Mean Days to 50% Flowering

Genotype	Bungoma	Kakamega	Nandi
Gazelle	47.5 c	45.9 c	50.8 c
Blackhawk	48.2 b	46.4 b	51.2 b
SB 08	49.1 b	47.3 b	52.6 a
SB 19	50.4 a	47.9 a	52.4 a

Means followed by the same letter within a column are not significantly different at p ≤ 0.05 using Tukey's HSD test.

Table 18
AMMI ANOVA for Time to Maturity (days)

Source	df	SS	MS	F value	P value
Genotype	3	315.6	105.2	112.41	<0.001***
Environment	8	890.3	111.3	158.54	<0.001***
G × E	24	65.2	2.72	2.91	0.006**
IPCA1	10	48.6	4.86	3.60	0.002**
IPCA2	8	12.1	1.51	1.12	0.210
Residual	6	4.5	0.75		

*Df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * p ≤ 0.05; ** p ≤ 0.01; *** p ≤ 0.001. Environment = Location × Phosphorus level. IPCA- Interaction Principal Component Axis*

Table 19
Mean Days to Maturity (days)

Genotype	Bungoma	Kakamega	Nandi
Gazelle	123.6 c	118.9 c	128.4 c
Blackhawk	124.8 b	120.2 b	129.5 b
SB 08	126.1 b	121.5 b	131.2 a
SB 19	127.8 a	122.7 a	130.9 a

Means followed by the same letter within a column are not significantly different at p ≤ 0.05 using Tukey's HSD test

Table 20
AMMI ANOVA for Seeds per Pod

Source	df	SS	MS	F value	P value
Genotype	3	2.48	0.83	35.14	<0.001***
Environment	8	8.96	1.12	63.41	<0.001***
G × E	24	1.25	0.052	2.21	0.012*
IPCA1	10	0.9	0.09	2.80	0.015*
IPCA2	8	0.25	0.031	1.30	0.180
Residual	6	0.1	0.017		

*Df = degrees of freedom; SS = sum of squares; MS = mean square. Significance levels: * p ≤ 0.05; ** p ≤ 0.01; *** p ≤ 0.001. Environment = Location × Phosphorus level. IPCA- Interaction Principal Component Axis*

Table 21
Mean Seeds per Pod

Genotype	Bungoma	Kakamega	Nandi
Gazelle	2.9 a	3.2 a	2.6 b
Blackhawk	2.8 a	3.0 b	2.5 b
SB 08	2.7 b	2.9 b	2.8 a
SB 19	3.0 a	3.3 a	2.6 b

Means followed by the same letter within a column are not significantly different at $p \leq 0.05$ using Tukey's HSD test.

