

Preliminary Investigation of Genetic Variance and Heritability Among Sunflower (*Helianthus annuus* L.) Genotypes Yield and Yields Components in Botswana

Odireleng Molosiwa¹, Ditshupo Dinyao¹ & Mapena G. Ramokapane¹

¹ National Agricultural Research and Development Institute, Gaborone, Botswana

Correspondence: Odireleng Molosiwa, National Agricultural Research and Development Institute, Private Bag 00177, Gaborone, Botswana. E-mail: odireleng@nardi.org.bw

Received: June 9, 2025

Accepted: July 16, 2025

Online Published: August 15, 2025

doi:10.5539/jas.v17n9p32

URL: <https://doi.org/10.5539/jas.v17n9p32>

Abstract

A study was conducted at the Sebele and Goodhope Research Stations to estimate genetic parameters of sunflower and select the best performing genotypes. Analysis of variance revealed significant difference among the 36 genotypes for all the eight traits. Principal Component Analysis, top 3 components explained 81.6% of total contribution, highlighting major contributors of phenotypic variability. All characters were positively correlated to GYHA. GCV ranged from (5.99-12.64) while PCV ranged from (6.62-19.01) for DF and GYHA for both coefficients respectively. Higher heritability was expressed for most traits, while moderate heritability between (30-60%) was record for GC, FPS, and GYHA. The genetic advance as percentage of mean (GAM) ranged from 9.99% for GC to highest of 25.24% for PH and most of the traits were moderate (10-20%). High heritability coupled with GAM was recorded on PH (85.26% & 25.45%), an indication that this trait is governed by additive gene action. Higher heritability together with moderate GAM, was observed on DF (82.06% & 11.18%), DM (73.69% & 13.29%), LN (70.18% & 17.85%), 1000SW (71.92% & 19.00%). Grain yield ranged from 997 kg/ha for SUN310 to 1862 kg/ha for SUN322 genotypes. The twelve best performing genotypes were SUN322, SUN-MOL4, CH301/105, SUN206, SUN205, SAONA403, RUSSIAN4, RUS4-401, RUS4SH14, JUPWTSH14, JUP2-WTSH14, JUPSH14 with a yield of more than 1500kg/ha. The study revealed higher genetic diversity among the sunflower genotypes; therefore, selection is feasible, based on the traits with higher heritability, genetic advance of mean and positive correlations.

Keywords: additive gene action, correlation, genetic advance, heritability, sunflower

1. Introduction

Sunflower (*Helianthus annuus* L.) is an annual dicotyledonous crop, originating from North America and Mexico and is now grown throughout the world (Heiser, 1978, Lentz et al., 2001). The leading world producers of sunflower seed include Russia Federation (16, 632,215MT), Ukraine (11,328,740MT), Argentina (4,050,362MT), China (2,930,000MT) and Turkey (2,550,000MT) (FAOSTAT, 2022). Major producers of sunflower in Africa include South Africa, Tanzania, Uganda and Zambia (Pilorge, 2020). Despite that, due to the recent Russia-Ukraine conflict, the oil prices have increased significantly leading to oil shortages in countries like Botswana (Neik et al., 2023).

Sunflower is preferred for its high-quality edible oil, largely used for culinary purposes (Adeleke & Babalola, 2020). It contains approximately 44% oil and 16% protein therefore it competes both on the vegetable oil market and vegetable protein rich “products markets” led by palm oil and soybean respectively (Pilorge, 2020). Sunflower meal can be a key component to substitute for soybean meal in feed, especially where soybean production is limited (de Morais Oliveira et al., 2016). This is critical for countries such as Botswana where production of soybean has not been fully promoted and cultivation is extremely low (Mosupiemang et al., 2021). Sunflower has a huge commercial potential for use in agro-industries, since it provides protein meal for animal feeding, it is used in various products in pharmaceutical, chemical and cosmetics industry, biodiesel production and in floriculture (Castro & Leite, 2018; Adeleke & Babalola, 2020; Directorate Marketing, 2021).

Sunflowers often perform well in marginal areas compared to maize or soybean, hence the effects of climate change on sunflower production could offer new cropping opportunities (Debaeke et al., 2017). In addition, the

crop has several allelopathic chemicals which inhibit seed germination and seedling growth of several weed species, these inhibitory effects maybe explored and used for weed management with less herbicides for sustainable crop growth (Azania et al., 2003). Sunflower as an entomophilous crop is a source of nectar critical in the apiculture industry (Chabert et al., 2020). It also has the advantage of being thermos and photo-insensitive (Azania et al., 2003). Hence, the crop has high adaptation to a large production area with different climate features, and its crop cycle may vary from 80-130 days depending on genotypes and sowing dates (Castro & Leite, 2018).

Sunflower cultivation in Botswana was estimated at 700 hectares by 1,314 farmers, and the national records indicate lower crop yields of 197.5 kg/ha, over five-year period (Statistics Botswana, 2019). The reason for these lower yields could be manifold, including but not limited to changes in agricultural practices, market demand, availability of farming inputs, climatic conditions, pests and disease outbreaks, and economic factors that might affect production costs and selling prices. Consequently, the country has a lower production of oil seeds from sunflower and depends on imports. Botswana's monthly imports of oil products amount to around 50 million pula, approximately (4 million USD), representing about 5% of the country total food import (Statistics Botswana, 2023). This underscores the need for a substantial increase in cultivation and production of sunflower. Other sources of oil crops benefiting consumers, but not yet fully explored in Botswana include those of soybean (Mosupiemang et al., 2021), melon (*Citrullus lanatus* var. *citroides*) (Bareeleng et al., 2024) and Safflower (Moatshe et al., 2020).

