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# Genetic variability, heritability, and genetic gain for yield and associated traits in recently introduced soybean genotypes in the Guinea Savannah zone of Ghana

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Abstract: Estimating genetic parameter optimizes the selection of complex traits. This study evaluated 150 soybean germplasm accessions from Ghana, Nigeria, USA and Columbia to assess the performance of recently introduced soybean genotypes for yield and associated traits. A 15x10 alpha lattice design with three replications was employed, each consisting of 10 incomplete blocks containing 15 genotypes. The results revealed significant genotypic differences among genotypes for all evaluated traits. Maturity days varied, with USA genotypes maturing earliest (82-115.33 days), followed by Columbia (97.33-136.00), IITA genotypes (106.67-142.0 days) and Ghana (114.00-135.33 days). Genotype PI 628866 (USA) exhibited the highest 100-seed weight (24.72g). Ghanaian genotypes, including Favour, SAR-Qua/Afa-18-6, SAR-SL2/USL-18-2, SAR-SL2/SPg-18-3, and Afayak, recorded the highest grain yields (2.89-2.54 t/ha). The genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged from 21 to 30% with high heritability estimates (>80%) observed for most traits, indicating strong potential for genetic improvement through selection. Correlation analysis showed strong associations: DFF-DM (r=0.79), GY-PHF (r=0.67), GY-PHM (r=0.55); a weak correlation was observed between GY-HSW (r=0.19). Moderate correlations were found for GY-PPP (r=0.37) and GY-terminal leaf length. PHF was identified as an effective selection criterion for GY, while a negative association between HSW and PHF suggests trade-offs. Multi-trait selection indices are necessary due to moderate correlations between GY and PPP. Path coefficient analysis identified days to flowering (0.550) and height at flowering (0.313) as traits with direct effects on grain yield, making them suitable for indirect selection. Overall, each germplasm source exhibited unique strengths and weaknesses. Ghanaian genotypes excelled in grain yield, while USA genotypes demonstrated early flowering and maturity. These findings can guide breeders in developing high-performing soybean varieties by leveraging desirable traits from each source.

Keywords: Path coefficient analysis, genetic advance, germplasm, correlation analysis, Glycine Max.

# Introduction

Soybean, a vital cash crop for smallholder farmers in Northern Ghana, has been cultivated in the country since its introduction in 1901, gaining prominence in the mid-1990s (Plahar, 2006). Although adoption was initially slow due to limited household knowledge and lack of industrial-scale processing (Plahar, 2006; Addae-Frimpomaah et al., 2022), soybean production has steadily increased, rising from 74,800 Mt in 2008 to 176,670 Mt in 2018 (MoFA, 2019). This growth is largely driven by its potential to generate income and improve nutrition for smallholder farmers and their families (Addae-Frimpomaah et al., 2022). However, poor grain yield remains a major constraint to soybean cultivation in Ghana due to late-maturing of commercial varieties, shortened rainfall patterns, poor pod filling, and terminal drought during pod development stages (Addae-Frimpomaah et al., 2022; Denwar et al., 2019).

Understanding the genetic basis of quantitative traits, including yield and yield components, is crucial for enhancing soybean productivity (Gosa et al., 2019). Heritability and genetic diversity among traits are critical for the success of breeding

programs (Dudhe et al., 2020). Traits with high heritability facilitate genetic improvement through selection, even for traits with low heritability (Hall and Richard, 2013). Strategic efforts to broaden the genetic base of commercial breeding programs, while ensuring timely release of new varieties, are necessary for achieving both long-term genetic gains and short-term breeding targets (Allier et al., 2020; Awad-Allah et al., 2022).

To achieve these goals, populations with high genetic variability, created through germplasm introduction, hybridization, or wild parent utilization, are essential (Cooper et al., 2001; Nachimuthu et al., 2015).

Evaluating genetic parameters, such as genotypic and phenotypic coefficient of variation, heritability and genetic advance, allows for informed decision-making in breeding programs (Aditya et al., 2011). Additionally, correlation analysis helps determine associations between traits. This study aims to assess genotypic variability, broad-sense heritability, and the genetic advance potential for yield and associated traits among newly introduced soybean genotypes, providing valuable insights for the soybean breeding program.

# Results

# Analysis of variance

The analysis of variance (ANOVA) revealed highly significant (P<0.001) genetic variation among the 150 soybean genotypes for most yield and yield-related traits (Table 1). The genotype source of variation was significant (p < 0.001) for all traits, highlighting substantial genetic differences among genotypes. This was evident in traits such as days to 50% flowering (mean square = 40.88), days to maturity (186.447 days), leaflet number (0.108347), number of node on main stem (16.1875), plant height at 50% flowering (54.668 cm), and plant height at maturity (211.862 mm).

Significant genetic variation was also observed for traits related to pod and seed production, including terminal leaf length (8.1369 cm), pod clearance (4.9642 cm), number of pod/peduncle (1.7466), number of pods per plant (718.11), pod length (0.64252 cm), number of seeds per pod (0.21937), 100-seed weight (11.4098 g) and grain yield (0.23993 t/ha). Mean squares for genotype variation ranged from 0.108347 (leaflet number) to 718.11 (number of pods per plant). Replication was not a significant source of variation for most traits. Error variance accounted for random variation, with relatively low values for all traits, ranging from 0.006088 (leaflet number) to 0.3756 (number of seeds per pod).