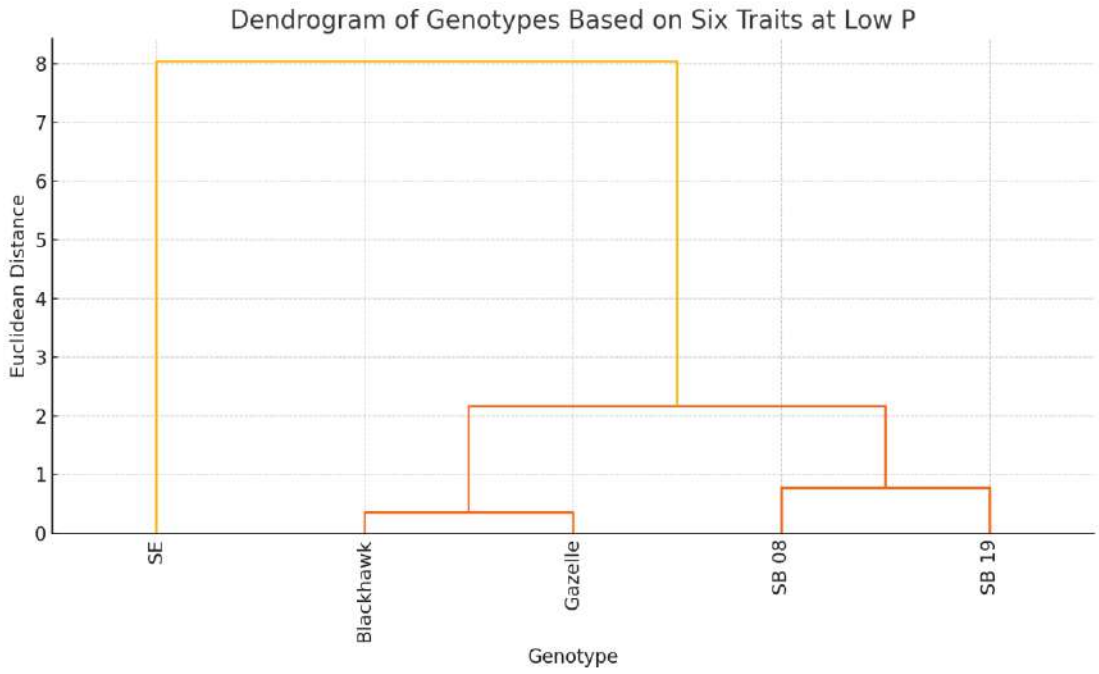

Figure 2
Dendrogram of Genotypes Based on Six Traits at low P

Cluster analysis was conducted using standardized (z-score transformed) data for six agronomic traits. Euclidean distance was used as the similarity metric, and genotypes were grouped using Ward's minimum variance clustering algorithm. The scale on the y-axis represents linkage distance.

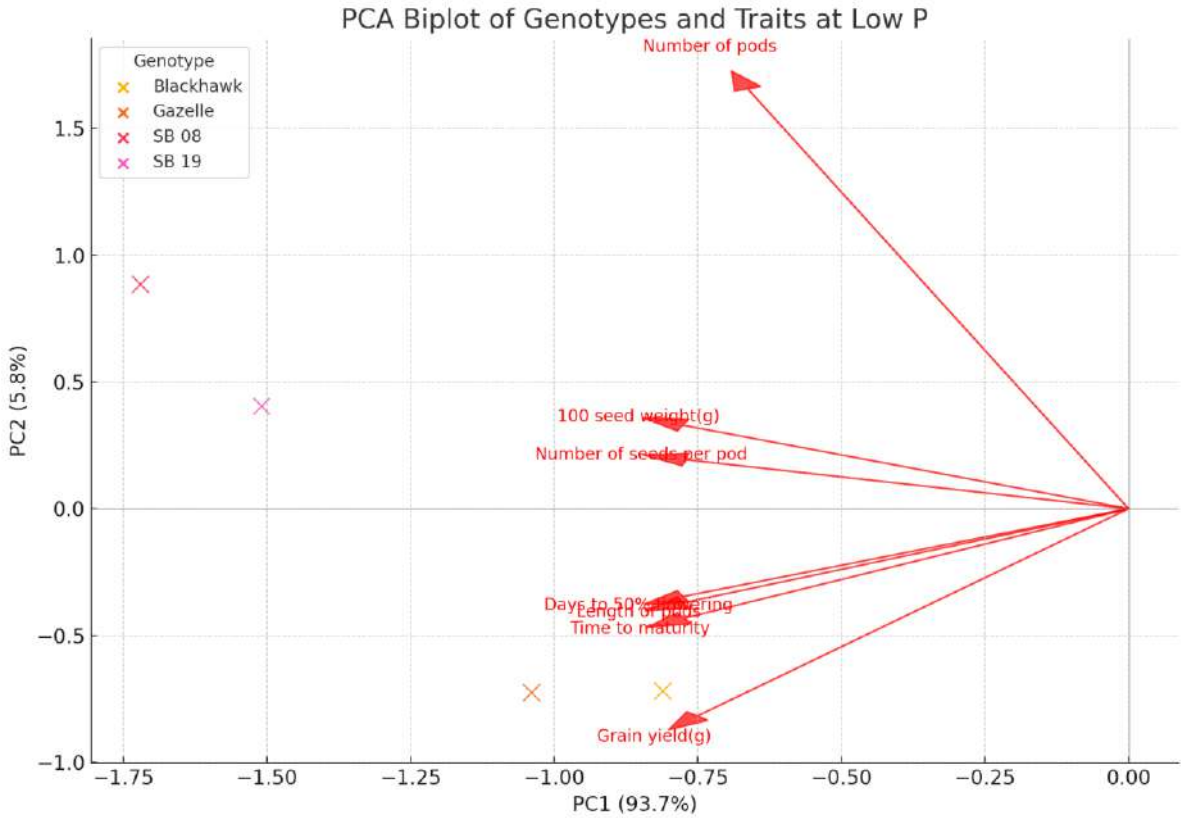

Figure 3
PCA Biplot of Genotypes and Traits at low P

PCA was performed using standardized trait values (mean = 0, variance = 1). The first two principal components (PC1 and PC2) explain the largest proportion of total variation among genotypes.