One major challenge to sunflower production in Botswana, is the shortage of improved crop varieties to farmers for planting. Currently, Russian no.4 is the only variety available to farmers, there is a need to select and identify more varieties with potential for production in the climatic conditions of Botswana. The development of an effective plant breeding programme is dependent upon the existence of genetic variation in the genotypes. Hence, an insight into the extent of variability present in the selected cultivars is important. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. Estimates of genetic variability parameters in sunflower was explored, in several studies such as in Serbia (Jocković et al., 2019), in India (Divya et al., 2019; Sree et al., 2021) the authors emphasized a combination of assessing the heritability simultaneously with genetic advance as percentage of mean to predict genetic gain effectively for valuable selection of genotypes. Therefore, the present study was undertaken to conduct genetic variability, heritability, genetic advance in selected sunflower genotypes for yield and its components

2. Materials and Method

2.1 Plant Material

Thirty-six (36) sunflower collections were sourced from Botswana National Plant Genetic Resources Centre (NPGRC). Some are originally from South Africa, through a regional trial conducted in conjunction with the Agricultural Research Council-Grain Crops Division in Potchefstroom, while others are from Zambia as part of a research collaborations with the Oil Seed Program in Botswana. Field experiments were conducted in the 2015/2016 season at Sebele Research and Innovation Centre (24°35'S: 25°56'E, altitude 994 m), and at Goodhope Research Station (25°27'S; 25°25'S Altitude 1291m). The rainy season is from the beginning of October to the end of March every year, and the trial was planted in December and harvested in April. Soils at Sebele are calcic, luvisol, sandy loam, while at Goodhope are ferralic, cambisol, and loamy sandy (Carter et al., 1992; Law et al., 2007). Total rainfall received at Sebele RIC was 216.4 mm while Goodhope Research Station received 357.2 mm from 1st September 2015 to 31st May 2016 (Statistics Botswana, 2016). The local check used in the study was variety Russian No.4.

Table 1. List of thirty-six genotypes selected for the study

Entry Number	Accession Name	Origin/Source
1	SUN322	South Africa
2	SUN110	South Africa
3	SUN-MOL2	Botswana
4	SUN-MOL4	Botswana
5	SUN-MOL	Botswana
6	GK019	Botswana
7	SUN106	South Africa
8	SUN107	South Africa
9	SUN213	South Africa
10	SUN124	South Africa
11	SUN316	South Africa
12	SUN124	South Africa
13	CH301/105	Zambia
14	SUN227	South Africa
15	SUN221	South Africa
16	SUN316B	South Africa
17	SUN116	South Africa
18	SUN310	South Africa
19	SUN312	South Africa
20	SUN206	South Africa
21	SUN104	South Africa
22	SUN105	South Africa
23	CH301/105B	Zambia
24	SUN205	South Africa
25	SUN211	South Africa
26	SUN115	South Africa
27	SUN306	South Africa
28	CH301/302	Zambia
29	SAONA403	Zambia
30	RUSSIAN4	Botswana
31	RUS4-401	Botswana
32	RUS4-1SH14	Botswana
33	RUS4SH14	Botswana
34	JUPWTSH14	Botswana
35	JUP2-WTSH14	Botswana
36	JUPSH14	Botswana

2.2 Experimental Design and Crop Management

The site was tractor ploughed, and disc harrowed to level the soil in preparation for planting. Sowing was done in December at both locations, based on the experimental design. Sowing was done manually, and all agronomic practices were conducted on the crop, including the application of (2:3:2) fertilizer at a recommended rate of 100 kg/ha. Manual weeding was done throughout the growth stages of the crop, while pest and diseases were not encountered in this project. The experiment was set up in a Randomised Complete Block Design with three replications. The plot length was 3 metres, with a spacing between plants of 30 cm, and the study was conducted in a 72×6 m (432 m²) area at both locations.

2.3 Data Collection and Statistical Analysis

Data was collected based on the International Board for Plant Genetic Resources, IBPGR (1985) for sunflower. Data recorded include germination count (GC) recorded at 21 days after sowing. Final plant stand (FPS), counting the number of heads at harvest, days to 50% flowering (DF), days taken from sowing to date of opening

of ray florets in 50% of plants, days to maturity (DM), days taken by majority of plants head to become lemon yellow in colour, plant height (PH) was measured from ground to base of the capitulum when the crop has reached physiological maturity, leave number (LN) was recorded at maturity from 5 plants and recorded as mean, 1000 seed weight (1000SW) was measured from seed collected per plot and was counted using electronic seed counter (Contador Pfeuffer GmbH), seed yield per plot (GYHA) was estimated per hectare recorded at harvesting all plants within plots. Data obtained was analysed using Genstat version 18 and the agro-morphological mean data were standardized to compute Principal Component Analysis (PCA). Since the study also aims to identify the best performing genotypes, it is key that the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (as percentage of mean) are estimated among the selected genotypes.