# Yield and yield-related traits performance of genotypes based on source

The performance of soybean genotypes varied significantly by source (Table 2). Genotypes from the USA exhibited the highest 100-seed weight (9.37-20.20g, mean=14.19g), followed by those from Columbia (8.10-19.47g, mean=13.86g). Ghanaian and IITA genotypes showed similar 100-seed weights (13.54g and 13.33g, respectively). Flowering days ranged from 26.33 to 55.33 days, with USA genotypes flowering earliest (mean = 37.64 days) and Ghanaian genotypes latest (44.0-55.33 days). Maturity days also differed, with USA genotypes maturing earliest (82-115.33 days, mean=101.08 days) and IITA genotypes latest (106.67-142.0 days, mean=119.23 days).

Ghanaian genotypes exhibited the highest average grain yield (1.58-2.58 t/ha, mean=2.34 t/ha), outperforming IITA (1.92 t/ha), USA (mean = 0.82 t/ha), and Columbia genotypes (mean = 0.81 t/ha). Ghanaian genotypes also had the highest average pods per peduncle (4.16), surpassing IITA (3.83), Columbia (3.76) and USA (3.56). Columbia genotypes displayed the highest average number of nodes on the main stem (11.99). Ghanaian genotypes were the tallest at flowering (32.20 cm) and maturity (45.65 cm), followed by IITA and USA genotypes.

Pod length ranged from 3.71 to 3.87 cm, with Ghanaian genotypes showing the highest average number of pods per plant (78.10) and pod clearance (6.15 cm). Moderate to high variability was observed among genotypes, with coefficient of variation (CV) ranging from 2.0% (grain yield in IITA genotypes) to 22% (pods per plant in USA genotypes). Least significant difference (LSD) values, indicating significant differences among genotypes, ranged from 0.062 (grain yield in IITA genotypes) to 12.155 (number of pods per plant in USA genotypes), and varied across traits.

# Evaluation of 150 genotypes for key agronomic traits

The top 15 soybean genotypes demonstrated superior performance in desirable traits, such as early flowering, maturity, high 100-seed weight, and increased grain yield. Genotype PI 628852 flowered earliest at 23.85 days, while PI 597468 matured earliest at 83 days (Table 3). PI 628866 recorded the highest 100-seed weight (24.72g), and the genotype Favour achieved the highest grain yield (2.89 t/ha). In contrast, the bottom 15 genotypes showed delayed flowering (48.92-56.02 days), delayed maturity (121.60-139.10 days), lower 100-seed weight (11.25-15.94g), and significantly lower grain yield (0.35-0.46 t/ha). Comparative analysis revealed significant differences between the top and bottom-performing genotypes. Specifically, the top genotypes flowered 20-30 days earlier and matured 30-40 days earlier than the bottom genotypes. Additionally, they exhibited 100-seed weights that were 2-5g heavier and grain yields 1.5-2.5 t/ha higher than the bottom genotypes. Statistical analysis confirmed the significance of these differences, with F-probability values less than 0.001 for all traits. The coefficient of variation (CV) ranged from 2.0 % (days to maturity) to 13.0 % (grain yield), indicating moderate to high variability among genotypes. Least significant difference (LSD) values were 1.942 (days to 50% flowering), 1.768 (days to maturity), 1.051 (100-seed weight) and 0.172 (grain yield), serving as thresholds for distinguishing significant differences among genotypes.

# Estimation of variance components

The estimates of phenotypic  $(\sigma_p^2)$ , genotypic  $(\sigma_g^2)$  and environmental  $(\sigma_e^2)$  variances, along with phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), are presented in Table 4. Genetic variance ranged from 0.03 for leaflet number to 226.91 for number of pods per plant, while phenotypic variance ranged from 0.04 for leaflet number

#### **Table 1.** Analysis of variance for yield and yield related traits of 150 soybean genotypes.

Source	DF	Days to 50% flowering	Days to maturity	Leaflet number.	Node on main stem	Plant height at 50% flowering	Plant height at maturity	Terminal leaf length	Pod clearance	No. of pod/ peduncle	No. of pods per plant	Pod length	No. of seeds per pod	100 seed weight	Grain yield
Rep Rep (Block)	2 42	39.076 225.918	16.642 712.145	0.008889 0.07873	0.2475 20.4421	11.966 208.384	14.423 466.011	4.9011 10.7349	0.049 2.7624	0.1644 1.1484	0.84 1558.67	0.05216 0.46794	0.04136 0.07994	0.2148 6.5301	0.00594 3.89279
Genotype	149	40.88***	186.447 ***	0.108347***	16.1875***	54.668***	211.862***	8.1369***	4.9642***	1.7466***	718.11***	0.64252***	0.21937***	11.4098***	0.23993***
Error	257	1.573	5.625	0.006088	0.577	1.605	3.505	0.4845	0.2559	0.1078	37.39	0.05024	0.01811	0.3756	0.01411