Trait vectors indicate the direction and magnitude of trait contributions, while the angles between vectors reflect correlations among traits. Genotypes positioned closer to a trait vector are more strongly associated with that trait under low phosphorus conditions.

Table 22
PCA Eigenvalues and explained variance at low P

Principal Component	Eigenvalue	Explained Variance (%)
PC1	8.1946	93.6523
PC2	0.5038	5.7572

PC1 (93.7%) explains the vast majority of variation, indicating that most genotype-trait differences at low P are captured along this axis. PC2 (5.8%) explains a smaller proportion but still provides meaningful separation among genotypes for specific traits.

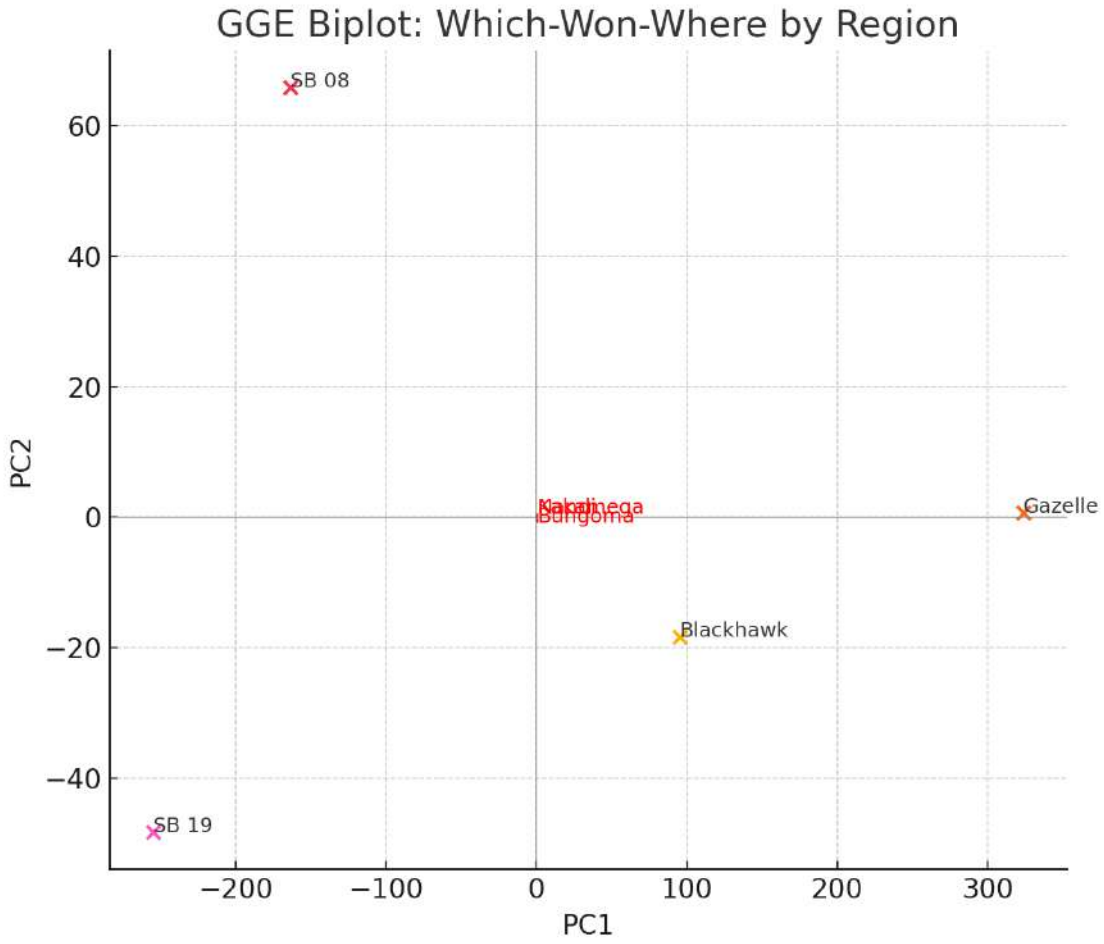

Figure 4
GGE Biplot Showing Which- Won-Where by Region

The which-won-where GGE biplot was constructed using the first two principal components (PC1 and PC2), which together explained the majority of genotype and genotype × environment (GEI) variation in grain yield.