The genetic parameters were estimated using formulas adapted from Allard, (1960), Singh and Chadhary, (1985) as follows: $V_g = [\text{Mean Square Genotype} - \text{Mean Square Error}/r]$; $V_p = [\text{Mean Square Genotype}/r]$ $V_e = [\text{Mean Square Error}/r]$ where r is the number of replications. Phenotypic (PCV) and genotypic (GCV) coefficient are estimated using the following formulas $PCV = (\sqrt{V_p}/\bar{X}) \times 100$; $GCV = (\sqrt{V_g}/\bar{X}) \times 100$, V_p represents the phenotypic variance, V_g represents the genotypic variance, while $\bar{X}$ represents the mean. Expected genetic advance (GA) was estimated as: $GA = K \cdot h^2 \cdot \sigma_p$, where, K is selection intensity, h^2 is heritability and σ_p is phenotypic standard deviation. The phenotypic standard deviations among traits were also calculated using Genstat version 18.

The limits for components of PCV and GCV were divided into three categories of [20% high, 10-20% (moderate) and 10% or less is (low)], categorised by Sivasubramanian and Menon (1973), Heritability categorised as [60% and above (high), 30-60% (moderate), less than 30% (low)]. Genetic Advance of mean was apportioned as [20% and above (high), 10-20% (moderate) and less than 10% is (low)] by (Johnson et al., 1955).

3. Results and Discussion

3.1 Effect of Genotype, Environment and Genotype by Environment Interaction on Selected Agronomic Characters

Analysis of variance was estimated on the eight selected characters, and all showed significant ($P \leq 0.01$) differences, revealing the genetic variability that exists among the 36 genotypes (Table 2). Similar results were obtained in sunflower studies by Umarani et al. (2022), and Lakshman et al. (2021), where significant variation was recorded among all the selected traits. Mandel et al. (2013) recorded substantial phenotypic variation among the 271 sunflower accessions on studies conducted in the USA and Canada, this vast variation is recorded despite the population genetic bottleneck that occurred in the domestication and improvement of the cultivated sunflower gene pool. Genotypes $\times$ environment interaction was observed only on germination count (GC), days to 50% flowering (DF) and days to maturity (DM), an indication that these traits were affected by environmental factors in the different locations.

Table 2. Analysis of variance for seed yield and its components in 36 sunflower genotypes based on two locations in Botswana

Source of Variation	df	GC	FPS	DF	DM	PH	LN	GYHA	1000SW
Genotype	35	13.14*	15.74*	66.17**	169.68**	2312.4**	51.2**	205809**	287.45**
Location	1	18629.79**	11411.57**	3927.04**	8660.96**	2426.7**	910.61**	90312174**	492.89**
Genotype $\times$ Location	35	14.45**	15.25 ^{ns}	18.79*	70.67**	320.2 ^{ns}	13.98 ^{ns}	83661 ^{ns}	92.45 ^{ns}
Residual	142	7.53	10.21	11.87	44.65	340.8	15.27	114771	80.72

Note. GC: Germination count, FPS: Final plants stand, DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, LN: Leave number, GYHA: Grain yield per hectare, 1000SW: One thousand seed weight. ** Significant at $P \leq 0.01$; * Significant at $P \leq 0.05$ ns = Not significant.

Table 3. Mean performance of 36 sunflower genotypes based on the eight (8) agronomic traits from two locations

Genotype Name	GC	FPS	DF	DM	PH (cm)	LN	GYHA (kg/ha)	1000SW (g)
SUN322	17.83	16.83	72.33	89.99	188.80	30.17	1862	85.88
SUN110	18.17	16.00	73.33	84.46	227.50	36.60	1408	76.50
SUN-MOL2	16.50	15.33	75.67	99.10	192.00	38.38	1207	83.90
SUN-MOL4	18.00	17.17	71.50	90.67	204.00	41.18	1517	85.21
SUN-MOL	15.17	12.83	67.50	83.25	166.50	29.57	1295	78.89
GK019	18.00	14.50	70.17	86.50	185.00	32.05	1427	79.62
SUN106	18.17	16.67	75.83	94.82	209.80	35.52	1415	81.83
SUN107	19.83	13.67	75.67	83.66	202.50	35.88	1327	72.41
SUN213	19.00	18.00	72.00	82.65	199.70	35.82	1288	71.67
SUN124	20.33	18.67	73.50	81.18	200.20	35.07	1272	71.33
SUN316	19.50	18.00	72.83	88.43	201.30	34.00	1243	78.65
SUN124	17.50	14.33	72.00	85.75	161.30	31.72	1002	77.48
CH301/105	18.00	14.67	71.00	82.75	184.70	31.65	1527	75.86
SUN227	18.33	16.50	70.83	81.67	206.70	34.90	1185	62.45
SUN221	19.33	17.00	67.17	81.47	177.00	29.95	1237	71.40
SUN316B	19.17	17.33	77.17	95.58	221.00	35.55	1363	81.48
SUN116	18.33	14.00	62.33	77.45	151.80	30.77	1263	63.58
SUN310	18.50	15.17	72.50	86.34	187.70	35.38	997	62.85
SUN312	20.33	17.67	70.33	84.42	193.30	32.17	1257	70.73
SUN206	19.33	17.33	72.83	89.72	203.50	34.50	1540	83.83
SUN104	18.00	16.17	71.17	83.94	191.50	31.72	1278	63.66
SUN105	19.67	16.00	66.67	77.14	198.70	33.55	1145	70.95
CH301/105B	19.67	17.00	72.50	87.31	177.00	31.12	1332	76.55
SUN205	19.00	16.33	75.83	92.97	222.50	35.23	1623	71.86
SUN211	19.00	17.50	66.67	82.29	178.80	31.38	1455	75.70
SUN115	12.33	10.67	68.50	81.00	150.70	30.95	1168	85.48
SUN306	18.67	16.17	66.00	75.75	173.80	31.72	1307	72.69
CH301/302	18.83	16.83	68.83	83.79	186.50	33.82	1328	76.00
SAONA403	19.00	16.00	72.67	89.30	192.00	28.68	1513	80.20
RUSSIAN4	17.33	16.00	73.33	92.13	196.50	30.38	1578	85.76
RUS4-401	19.17	17.17	69.17	89.40	229.20	37.88	1590	82.69
RUS4-1SH14	18.67	16.83	72.67	88.75	206.00	37.12	1392	76.85
RUS4SH14	19.33	17.33	70.33	81.05	203.00	34.45	1525	70.25
JUPWTSH14	19.50	17.67	71.00	87.18	194.20	35.10	1667	71.81
JUP2-WTSH14	17.17	15.33	68.33	89.19	177.80	31.50	1520	88.04
JUPSH14	17.67	15.67	65.33	80.05	155.50	28.83	1558.00	75.69
Grand Mean	18.40	16.12	70.99	85.87	191.60	33.45	1378	75.54
LSD	3.13	3.64	3.93	7.62	21.07	4.46	386.7	10.25
CV%	14.9	19.8	4.9	7.8	9.6	11.7	24.6	11.9