#### **Table 2.** Average performance of groups of genotypes from the different sources.

	Ghana (n=10)	IITA (n=37)		USA (n=55)		Columbia (n=48)										
												-	<b>27 1</b> 0 <i>1</i>			
Traits	Mean (±SD)	Range	CV%	LSd	Mean± (SD)	Range	CV%	LSd	Mean ± (SD)	Range	CV%	LSd	Mean±(SD)	Range	CV%	LSd
100 seed	13.54±1.133	12.13-	3.6	0.840	13.33±1.583	0.40-	3.2	0.688	14.19±2.660	9.37-	4.8	0.962	13.86±1.936	8.1-	4.7	1.051
weight (g)		15.60				17.47				20.20				19.47		
Days to 50%	48.10±3.428	44.00-	1.7	1.373	47.76±2.958	42.67-	2.9	2.293	37.64±5.382	26.33-	3.3	1.719	41.78±3.772	34.00-	2.9	1.942
flowering		55.33				53.33				48.67				49.00		
Days to	121.20±6.299	114.00-	1.8	3.797	119.23±8.871	106.67-	1.6	3.163	101.08±9.538	82.00-	2.7	3.814	110.13±7.455	97.33-	2.0	3.51
maturity		135.33				142.00				115.33				136.00		
Grain yield	2.34±0.349	1.58-	2.0	0.079	1.92±0.259	1.54-	2.0	0.062	$0.82 \pm 0.414$	0.44-	20.5	0.235	0.81±0.388	0.45-	13.0	0.172
(t/ha)		2.58				2.50				2.39				2.17		
No of	4.16±1.122	2.37-	8.1	0.577	3.83±1.048	2.33-	6.9	0.430	3.56±0.683	2.93-	10.9	0.543	3.76±0.791	2.17-	8.0	0.49
pod/peduncle		5.50				6.93				5.53				5.50		
Nodes on the	10.06±2.439	5.83-	9.6	1.651	9.38±2.626	5.87-	6.0	0.910	9.17±1.978	6.29-	8.2	1.059	11.99±2.797	8.00-	7	1.36
main stem		13.33				18.27				12.00				18.67		
Plant height	32.30±4.683	26.60-	4.7	2.596	29.04±3.989	22.00-	4.4	2.057	21.58±5.266	12.81-	6.4	1.935	21.85±5.185	14.80-	4.9	1.737
at flowering		39.30				42.40				32.30				33.37		
(cm)																
Plant height	45.65±6.777	38.13-	3.4	2.633	43.35±8.943	34.10-	3.3	2.294	30.96±8.717	18.87-	7.3	3.178	40.20±10.39	26.20-	2.9	2.563
at maturity		58.23				65.73				47.10				63.63		
(cm)																
Pod length	3.82±0.487	3.30-	7.3	0.475	3.80±0.399	3.23-	5.4	0.337	3.71±0.677	2.60-	7	0.364	3.87±0.429	2.80-	4.7	0.292
(cm)		4.40				4.53				5.10				4.60		
Pods per	78.10±15.18	57.80-	6.7	8.953	55.64±12.48	41.37-	5.3	4.766	39.38±17.49	15.20-	22	12.155	61.28±18.16	25.83-	5.4	5.362
plant		113.43				96.43				71.3				87.43		
Pod clearance	6.15±1.761	3.93-	13.2	1.387	6.12±1.594	3.90-	7.6	0.754	5.45±1.250		9.9	0.758	5.47±1.317		7.3	0.646
(cm)		10.13			8.57					3.00-			3.20-			
										9.63				8.73		

SD= Standard deviation, CV= Coefficient of variation, LSD = Least significant difference.