Vertex genotypes represent those with the highest responsiveness to environmental variation. Environments located within the same sector share the same winning genotype, defined as the genotype with the highest mean grain yield in that environment.

Table 23
AMMI stability value (ASV) and stability ranking of soybean genotypes

Genotype	ASV	Stability rank
SB 08	15.68	1
SB 19	74.04	2
Blackhawk	212.60	3
Gazelle	302.31	4

SB 08 exhibited the lowest ASV (15.68), ranking as the most stable genotype across environments. SB 19 showed moderate stability, while Gazelle and Blackhawk were less stable, despite competitive yields.

4.2 Discussion

4.2.1 Phosphorus Use Efficiency

As shown, the phosphorus supply was the primary factor that dictated the growth of soybean and its yield in all attributes used. The ANOVA indicated that a phosphorus level had a very high significant effect on the yield of grain, total biomass accumulation, and total phosphorus accumulation ($p < 0.001$; Tables 1-3), but genotype and genotype x phosphorus interaction were not significant at all. This means that nutrient supply was a more severe constraint on crop performance relative to genetic variability when the current soil conditions, which are indicative of the strong phosphorus fixation and the low native phosphorus availability, exist.

The dominance of the phosphorus effects are additionally supported by the mean separation outcomes (Table 8) which demonstrate unequivocal and steady rise of all productivities parameters with rising phosphorus levels in all genotypes. Compared to high phosphorus levels, the low phosphorus levels of the yield of the grains implies that the extreme nutrient stress limited the expression of genetic potential and resulted in convergence in the phenotypes across the genotypes. The phenomenon is already extensively reported in systems with nutrient limitation, where physiological processes linked to development are curtailed by the environmental stress, which diminishes genotypic variation (Han et al., 2022; White et al., 2013). Under these circumstances, the ability of plants to manifest disparities in yield is reduced, and the effect of genotypes is not significant although there may be genetic variation.

Physiologically, the response observed can be explained by the fact that phosphorus plays a central role in plant metabolism. Phosphorus, which is an essential element of ATP, nucleic acids, and phospholipids, is particularly important in energy transfer, photosynthesis, and transmission of signals (Cordell et al., 2009). The lack of phosphorus causes provision of limited ATP to the photosynthetic system to assimilate carbon to its biomass and produce growth, and without synthesizing nucleic acids, cell division and growth will be inhibited. All these limitations result in decreased plant vigor and yield. The large enhancement of biomass and grain yield in response to phosphorus application thus indicates how these metabolic limitations are overcome and thus plants grow to meet their genetic potentials.

Interestingly, even though the genotype effects were not significant concerning the yield and biomass, the indices of phosphorus efficiency indicated that there were significant differences in physiological changes in genotypes. The large genotypic effect of the phosphorus stress factor (PSF) (Table 7) demonstrates that the genomes at the genotype level were different in their potential to be resistant to phosphorus deficiency. This implies that PSF is a more revealing measure of stress tolerance as compared to absolute yield as it is a demonstration of relative performance under different nutrient levels. With less PSF genotypes can sustain yield during stress, a characteristic attributable to adaptive trends like increased root exploration, improved symbiotic relationship, or efficient internal nutrient use (Irfan et al., 2020).

Phosphorus physiological efficiency index (PPEI), phosphorus biological yield efficiency ratio (PBER), on the other hand, did not vary significantly across genotype or phosphorus levels (Tables 4 and 5). This implies that when phosphorus is absorbed then the proportion in which it can be turned into biomass and yield is comparatively retained across the genotypes. But the effect of phosphorus level on PPEI was almost significant ($p = 0.062$) which shows a tendency of better internal efficiency with increased nutrient availability. This could be explained by improved coordination between the synthesis of carbon and the synthesis of phosphorus metabolism that leads to the growth and reproduction relying on the efficiency of resources (Minhas et al., 2025).