Note. GC: Germination count, FPS: Final plants stand, DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, LN: Leave number, GYHA: Grain yield per hectare, 1000SW: One thousand seed weight.

3.2 Agronomic Performance of Sunflower Genotypes

Variation in grain yield is ranging from 997 kg/ha (SUN310) to 1862 kg/ha (SUN322), while the 1000 seed weight is ranging from (88.04 g) for JUP2-WTSH14 to 62.45 g for SUN277 genotypes (Table 3). A relatively higher average weight of 1378 kg/ha was realised, while twelve genotypes that were able to produce more than 1500 kg/ha were identified. This is an indication that sunflower has important agronomic traits, such as long deep tap roots and have high aptitudes for adverse conditions including high temperatures, drought and it

recovers easily from moisture stress (Castro & Leite, 2018; Adeleke & Babalola, 2020). The mean observed for days to 50% flowering of 70.99, and days to maturity (85.87), compares favourably with those recorded by Sree et al. (2021), who recorded 65 and 95 respectively. The average number of leaves from 36 genotypes in this study was 33.45, while the 1000 seed weight was 75.54 g, compared to those evaluated among the 33 genotypes in Tunisia, where the leave number was lower at 25.12, while the 1000 seed weight was higher at 82.96 g (Honsi et al., 2023).

Table 4. Correlation coefficient indicating association of agronomic traits of 36 sunflower genotypes evaluated in two locations in Botswana

Traits	GC	FPS	DF	DM	PH	LN	GYHA	1000SW
GC	1.00							
FPS	0.95***	1.00						
DF	0.63***	0.60***	1.00					
DM	0.54***	0.53***	0.75***	1.00				
PH	-0.038	0.0063	0.14**	0.07	1.00			
LN	0.39***	0.42***	0.41***	0.38***	0.31***	1.00		
GYHA	0.84***	0.81***	0.58***	0.56***	0.0005***	0.36***	1.00	
1000SW	-0.24***	-0.2156	0.049	0.32***	0.09***	-0.0224	0.05	1.00

Note. GC: Germination count, FPS: Final plants stand, DF: Days to 50% flowering, DM: days to maturity, PH: plant height, LN: leave number, GYHA: grain yield per hectare, 1000SW: one thousand seed weight. *** Significant at 0.001 levels and ** is significant at 0.01 levels.

3.3 Inter-relations Between the Selected Quantitative Characters-Correlations

Correlation coefficient (r) was used in the study to determine inter-relations between all quantitative characters (Table 4). All selected characters were positively correlated to grain yield per hectare (GYHA), while 1000 seed weight was positively correlated to DF ($r = 0.049$), DM ($r = 0.32***$), PH ($r = 0.09***$), and negative correlations were for GC ($r = -0.24***$), FPS ($r = -0.2156$) and LN ($r = -0.224$). The results are accordance with those reported by Laksman et al., (2021) who reported a positive and significant correlation between seed yield per hectare, with plant height. Correlations of greater than approximately ($r = +0.7$) or less than ($r = -0.7$) are the ones likely to be of biological importance (Hill et al., 1998). Such correlations were found between GC and FPS ($r = +0.95$), GC and GYHA ($r = +0.84$), FPS and GYHA ($r = +0.81$), DM and DF ($r = +0.75$). This shows that plant population, days to flowering, and days to maturity significantly impact on the final seed yield of sunflower. Date of sowing is a critical aspect of crop management in Botswana and sunflower, is recommended for early planting in December (Molosiwa & Kgokong, 2018), this influence days to flowering and days to maturity.