<u>1able</u>	3. Mean perform Genotype	Days to 50% flowering	Genotype	<u>15 soybear</u> Days to maturity	<u>i genotypes for 10</u> Genotype	100 seed weight	F, GY and DTM. Genotype	Grain yield (t/ha)
1	PI 628852	23.85	PI 597468	83.00	PI 628866	24.72	Favour	2.89
2	PI 597468	25.55	PI 628805	86.40	PI 567053	20.13	SAR-Qua/Afa- 18-6	2.65
3	PI 628838	26.21	PI 567315	89.10	5232	18.87	SAR-SL2/USL- 18-2	2.64
4	PI 628805	28.53	PI 628852	91.20	PI 597468	18.18	SAR-SL2/SPg- 18-3	2.57
5	PI 628835	30.73	PI 628838	92.00	TGX 1990-46F	18.06	Afayak	2.54
6	PI 628812	31.88	PI 578330	92.10	PI 628840	17.41	TGX 1988-3F	2.53
7	PI 628847	33.01	PI 628886	92.30	PI 628848 C	17.35	Jenguma	2.52
8	5522	33.98	PI 594540	92.60	PI 628918	17.21	TGX 1740 - 2F	2.50
9	PI 628813	34.03	PI 628835	92.90	5546	17.15	BRS TIANA	2.44
10	PI 567315	34.42	PI 628885	94.00	TGX 1990- 114FN	17.04	TGX 1903-7F	2.43
11	PI 628803	34.75	PI 548659	95.80	TGX 1990-57F	16.47	TGX 1485-1D-C	2.37
12	5519	34.98	PI 628918	96.00	TGX 2017-6E	16.35	TGX 1990-52F	2.36
13	PI 628848 C	35.06	PI 628919	96.30	5510	16.34	FT CRISTALINE	2.29
14	PI 548654	35.34	PI 628854	96.70	PI 628862	16.05	TGX 1989- 68FN	2.26
15 "	PI 628816	35.37	PI 628875	97.60	PI 567056 A	15.94	Soung Pungun	2.22
0								
136	BRS TIANA	48.92	Favour	121.60	PI 628876	11.25	5544	0.46
137	PI 567099 A	48.94	SAR- Qua/Afa-18- 6	121.90	PI 548659	11.22	PI 548659	0.45
138	TGX 2019-1E	49.01	TGX 2009- 12F	122.00	5239	11.21	PI 628866	0.44
139	TGX 1989-11F	49.11	TGX 1990- 95F	122.20	5505	11.14	PI 594540	0.44
140	TGX 1989-20F	49.19	SAR- SL2/USL-18- 1	122.70	PI 628882	11.13	5528	0.43
141	TGX 1990-95F	49.19	PI 628850	124.50	5554	11.05	5545	0.43
142	TGX 1990-93F	49.43	5538	126.90	5520	11.01	5508	0.43
143	TGX 1990-78F	49.44	TGX 1990- 40F	128.50	TGX 1989-49FN	10.92	PI 628803	0.42
144	TGX 1988-3F	49.61	TGX 1990- 57F	131.30	PI 548469	10.86	5549	0.41
145	TGX 2009-16F	51.06	SAR- Jen/USL-18-3	132.70	5518	10.68	PI 628854	0.41
146	TGX 1990-57F	51.11	TGX 1990- 21F	132.90	TGX 1740 - 2F	10.60	5519	0.39
147	SAR-Jen/USL- 18-3	51.51	TGX 1990- 114FN	134.00	5212	10.57	5511	0.39
148	TGX 2017-6E	52.50	TGX 1990- 55F	134.30	PI 567099 A	9.23	5504	0.38
149	SAR-SL2/USL- 18-1	54.44	5205	137.10	5205	7.39	5518	0.37
150	TGX 1989-48FN	56.02	TGX 2017-6E	139.10	PI 594540	6.37	5205	0.35
	Grand mean	42.19		109.86		13.83		1.19
	F. prob	<.001		<.001		<.001		<.001
	LSD	1.942		1.768		1.051		0.172
	CV	2.9		2.0		4.7		13.0

CV= Coefficient of variation, F. prob = F. probability, LSD = Least significant difference.

Traits	Mean	Genotypic	Phenotypic	$H^2$	GCV	PCV	CVr (%)	Genetic	Genetic advance as %
		variance	variance ( $\sigma^{2}_{p}$ )		(%)	(%)		advance	of the mean
		$(\sigma^2_g)$							
Days_to_50%_flowering	42.16	13.50	15.07	89.57	8.72	9.21	1.56	0.87	2.06
100 seed weight	13.83	1.93	2.30	83.70	10.04	10.98	2.86	0.36	2.62
Days to maturity	109.80	62.14	67.77	91.70	7.18	7.50	1.59	1.80	1.64
Grain yield /ha	1.19	0.08	0.09	84.21	23.04	25.11	1.55	0.07	5.96
Leaflet number	3.05	0.03	0.04	84.85	6.05	6.57	1.55	0.05	1.55
No of pod peduncle	3.73	0.55	0.65	83.52	19.81	21.68	1.54	0.19	5.19
Nodes on the main stem	10.18	5.20	5.78	90.02	22.41	23.62	1.62	0.53	5.25
No of seeds/pod	2.45	0.07	0.09	78.74	10.56	11.90	1.48	0.07	3.02
Plant height at flowering	24.22	17.69	19.29	91.68	17.37	18.14	1.64	0.96	3.96
Plant height at maturity	37.95	69.45	72.96	95.20	21.96	22.51	1.68	1.79	4.73
Pod length	3.79	0.20	0.25	79.71	11.73	13.14	1.49	0.12	3.30
Pods per plant	52.98	226.91	264.30	85.85	28.43	30.68	1.57	3.79	7.15
Terminal leaf length	9.60	2.55	3.04	84.04	16.64	18.16	1.54	0.41	4.32
Pod clearance	5.67	1.57	1.83	85.98	22.10	23.83	1.57	0.31	5.54

**Table 4.** Estimates of variance components, broad sense heritability, GCV and PCV, GA and GAM of 150 soybean traits evaluated in 2020.

Table 5. Pearson's correlation coefficients for fourteen traits evaluated among 150 *Glycine max* genotypes.