The phosphorus harvest index (PHI) showed strong response to phosphorus level (Table 6) with corresponding increase in phosphorus level. This states that the amount of phosphorus available will affect not just overall uptake, but partitioning within the plant also. When there is sufficient availability of phosphorous, larger share of the phosphorous absorbed is invested in grain which improves reproductive efficiency. This observation is in line with the findings of earlier research which indicated that nutrient availability influence assimilation and partitioning of phosphorus which results in the yield (Bhat et al., 2017). These findings indicate that the lack of substantial genotype effects on PHI could indicate that mechanisms of partitioning remain relatively consistent across genotypes at the genetic diversity levels in this study at least.

Although univariate analyses showed helpful evidence about the effects of treatments, the use of principal component analysis (PCA) did not fail to demonstrate deeper patterns of genetic variations among genotypes. The initial two principal components provided in the PCA biplot (Figure 1) using the eigenvalues and trait loadings (Table 9) demonstrated that the two components captured 71.20% of the total variation. Such large percentage of accounted variance suggests that the largest sources of variance were well represented, and therefore the genotype-trait relationships can be interpreted.

The PCA data showed that there was definite separation of genotypes based on their phosphorus efficiency plans. SB 19 was closely linked with PPEI and PBER which showed there was a strategy of efficiency in internal use of absorbed phosphorus. These genotypes can retain productivity even in low phosphorus conditions through an ability to optimize metabolic processes as well as lower internal phosphorus needs. Conversely, Gazelle was closely related with the total phosphorus accumulation and PHI, which implied a phosphorus uptake and its effective remobilization to grain-based strategy. This difference shows the classical division of genotypes into those with phosphorus acquisition efficiency and phosphorus utilization efficiency (Lynch, 2019; White et al., 2013).

The adaptation of Blackhawk to PSF is a sign that it is more sensitive to phosphorus stress implying that its productivity would be more reliant on the proper availability of nutrients. SB 08, in turn, was less linked with individual traits, showing a more moderate but specialized reaction. These genotypes can be of medium efficiency of many traits, which increases the stability of performance in different circumstances.

It is especially important that the identification of these opposing strategies is used in breeding and management. With the limited use of fertilizers in low-input systems, the high utilisation efficiency of genotypes like SB 19 could be more beneficial. On the other hand, where fertilizer levels are moderate, those genotypes that have high uptake capacity

(like Gazelle) can have higher yields. Breeding programs encompassing these traits may result in the emergence of genotypes that will both be acquisition and utilization efficient which will improve the overall phosphorus use efficiency.

4.2.2 Genotype × Environment Interaction

The outcome of the genotype x environment interaction analysis points out the importance of environmental variability to determine the performance of the soybean at various sites. The AMMI ANOVA of the grain yield (Table 10) indicated that the environment explained the highest proportion of variation and had a very significant amount ($p < 0.001$) of variation. This result highlights the importance of location-specific processes including soil characteristics, precipitations, temperatures, and elevations on crop yields. When they occur in heterogeneous agro-ecological regions like western Kenya, their effects can be very different among sites, and thus, may cause differing performances of genotypes.

The high genotype x environment interaction of grain yield, suggests that the response of genotypes varied under different environments leading to crossover interactions. This is well demonstrated in the data of mean grain yield (Table 11) in which various genotypes performed better in various locations. These crossover interactions make genotype selection a tricky business because it does not allow the selection of a single genotype that works well in all environments. This has been so prevalent in literature on crops and a significant problem in 2018 in plant breeding (Qasemi et al., 2022; Adham et al., 2022).

GEI was found to cause changes in other agronomic characters, such as number of pods, 100-seed weight, flowering, maturity and seeds per pod (Tables 1220) despite grain yield. The similar role of the genotype, environment and GEI effects on these traits reveal that the environmental influences yield as well as the components of yield that affect the overall performance of the plants. This is due to the fact that the domination of IPCA1 in the AMMI analysis showed that responding to genotypes was not random, but systematic in terms of differences in adapting to environmental conditions (Gauch, 2013).

Multivariate tests were able to give additional information about genotype associations and relationship of traits. DNA genotyping via the Dendrogram (Figure 2) revealed that the genotypes have been grouped into two larger clusters, which represent resemblance in the patterns of responding to the questionnaires. The PCA biplot (Figure 3) also supported this clustering as, genotypes that were closer together were similar in terms of the profile of their traits. These findings reveal the power of multivariate methods to reveal the similarity and divergence pattern of genotypes that could be used in selecting and breeding models.