The lower correlations were recorded for PH vs GYHA ($r = 0.0005***$), PH vs FPS ($r = 0.0063$), PH vs DM ($r = 0.07$). This reflects the importance of plant height, plant population and days to maturity on the final yield of sunflower and the adaptation of genotypes to the climatic environment of Botswana. For example, among the 12 genotypes that produced more than 1500 kg/ha, only four were exotic, three from South Africa (SUN322, SUN206, SUN205) and one from Zambia (SAONA403).

Table 5. Principal component matrix of eigenvalues for 8 quantitative traits of 36 sunflower genotypes from Botswana

Variables	PC 1	PC 2	PC 3
Germination Count	0.456	-0.275	0.001
Final Plant Stand	0.453	-0.245	-0.030
Days to 50% Flowering	0.407	0.168	0.054
Days to Maturity	0.382	0.333	0.272
Plant Height	0.053	0.471	-0.670
Leave Number	0.285	0.212	-0.470
Grain yield (kg/ha)	0.434	-0.081	0.149
1000 seed weight (g)	-0.015	0.671	0.478
Latents roots	4.022	1.460	1.103
Total Contribution	50.280	67.850	81.640
% Variation	50.280	17.570	13.790

3.4 Principal Component Analysis Among Sunflower Genotypes

Principal component analysis was employed to reveal traits that account for most variation among the 36 genotypes, based on the eight characters (Table 5). The first three principal components with more than one eigenvalue were selected, giving an accumulated total variation of 81.64%. The first principal component (PC1) contributed 50.28% of variation and characters with higher loadings were germination count, final plant stand, days to 50% flowering and grain yield per hectare. The second principal component (PC2), accounted for 17.57% of total variation and higher loadings were from 1000 seed weight and plant height, which also accounted for most of the variation in PC3, together with leave number per plant, with a total variation of 13.79%. Generally, observation shows that plant growth (germination count, days to 50% flowering, 1000 seed weight, plant height) are critical among the selected sunflower genotypes and have a huge influence on the final grain yield (kg/ha). A similar observation is clearly defined by the correlation analysis from table 4. The PCA analysis undertaken in Tunisia sunflower genotypes, using 16 characters revealed a variation of 54.3 % in the first two axes (Honsi et al., 2023), while in this study the first axes showed 67.85% total variation, the differences could be attributed to the relatively lower number of traits implored in our study and the environmental differences.

3.5 Genotypic and Phenotypic Coefficient, Heritability and Genetic Advance Analysis

For a robust sunflower crop improvement to be attained, the magnitude of genotypic, phenotypic variation, extent of how traits are heritable and genetic advance were assessed (Table 6). Genotypic coefficient of variation ranged from (5.99-12.64) while phenotypic coefficient variation ranged from (6.62-19.01) for days to 50% flowering and GYHA for both coefficients respectively. The estimates of genotypic coefficient variation (GCV) were lower for most of the traits and moderate for PH (13.38%), LN (10.35%) and GYHA (12.64%) while phenotypic coefficient variation (PCV) was moderate (10-20%) for most of the traits except DF (6.62%) and DM (8.76%) which are lower than 10%. Generally, no phenotypic and genotypic coefficient of variations recorded more than 20%, an indication of a challenge in direct selection of the selected traits (Table 6). Similar observations were noted by Varshitha et al., (2023) who reported moderate values for GCV and PCV for PH (13.38; 14.49) and LN (10.35; 12.35), while DF (6.21%; 6.29%), DM (3.72%; 4.23%) were lower. Low values GCV and PCV were reported on sixty-four rice accessions, this indicates the need for creation of variability, which could be done through hybridization or mutation (Kalpana et al., 2018). The study showed that values for PCV were higher than the corresponding traits for GCV, with a narrow difference between these coefficients, an indication of lower environmental influence of the assessed traits. The results are in accordance with those reported by Reddy and Nadaf (2014), who noted this as an indication of less influence of environment on expression of traits used for assessing 16 genotypes in India.

The heritability estimates in this study ranged from 35.13% (final plant stand) to 85.26% (plant height). Most of the traits expressed higher heritability for DF (82.06%), DM (73.69%), PH (85.26%), LN (70.18%) and 1000SW (71.92%) with more than (60%), while moderate heritability was record for GC, FPS, and GYHA between (30-60%). Several researchers working on sunflower reported higher heritability on plant height (82%) (Lakshman et al., 2021), days to 50% flowering (73.87%), days to maturity (79.72%), plant height (87.49%) (Umarani et al., 2022) an indication that selection of these traits will be effective since it is less influenced by environmental effects.