HSW (g)	1	-													
DFF(days)	2	-0.15**	-												
DM (days)	3	-0.15**	0.79***	-											
GY (t/ha)	4	0.19***	0.67***	0.58***	-										
Leafletno/plt	5	-0.04NS	0.21***	0.12*	0.25***	-									
NPP/plt	6	0.01NS	0.15**	0.16**	0.10*	0.01NS	-								
NNMS/plt	7	0.01NS	0.03NS	0.08NS	-0.10*	-0.01NS	0.22***	-							
Noseeds/pod	8	-0.01NS	-0.10*	-0.03NS	-0.14*	0.15**	-0.02NS	0.03NS	-						
Ht@flowering	9	-0.14**	0.66***	0.62***	0.74***	0.15**	0.13**	-0.15**	-0.08NS	-					
(cm)															
Ht@maturity	10	-0.11*	0.55***	0.56***	0.51***	0.08NS	0.11*	0.15**	0.07NS	0.63***	-				
(cm)															
Podlength (cm)	11	0.13**	0.10*	0.07NS	-0.01NS	-0.05NS	0.36***	0.21***	0.18***	-0.02NS	0.05NS	-			
Pods/plt	12	-0.03NS	0.49***	0.47***	0.37***	0.25***	0.43***	0.34***	-0.14**	0.37***	0.50***	0.21***	-		
TLL (cm)	13	-0.09NS	0.45***	0.42***	0.36***	0.14**	0.11*	0.11*	-0.08NS	0.32***	0.34***	0.11*	0.31***	-	
Podcle (cm)	14	-0.02NS	0.15**	0.15**	0.22***	-0.03NS	0.24**	0.09Ns	-0.07NS	0.25***	0.17**	0.09NS	0.07NS	0.09NS	-
		1	2	3	4	5	6	7	8	9	10	11	12	13	14

1234567891011121314\*, \*\*. \*\*\* = significant at P<0.05, P<0.01, P<0.001 respectively, NS= not significant (P>0.05), HSW= 100 seed weight DFF=Days to 50% flowering, DM=Days to maturity, GY(t/ha)=Grain yield (t/ha),<br/>Leafletno/plt= leaflet number/plant, NPP/plt=Number of pod peduncle, NNMS/plt=Number of nodes on the main stem, Noseeds/pod=Number of seed per pod, Ht@flowering =Plant height at flowering<br/>(cm), Ht@maturity= Plant height at maturity (cm), Podlength= Pod length (cm), Pods/plt = Number of pods per plant, TLL (cm)= Terminal leaf length (cm), Podcle (cm)=Pod clearance (cm)

to 264.30 for pod per number. PCV values (6.57 to 30.68 %) were slightly higher than GCV values for all 14 traits, with leaflet number recording the lowest PCV value and pods per plant the highest. The traits with the highest GCV values included number of pods per plant (28.43%), grain yield (23.04%), number of nodes on the main stem (22.41%) and pod clearance (22.10%). All agronomic traits recorded high broad sense heritability estimates, ranging from 78.74% for the number of seeds per pod to 95.20% for plant height at maturity (Table 4). The relative coefficient of variation ranged from 1.48 (seeds per plot) to 2.86 (100 seed weight). Estimates of genetic advance varied from 0.05 for leaflet number to 3.79 for number of pods per plant. Genetic advance as a percentage of the mean (GAM) ranged between 1.55% for leaflet number to 7.15% for number of pods per plant.

#### Pearson correlation among traits

Correlation analysis revealed highly significant associations (P<0.001) between grain yield and various traits (Table 5). The weight of 100 seeds showed a negative correlation with most traits, except for the number of pods per peduncle (r=0.15), the number of nodes on the main stem (r=0.10) and pod length (r=0.10). Days to 50% flowering exhibited positive correlations with all traits except the number of seeds per pod, demonstrating significant associations with days to maturity (r=0.79), grain yield (r=0.69), leaflet number (r=0.21), number of pod per peduncle (r=0.15), plant height at flowering (r=0.66), plant height at maturity (r=0.55), pods per plant (r=0.49), terminal leaf length (r=0.45) and pod clearance (r=0.15). Similarly, days to maturity positively correlated with all traits except the number of seeds per pod, with strong associations observed for grain yield (r=0.58), plant height at flowering (r=0.62), plant height at maturity (r=0.56), number of pods per plant (r=0.47), terminal leaf number (r=0.42) and pod clearance (r=0.15). Grain yield was positively correlated with all traits except for the number of seeds per pod, showing strong associations with plant height at flowering (r=0.74), plant height at maturity (r=0.51) and the number of pods per plant (r=0.34).

Leaflet number showed weak or non-significant correlations with most traits, except for the number of seeds per pod (r=-0.14), plant height at flowering (r=0.15), number of pods/plant (r=0.25) and terminal leaf length (r=0.14). The number of pods per peduncle displayed positive but weak correlations with most traits, except the number of seeds per pod (r=-0.14). In contrast, the number of nodes on the main stem showed no correlation with the number of seeds/pod (r=-0.10) and only a weak correlation with pod clearance (r=0.05).

#### Principal component biplot

The principal component analysis (PCA) biplot indicated that 41.4% of the total variation among soybean genotypes was explained by the first two principal components (PC1 and PC2) (Figure 2). Genotypes with high plant height at maturity (PHM), grain yield (GY), number of pods per plant (PPP), and late flowering and maturity clustered in quadrants 1 and 4. Conversely, shorter genotypes with early flowering, few pods per plant, high 100-seed weights, and more number of seeds/pod clustered in quadrants 2 and 3. Strong correlations were observed between GY and PHF (r=0.74), DFF (r=0.69), DM (r=0.58), and PHM (r=0.51). Acute angles between vectors signified positive correlations, while near-right angles (e.g., PL vs TLL and DM) suggested independence. Obtuse angles (PL vs GY and PHF) indicated negative correlations. Vector lengths highlighted that 100-seed weight, number of seeds/pod, lodging score and pod length had minimal impact, whereas grain yield, plant height at flowering, plant height at maturity, days to 50% flowering, days to maturity and number of pods per plant were critical yield traits.