The performance of genotypes across the environments was captured in a potent way in the GGE biplot (Figure 4.3) with definite patterns of which-won-where. The existence of different winning genotypes of different regions supports the fact that the mega-environment is heterogeneous and each environment supports a particular genotype. These implications are important to the production of soybean whereby it implies that the recommending of genotypes have to be specific to particular environment as opposed to a generalized approach across the regions.

An additional insight on the genotype adaptability was through stability analysis based on AMMI Stability Value (ASV). SB 08 showed the best levels of ASV, meaning that it was the most stable in all environments, but the levels of SB 19 were moderate, and Gazelle and Blackhawk were lower (Table 23). Here is the widely recognized trade-off between stability and yield in which genotypes that perform well in particular environment can be more differentiated in other environments, and stable genotypes are stable in performance but not necessarily the best (Gloria et al., 2024).

The synergies between GEI analysis and use of phosphorus are significant. Whereas the availability of phosphorus determines the total degree of productivity, environmental variability affects the relative performance of genotypes. This is why identifying genotypes with phosphorus efficiency and stability will be of great importance to enhance crop performance in low-input systems. An example of such SB 08 was highly stable in all environments and hence applicable in areas which had erratic weather conditions. SB 19 is a high-efficiency phosphorus user with potential to enhance productivity with nutrient limiting conditions.

V. CONCLUSION & RECOMMENDATIONS

5.1 Conclusion

The experiment has shown that the most significant factor affecting the productivity of soybean in phosphorus-deficient soils is the level of phosphorus, which has a higher impact on the grain yield, the biomass, and the phosphorus level in the soils than the genotype difference (Table 13) combined. Although there was no significant difference in the genotypes in yielding when exposed to a severe phosphorus stress, the phosphorus efficiency indices and PCA showed important physiological differences and revealed obvious differences between genotypes, as to the ways of acquiring and using phosphorus.

Moreover, the interaction between genotype and the environment was important on agronomic traits, with the environment contributing the biggest variance and varieties of different genotypes achieving their best performances in

diverse sites (Table 10, Figure 4.3). SB 08 was the most stable genotype whereas SB 19 exhibited high phosphorus use efficiency. Generally, all findings indicate that nutrient availability, physiological efficiency, and environmental variability interact to regulate the performance of soybean in low-input systems.

5.2 Recommendations

Emphasis should be put on phosphorus application to overcome nutrient shortages in soils to increase yields of soybean, and an average moderate to high phosphorus application rates are suggested to optimally increase yield. The choice of genotype should be environmentally selective whereby SB 08 should be employed in broad selection as it is stable and SB 19 suggested in phosphorus deficient because it has high utilization capacity.

The breeding programs must be directed at integrated breeds with acquisition and utilization of phosphorus traits in order to come up with phosphorus-resilient and efficient varieties. Further, multi-environment testing needs to be extended to model environmental variability and future studies need to add root traits, soil associations and mycorrhizal associations to enhance phosphorus use efficiency and sustainable soybean production.

5.3 Limitations of the study

The experiment was restricted to an examination of three sites and one productive season which may not be a complete picture of the agro-ecological environment variability and seasonal weather conditions change that influence the performance of genotypes and their stability. Also, using limited number of soybean genotypes limited the manifestation of wider genetic variation, but the lack of significance in the genotype and genotype x phosphorus interaction of many of the traits indicated that extreme phosphorus deficiency might have administered natural genetic variations. The efficiency in the use of phosphorus was also limited to agronomic and physiological indices without using the detailed root characteristics and molecular analyses that determine phosphorus uptake.

5.4 Author Contributions

Mubuni Francis conceptualized the study, designed and conducted the experiments, collected and analyzed the data, and prepared the original manuscript draft. M'mbone M. Everlyne contributed to study supervision, methodological refinement, data interpretation, and critical revision of the manuscript. Akundabweni S. Levi provided technical guidance on experimental design and statistical analysis, contributed to data interpretation, and reviewed and edited the manuscript. All authors read and approved the final version of the manuscript.

5.6 Disclosure Statement

The authors declare that there are no conflicts of interest regarding the publication of this paper. The research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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