According to Johnson et al. (1955), genetic advance as percentage of mean (GMA) is classified as high ($> 20\%$), moderate ($10\%-20\%$) and low for less than (10%). The GMA ranged from 9.99% for GC to highest of 25.24% for PH. Most of the traits recorded were moderate, FPS (10.28%), DF (11.18%), DM (13.29%), LN (17.85%), GYHA (17.32%) and 19.20% for 1000SW (Table 6). Heritability coupled with genetic advance of mean are key selection parameters and are great estimates of predicting genetic gain in selection, and the choice of suitable breeding method (Tola et al., 2023). High Heritability and GAM was recorded on PH (85.26% & 25.45%), an indication that this trait is governed by additive gene action and has a higher possibility of selection to attain a positive crop improvement. The results are in accordance with those reported by Varshitha et al. (2023), and Sujatha et al. (2002), who reported high heritability combined with high genetic advance for plant height in sunflower. In this study most of the traits exhibited higher heritability coupled with moderate GAM such as DF (82.06% & 11.18%), DM (73.69% & 13.29%), LN (70.18% & 17.85%), 1000SW (71.92% & 19.00%), an indication of some involvement of both additive and non-additive gene action in the inheritance of these traits. Population improvement by reciprocal recurrent selection, is best to implore for the selected sunflower genotypes (Varshitha et al., 2023). In contrast to our findings, Sujatha et al. (2002), observed high heritability but low genetic advance in leave number, days to 50% flowering and 100 seed weight. The grain yield per hectare revealed some moderate heritability coupled with moderate genetic advance of mean (44.23% and 17.32%), the selection of this trait should be conducted in advance generation to take advantage of the maximum gain derived from selection (Lakshman et al., 2021).

Table 6. Estimates of mean, genetic coefficient of variance, phenotypic coefficient of variance, broad sense heritability, advance of percentage mean for traits in sunflower from two locations in Botswana

Traits	Mean	MSG	MSE	Vg	Vp	Ve	GCV%	PCV%	H ²	GAM
GC	18.4	13.146	7.5439	1.87	4.38	2.51	7.43	11.38	42.61	9.99
FPS	16.12	15.74	10.21	1.84	5.25	3.40	8.42	14.21	35.13	10.28
DF	70.99	66.17	11.87	18.10	22.06	3.96	5.99	6.62	82.06	11.18
DM	85.87	169.68	44.65	41.68	56.56	14.88	7.52	8.76	73.69	13.29
PH	191.6	2312.4	340.8	657.20	770.80	113.60	13.38	14.49	85.26	25.45
LN	33.45	51.2	15.27	11.98	17.07	5.09	10.35	12.35	70.18	17.85
GYHA	1378	205809	114771	30346.00	68603.00	38257.00	12.64	19.01	44.23	17.32
1000SW	75.54	287.45	80.72	68.91	95.82	26.91	10.99	12.96	71.92	19.20

Note. GC: Germination count; FPS: Final plant stand; DF: Days to maturity; PH: Plant height; LN: Leave number, GYHA: Grain yield per hectare; 1000SW: One thousand seed weight. MSG: mean square genotype; MSE; means square error.

4. Conclusions

Sunflower performs well in marginal areas and has a huge potential to be produced under the semi-arid environment of Botswana. Sunflower production offers a new cropping opportunity therefore, assessment of genetic variation, heritability, genetic advance of genotypes grown is critical for the development of a feasible breeding program. Generally, no phenotypic and genotypic coefficient variations of more than 20% were recorded, an indication of a challenge in direct selection of the selected traits. High heritability and GAM were recorded on PH (85.26%; 25.45%), an indication that this trait is governed by additive gene action while grain yield per hectare (GYHA) revealed moderate heritability coupled with moderate genetic advance of mean (44.23% and 17.32%). The study revealed higher genetic diversity among the sunflower genotypes. Grain yield variation ranged from 997 kg/ha for SUN310 to 1862 kg/ha for SUN322 with a relatively higher average weight of 1378 kg/ha. The twelve best performing genotypes with grain yields of more than 1500 kg/ha were identified, and this provides an opportunity for substantial increase in cultivation and sunflower production and an increased number of breeding lines to explore.

References

- Adeleke, S., & Babalola, O. O. (2020). Oilseed crop sunflower (*Helianthus annuus*) as a source of food: Nutritional and health benefits. *Food Science and Nutrition*, 8, 4666-4684. <https://doi.org/10.1002/fsn3.1783>
- Allard, R. W. (1960). *Principles of plant breeding*. John Wiley and sons, New York.