# Path analysis

Grain yield was the primary trait of interest and served as the dependent (resultant) variable (Figure 3), while all the other traits were considered independent (causal) variables. Days to 50% flowering (0.550) and plant height at flowering (0.313) exhibited direct positive effect on grain yield. Pod number per plant (0.170), terminal leaf length (0.127) and plant height at maturity (0.688) demonstrated positive indirect effects on grain yield through their influence on days to 50% flowering (0.550). Additionally, the number of nodes on the main stem had an indirect effect on grain yield through days to 50% flowering. There was a strong positive correlation between days to maturity (0.430) and plant height at maturity (0.307), with moderate positive associations for pod clearance (0.174) and the number of nodes on the main stem (0.132), all of which indirectly influenced grain yield via plant height at flowering.

Conversely, lodging score negatively correlated with plant height at flowering. Moderate positive associations were also observed for days to maturity (0.169), pod clearance (0.261) and the number of nodes on the main stem (0.226) with nodes per plant, and these traits were strongly positively associated with pods per plant. Additionally, pods per plant were positively related to the number of seeds/pod and pod length.

#### Discussion

#### Agronomic traits evaluation of 150 soybean genotypes for genetic variation

Genetic variability is essential for successful breeding programs, as it provides the raw material for selection and genetic improvement (Sanchez et al., 2023).

The evaluation of 150 soybean genotypes revealed significant differences ( $p \le 0.001$ ) in yield and yield-related traits, indicating substantial genetic variation among *Glycine max* genotypes (Addae-Frimpomaah et al., 2021; Tewodros et al., 2021; Denwar et al., 2019). The comparison of germplasm from different locations showed distinct differences in traits such





**Figure 2.** Genotype by traits biplot that separated 150 soybean genotypes into clusters based on 15 yield and yield-related traits. GY=Grain yield, DFF = Days to 50% flowering, PHF = Plant height at flowering, PPP = Pods per plant, TLL = Terminal leaf length, NNSM = Number of nodes on the main stem, LS = Lodging score, PC = Pod clearance, PHM= Plant height at maturity, DM= Days to maturity, NSPP= Number of seeds/pod, HSW= Hundred seed weight, PL= Pod length and SHS= Shattering score



**Figure 3.** Path diagram showing direct and indirect relationship between grain yield and other traits. DFF = Days to 50% flowering, PHF = Plant height at flowering, PPP = Pods per plant, TLL = Terminal leaf length, NNSM = Number of nodes on the main stem, LS = Lodging score, PC = Pod clearance, PHM= Plant height at maturity, DM= Days to maturity, NSPP= Number of seeds per pod, NP= Nodes per pod, HSW= Hundred seed weight, PL= Pod length and SHS= Shattering score.

as days to flowering, maturity, 100-seed weight, grain yield and number of pods per plant. This variation offers opportunities to improve soybean varieties, particularly in terms of maturity groups and yield, for different agro-ecological zones in Ghana (Denwar et al., 2019). Consistent with previous findings by Denwar et al. (2019), significant variation was observed in 142 soybean accessions from various regions. Genotypes from the USA and Colombia exhibited genetic differences that influenced seed size and weight (Saryoko et al., 2017). Specifically, PI 628866 demonstrated the highest 100-seed weights, while PI 594540 had the lowest. Selective breeding of soybean genotypes from these regions could enhance desirable traits, such as seed weight. Additionally, the top 15 earliest-maturing genotypes originated from the USA and Colombia, whereas the 15 latest maturing genotypes came from Ghana and IITA-Nigeria. Poor adaptation effects may contribute to the early maturity but reduced grain yield observed in genotypes from the USA and Colombia, confirmed by previous studies (Saryoko et al., 2017).

#### Estimation of variance components

Estimating genetic parameters within germplasm collections is essential for effective crop improvement through selection (Awad-Allah et al., 2022). This studyrevealed significant genotypic variability among 150 soybean genotypes. The phenotypic coefficient of variation (PCV) values slightly exceeded the genotypic coefficient of variation (GCV) values, indicating a dominant role of genetic factors in trait expression (Yohannes et al., 2015; Owusu et al., 2018; Mofokeng, 2021). High PCV and GCV values were observed for traits such as the number of pods per plant, grain yield, and plant height (Baraskar et al., 2014; Mofokeng et al., 2021). Broad-sense heritability estimates were high (78.74-95.20%) for traits like plant height at maturity, days to maturity, and plant height at flowering, indicating strong genetic infuence (Crossa et al., 2017). However, these findings partially contradict previous studies (Tandekar et al., 2022; Baraskar et al., 2014), which may be due to differences in the genotypes analyzed and environmental interactions.

The relative coefficient of variation (CVr) exceeded 1 for all measured traits, highlighting high variability among genotypes. These findings suggest substantial genetic variation and potential for enhancement through selective breeding, aligning with previous research on soybean and other crops (Adhikari et al., 2018; Neelima et al., 2018; Jandong et al., 2020).