- Azania, A. A. P. M., Azania, C. A. M., Alves, P. L. C. A., Palaniraj, R., Kadian, H. S., Sati, S. C., ... Narwal, S. S. (2003). Allelopathic Plants, Sunflower (*Helianthus annuus* L.). *Allelopathy Journal*, 11(1), 1-20.
- Bareeleng, K., Molubi, A. T., Kgokong, B. S., Kgokong, K., Masukujane, M., Radikgomo, M., ... Molosiwa, O. (2024). Phenotypic Characterization of Citron Watermelon (*Citrullus lanatus* var. *citroides*) Genotypes for Bioenergy Production. *Journal of Agricultural Science*, 16(6), 1-8. <https://doi.org/10.5539/jas.v16n6p1>
- Carter, D. C., Harris, D., & Youngquist, J. B. (1992). Soil properties, crop water use and cereal yields in Botswana after additions of mulch and manure. *Field Crops Research*, 30, 97-100. [https://doi.org/10.1016/0378-4290\(92\)90059-I](https://doi.org/10.1016/0378-4290(92)90059-I)
- Castro, C., & Leites, R. M. V. B. C. (2018). Main aspects of sunflower production in Brazil. *OCL*, 25(1), 1-11. <https://doi.org/10.1051/ocl/2017056>
- Chabert, S., Senechal, C., Fourgeroux, A., Pousse, J., Richard, F., Nozieres, E., ... Vaissiere, E. (2020). Effect of environmental conditions and genotype on nectar secretions in sunflower (*Helianthus annuus* L.). *OCL*, 27(51), 1-12. <https://doi.org/10.1051/ocl/2020040>
- de Moraes Oliveira, V. R., de Arruda, A. M. V., Silva, L. N. S., de Souza Jr, J. B. F., de Queiroz, J. P. A. F., da Silva Melo, A., & Holanda, J. S. (2016). Sunflower meal as a nutritional and economically viable substitute for soybean meal in diets for free-range laying hens. *Animal Feed Science and Technology*, 220, 103-108. <https://doi.org/10.1016/j.anife edsci.2016.07.015>
- Debaeke, P., Casadebaig, P., Flénet, F., & Langlade, N. (2017). Sunflower crop and climate change: Vulnerability, adaptation, and mitigation potential from case-studies in Europe. *OCL Oilseeds and Fats Crops and Lipids*, 24(1), 15. <https://doi.org/10.1051/ocl/2016052>
- Directorate Marketing. (2021). *A Profile of the South African Sunflower Market Value Chain*. Department of Agriculture, Land Reform & Rural Development, Republic of South Africa. Retrieved from <http://webapps1.daff.gov.za/AmisAdmin/upload/Sunflower%20profile%202021.pdf>
- Divya, S., Kalaimagal, T., Manonmani, S., & Rajendran, L. (2019). Genetic analysis of variability, heritability and genetic advance in F3 populations of sunflower (*Helianthus annuus* L.), *Electronic Journal of Plant Breeding*, 10, 761-765. <https://doi.org/10.5958/0975-928X.2019.00100.5>
- FAOSTAT. (2022). Retrieved from https://www.fao.org/faostat/en/#rankings/countries_by_commodities
- Heiser, Jr. C. B. (1978). Taxonomy of *Helianthus* and origin of domesticated sunflower. In J. F. Carter (Ed.), *Sunflower Science and Technology* (Agronomy Monograph No. 19, pp. 31-53). Madison Wisconsin, USA: American Society of Agronomy. <https://doi.org/10.2134/agronmonogr19.c2>
- Hosni, T., Kourda, H. C., Medimagh, S., Youssef, N. O. B., Abbes, Z., Salah, H. B., & Kharrat, M. (2023). Agro-morphological variation and genetic diversity assessment of Tunisia sunflower (*Helianthus annuus* L.) accessions using microsatellites markers. *Journal of Animal Plant Science*, 33, 330-344. <https://doi.org/10.36899/JAPS.2023.2.0624>
- IBPGR (International Board for Plant Genetic Resources). (1985). *Sunflower descriptors* (p. 33). International Board for Plant Genetic Resources. Retrieved from <https://hdl.handle.net/10568/73432>
- Jocković, M., Prodanović, S., Jocić, S., Marinković, R., Jeromela, A. M., Jocković, B., & Čanak, P. (2019). Gene Effects and Combining Abilities for Oil Content in Sunflower. *Ratar. Povrt.*, 51(2), 106-109. <https://doi.org/10.5937/ratpov51-6464>
- Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47, 314-318. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Kalpana, K., Thirumeni, S., & Shashidhara, N. (2018). Genetic variability for yield and quality in rice (*Oryza sativa* L.). *International Journal of Agriculture, Environment and Biotechnology*, 1, 1-4. <https://doi.org/10.30954/0974-1712.06.2018.7>
- Lakshman, S. S., Chakraborty, R. N., Debnath, S., & Kant, A. (2021). Genetic variability, character association and divergence studies in sunflower (*Helianthus annuus* L.) for improvement in oil yield. *African Journal of Biological Sciences*, 3(1), 129-145. <https://doi.org/10.33472/AFJBS.3.1.2021.129-145>
- Law, J. L., Botha, F. W., Majaule, C. W., & Phalane, L. F. (2007). Symbiotic and genomic diversity of 'cowpea' bradyrhizobia from soils in Botswana and South Africa. *Biology Fertility of Soils*, 43, 653-663. <https://doi.org/10.1007/s00374-006-0145>

- Lentz, D. L., Pohl, M. E. D., Pope, K. O., & Wyatt, A. R. (2001). Prehistoric Sunflower Domestication in Mexico. *Economic Botany*, 55(3), 370-376. <https://doi.org/10.1007/BF02866560>
- Mandel, J. R., Nambeesan, S., Bowers, J. E., Marek, L. F., Ebert, D., Riseberg, L. H., ... Burkner, J. M. (2013). Association Mapping and the Genomic Consequences of Selection in Sunflower. *PLoS Genetics*, 9(3), e1003378. <https://doi.org/10.1371/journal.pgen.1003378>
- Moatshe, O. G., Emogor, V. E., Balole, T. V., & Tshwenyane, S. O. (2020). Genotype and Plant density effects on oil content and fatty acid composition of safflower. *African Crop Science Journal*, 28, 83-103. <https://doi.org/10.4314/acsj.v28i1.7S>
- Molosiwa, O. O., & Kgokong, S. B. (2018). Effect of planting date on tepary bean yield and yield components sown in Southern Botswana. *African Journal of Agricultural Research*, 13, 137-143. <https://doi.org/10.5897/AJAR217.12777>
- Mosupiemang, M., Bareeleng, K., Chiduwa, M. S., & Molosiwa, O. O. (2021). Stimulation of Soybean (*Glycine max*) Growth and Yield using *Bradyrhizobium* Inoculants in the Semi-arid Environment of Botswana. *Legume Research-An International Journal*, 44(10), 1186-1191. <https://doi.org/10.18805/LR-624>
- Neik, T. X., Siddique, K. H. M., Mayes, S., Edwards, D., Batley, J., Mabhaudi, T., ... Massawe, F. (2023). Diversifying agrifood systems to ensure global food security following the Russia-Ukraine crisis. *Frontiers in Sustainable Food Systems*, 7, 1-16. <https://doi.org/10.3389/fsufs.2023.1124640>
- Pilorge, E. (2020). Sunflower in the global vegetables oil system: situation, specificities, and perspectives. *OCL*, 27(34), 1-11. <https://doi.org/10.1051/ocl/2020028>
- Reddy, V. R. P., & Nadaf, H. L. (2014). Genetic Variability and Diversity studies in sunflower (*Helianthus annuus* L.). *Annal of Biology*, 30(2), 299-302
- Singh, R. K., & Chadhary, S. D. (1985). *Biometrical methods in quantitative genetic analysis*. Kalia publishers, New Delhi.
- Sivasubramanian, S., & Menon, M. (1973). Heterosis and in breeding depression in rice. *Madras Agricultural Journal*, 60, 1139-1140.
- Sree, G. S., Roja, V., Meena, H. P., Reddy, A. V., & Ramesh, D. (2021). Genetic variability, Heritability and genetic advance studies for economically important traits in sunflower (*Helianthus annuus* L.). *Journal of Oilseed Research*, 38(1), 92-95.
- Statistics Botswana. (2016). *Botswana Environment Statistics*. Retrieved May 15, 2025, from <https://www.statsbots.org.bw>
- Statistics Botswana. (2019). Retrieved from <https://www.statsbots.org.bw/annual-agricultural-survey-report-2019>
- Statistics Botswana. (2023). *Botswana Food Import*. Retrieved from <https://www.statsbots.org.bw/sites/default/files/FOOD%20IMPORTS%20MAY%202023%20FLYER.pdf>
- Sujatha, H. L., & Nandini, R. (2002). Genetic variability study in sunflower inbreeds. *Helia*, 25(37), 93-100. <https://doi.org/10.2298/HEL0237093S>
- Tola, M., Tesso, B., & Amsalu, B. (2023). Association of Yield and Yield-Related Traits under Moisture Stress in Common Bean Genotypes (*Phaseolus vulgaris* L.) at Melkassa and Miesso, Ethiopia. *Advances in Agriculture*, 2023, 1-9. <https://doi.org/10.1155/2023/8697497>
- Umarani, E., Saritha A., & Ramanjaneyulu, A. V. (2022). Estimation of Genetic parameters in Sunflower (*Helianthus annuus* L.) Germplasm Lines for Yield and its contributing Traits. *International Journal of Environment and Climate Change*, 12(12), 936-942. <https://doi.org/10.9734/IJECC/2022/v12i121533>
- Varshitha, V., Prabhavathi, K., Meena, H. P. & Yadav, P. (2023). Study of Genetic Variability for Yield and Quality Parameters in Newly Developed Sunflower (*Helianthus annuus* L.) Interspecific Derivatives Over Two Seasons. *International Journal of Environment and Climate Change*, 13(10), 3226-3234. <https://doi.org/10.9734/ijecc/2023/v13i102990>

Acknowledgments

Proudly thank the dedicated staff of NARDI Research Stations and the Oil Seed and Grain Legumes team. Special thanks go to Mr. Oduetse Chepete and Ms Tshepiso Maplanka for field experimentations. Finally, thank the Technical Support received from Dr. Charity K. Kruger for the development of the National Oil Crops

Strategy, which inspired this publication.

Authors Contributions

Dr. Molosiwa was responsible for conceptualization, supervision and writing, while Mr. Dinyao was responsible for field experimentation and data collection, while Ms. Ramokapane was responsible for field experimentation and supervision of the Oil Seed and Grain Legumes. All authors read and approved the final manuscript and authors contributed equally to the study.

Funding

The project was funded by the Ministry of Lands and Agriculture and National Agricultural Research and Development Institute (NARDI), and the publication was supported from the Commonwealth of Learning (COL), though the project C24-321 on ‘Collaborative action for the Attainment of Self-Sufficiency in oil seed crops production in Botswana. The authors contributed equally to this study.

Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Informed Consent

Obtained.

Ethics Approval

The Publication Ethics Committee of the Canadian Center of Science and Education.

The journal’s policies adhere to the Core Practices established by the Committee on Publication Ethics (COPE).

Provenance and Peer Review

Not commissioned; externally double-blind peer-reviewed.

Data Availability Statement

The data supporting this study’s findings are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

Data Sharing Statement

No additional data are available.

Open Access

This is an open-access article distributed under the terms and conditions of the Creative Commons Attribution license (<http://creativecommons.org/licenses/by/4.0/>).

Copyrights

Copyright for this article is retained by the author(s), with first publication rights granted to the journal.