The combination of heritability with genetic advance (GA) is critical for effective selection. The genetic advance as a percentage of the mean (GAM) showed moderate progress potential for traits of interest, with values ranging from 1.54% (leaflet number) to 7.14% (number of pods per plant) (Johnson et al., 1955). However, low GA (<10%) was observed for all traits, indicating relatively low expected genetic gain from selection. This combination of low genetic advance and high heritability suggests that non-additive genetic effects significantly influence trait expression. Alternative breeding strategies, such as chemical or physical mutagenesis, recombination breeding, and recurrent selection, may be necessary to achieve significant genetic gains (Roychowdhury and Tah, 2013).

#### Correlation analysis of yield and yield related traits

Soybean yield is a complex trait influenced by multiple quantitative traits, making it amenable to indirect selection (Nagarajan et al., 2022; Rao et al., 2017). Correlation analysis revealed positive associations between days to 50% flowering, maturity, grain yield, and yield-related traits, with the exception of the number of seeds/pod (Li et al., 2020). Days to 50% flowering and maturity showed positive correlations with grain yield, plant height, number of pods per plant, and terminal leaf length. These findings are consistent with prior studies (Jiang et al., 2014; Zhai et al., 2014; Pushpavalli et al., 2018; Addae-Frimpomaah et al., 2021; Sulistyo et al., 2018), underscoring the importance of flowering and maturity timing in soybean yield. Strong positive correlations between grain yield and traits such as plant height, leaflet number, number of pods per plant, and pod clearance suggest that enhancing these traits could improve soybean yield (Li et al., 2013; Sulistyo et al., 2018).

#### Principal component analysis biplot

Principal component analysis (PCA) biplot visually represents relationships among variables, with vector lengths indicating the explained variability (Sultana, 2019). This biplot analysis identified days to 50% flowering, plant height, number of pods per plant, and terminal leaf length as differentiating traits among soybean genotypes due to their long vectors. In contrast, traits such as 100-seed weight, pod length, and lodging score exhibited shorter vectors, signifying lesser importance in distinguishing genotypes and assessing yield potential. This finding aligns with prior studies by Rani et al. (2023) and Li et al. (2020), which also found these traits less critical in evaluating soybean genetic diversity and yield.

#### Path coefficient analysis

Path coefficient analysis highlighted significant relationships between soybean yield and various traits, offering insights for breeding programs. Days to 50% flowering and plant height at flowering had direct positive effects on yield, with days to flowering completion showing the highest direct effect (0.550). These traits are vital for determining soybean yield, suggesting that selective breeding breeding targeting these traits could enhance grain yield (Chavan et al., 2016; Dubey et al., 2015; Muhammad et al., 2007). Traits such as number of pods per plant and plant height at maturity exhibited indirect positive effects on yield. Focusing on flowering and height traits can improve soybean yield, making them priority criteria for selection.

# **Materials and Methods**

#### Description of experimental location

The experiment was conducted at the research field of the Council for Scientific and Industrial Research (CSIR)-Savanna Agricultural Research Institute (SARI) in Nyankpala (Figure 1), Northern region of Ghana (9°25'N, 0°58'W) during the rainy season from July to November 2020. The soil is a sandy loam developed from the Voltaian sandstone, classified as the Nyankpala series (SARI, 2016). Nyankpala is situated within the Guinea Savannah Zone, characterized by a monomodal rainfall pattern averaging 1,200 mm annually. The rainy season lasts 100-120 days, with an estimated annual reference evaporation of about 2,000 mm.

The area experiences a prolonged dry season (4-6 months) typically starting in November and ending in April. Intermittent drought during the wet season, lasting up to two weeks, can impact crop performance in the field. Relative humidity ranges from 46% to 76.8% (Abbam et al., 2018).

#### Planting material selection

The planting material comprised 150 soybean genotypes through collaboration with international and local institutions, including the University of Illinois, the Soybean Innovation Laboratory and the University of Missouri. These institutions, known for their expertise in African soybean breeding, facilitated the selection of climate-resilient germplasm from American and USDA sources. Genotypes were obtained from the Council for Scientific and Industrial Research-Savanna Agricultural Research Institute (CSIR-SARI), Ghana, (10 accessions), the International Institute of Tropical Agriculture (IITA), Nigeria (38 accessions), the University of Illinois, USA (55 accessions), and Colombia (47 accessions). The selection criteria emphasized diversity in yield, maturity, plant height, and seed characteristics, capturing a broad genetic base from Asia, Africa, North America and South America. Six check varieties were included, comprising four commercially viable varieties – (Jenguma, Afayak, Favour, and Soung Pungun) and two advanced breeding lines (BRS Tiana and FT Cristaline) introduced by the University of Illinois, USA, to the CSIR-SARI Soybean Breeding Programme in 2015. These check varieties are well adapted to tropical conditions, with yield potentials ranging from 1.0 to 3.0 tonnes/ha.

#### Experimental procedure and design

The experimental design was a 15 x 10 alpha lattice with three replications. Each replication comprised of 10 incomplete blocks, each containing 15 genotypes. Each genotype was planted in two-row plots, 4 meters long, with 60 cm spacing between rows and 5 cm spacing between plants within rows. Two seeds were sown per hill at a depth of 5 cm. A 1-meter alley was left between blocks, and a 2-meter space was maintained between replications. Ten plants per plot were randomly tagged for data collection. Weeding was performed manually as needed.

#### Data collection

Data collection included the following traits: pods per peduncle, seeds/pod, plant height at flowering and maturity, days to 50% flowering and maturity, pod length, number of pods per plant, terminal leaf length, leaflet number, 100-seed weight, grain yield, plant stand, pod clearance, and nodes per plant. Measurements followed standard protocols.

#### Data analysis

The collected data were subjected to analysis of variance (ANOVA) for alpha lattice design using PROC GLM in SAS (SAS Institute, 2017). Pearson correlation analysis was conducted to evaluate the degree of association among the traits. Principal Component Analysis (PCA) and biplot analysis were performed using SAS-based JMP software (SAS Institute, 2017) to identify trait contributions to accession differentiation. Stepwise multiple regression (Mohammadi et al., 2013) and sequential path diagrams were used to examine trait associations and the secondary traits influencing grain yield. SPSS version 17.0 (2007) Traits were categorized by order of contribution, minimizing multicollinearity using SPSS version 17.0 (2007) (Talabi et al., 2016). Significant traits ( $P \le 0.05$ ) were classified as first-order, and path coefficients were determined using standardized beta values and t-test significance at the 5% probability level.

# **Estimation of variance components**

# **1.** Genotypic Variance $GV = \frac{(MSg - MSe)}{2}$

where;

- MSg (Mean Square of genotypes): a measure of genetic variation among genotypes

- MSe (Mean Square of error): a measure of environmental variation
- r (number of replications): the number of times each genotype is repeated in the experiment

# 2. Phenotypic Variance,

PV = GV + MSe represents this partitioning, where:

- PV (Phenotypic Variance) is the total variation observed in a trait
- GV (Genotypic Variance) is the variation due to genetic differences among individuals
- MSe (Mean Square of error) is the variation due to environmental and other non-genetic factors;

# 3. Genotypic Coefficient of Variation,

$$GCV_{[]}(\%) = \left(\frac{\sqrt{\sigma_g^2}}{x}\right) * 100 \qquad \text{where}$$

 $\sigma_g^2$  = the Genotypic Variance X = the overall mean of the trait

# 4. Phenotypic Coefficient of Variation,

$$\text{PCV}_{\text{III}} (\%) = \left(\frac{\sqrt{\sigma_p^2}}{x}\right) * 100$$

where  $\sigma_p^2$  = Phenotypic Variance and *x* = mean of the character.

**5.** Broad sense heritability (H<sup>2</sup>) is a measure of the proportion of phenotypic variance attributable to genetic factors (Allard, 1960), and it's calculated as:

 $\mathrm{H}^2 = \left(\frac{\sigma_{\mathrm{g}}^2}{\sigma_{\mathrm{p}}^2}\right) * 100$ 

where:

-  $\sigma^{2}{}_{\mathrm{g}}$  is the genotypic variance

-  $\sigma^{2}{}_{p}$  is the phenotypic variance.

**6. Genetic Advance** Genetic Advance (GA) is a measure of the expected improvement in a trait due to selection (Allard, 1960), and it's calculated as:

 $GA = K \times \sigma_p \times H^2$ where:

- GA = expected genetic advance

- K = the standardized selection differential (at 5% selection intensity, K = 2.063)

-  $\sigma_p$  = phenotypic standard deviation (on a mean basis)

-  $H^2$  = broad-sense heritability

**7.** Genetic advance as a percentage of population means (*GAM*) is a measure of the expected improvement in a trait due to selection, expressed as a percentage of the population mean (Johnson et al., 1955). It's calculated as:

 $GAM = \left(\frac{GA}{X}\right) * 100$ 

where: GA = Genetic Advance, X = mean of the population

# Conclusion

This study offers valuable insights into the genetic variation, heritability, and trait relationships in soybean genotypes, aiding the development of effective breeding strategies for enhanced crop performance. High heritability estimates for traits related to plant height and maturity indicate their strong potential for genetic improvement. Path coefficient analysis highlighted days to 50% flowering and plant height at flowering as key direct contributors to grain yield, while traits such as number of pods per plant and terminal leaf length had indirect positive effects. Biplot analysis further distinguished soybean genotypes based on traits like days to 50% flowering, plant height, and number of pods per plant. These findings emphasize the importance of targeting specific traits to boost soybean yield and demonstrate the value of statistical methods such as PCA, biplot analysis, and path coefficient analysis in optimizing breeding programs (Chavan et al., 2016). The results provide a foundation for evidence-based strategies to improve soybean productivity

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# Statement of contribution

The authors contributed to this study as follows: F.A-F. led conceptualization, investigation, and drafting manuscript; G.A. designed the methodology and supervised the study; F.L.S. reviewed and edited; G.A.A. collected data; S.A. reviewed and edited under supervision, J.A-D. reviewed, C.N. conducted data analysis, J.Y. set up field experiments, O.A.A. assembled germplasm; and H.A. provided overall supervision.

# **Conflict of Interest**

The authors have no competing interests to declare

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