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Growth, development and yield of safflower genotypes in response to environmental variations

Marang Mosupiemang¹, Vallantino E. Emongor¹, Goitseone Malambane^{1*}, Renameditswe Mapitse²

¹Department of Crop and Soil Sciences, Botswana University of Agriculture and Natural Resources, Private Bag 0027, Gaborone, Botswana, ²Department of Chemistry, University of Botswana, Private Bag UB 0022, Gaborone, Botswana

ABSTRACT

Safflower (*Carthamus tinctorius* L.) is a crop that is drought tolerant and grown in arid and semi-arid lands (ASALs) for its commercial utility as vegetable oil, animal feed, cut flower, leafy vegetable, pharmaceuticals, foods colorant, textile dye, cosmetics, and biofuel production. These important attributes make safflower an ideal crop to diversify the economy and improve the socioeconomic status of many smallholder farmers in ASALs. This study evaluated the growth, development, and yield of five safflower genotypes in three different locations in the southern part of Botswana under farmers' fields during winter and summer. The results showed that there was a significant ($P \leq 0.05$) genotypic variability for all phenological development (days to emergence, stem elongation, and flowering), plant growth (plant height and shoot biomass), the yield and yield components (number of branches/plant, number of capitula/plant and 1000-seed weight), oil content and oil yield. However, genotypes did not vary significantly ($P \geq 0.05$) in number of primary branches/plant. The results showed that winter planting significantly ($P \leq 0.05$) promoted safflower growth and yield than planting in summer. The growth, development, yield, and yield components of safflower genotypes varied across locations with Ramonaka being the most favorable. The GGE biplot revealed that genotype Kenya-9819 was found to be the most stable and adaptable with above-average yields. Sebele winter planting was the best representative environment and most suitable for discriminating genotype performance. The genotype by yield*trait combination (GYT) biplot revealed that genotypes ranked as Kenya9819 > Turkey > Sina > PI537636 > Gila. The results suggested that safflower was best planted in winter and that Kenya9819 was the best genotype to be planted in the greater Gaborone region.

KEYWORDS: Genotype-environment interaction, GGE biplot, Genotype by yield*trait combination (GYT) biplot, Safflower

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***Corresponding Author:**
Goitseone Malambane
E-mail: gmalambane@buan.ac.bw

INTRODUCTION

Safflower (*Carthamus tinctorius* L.) is the most drought and saline-tolerant crop as compared to other oilseed crops that are commonly grown in ASALs. It is highly esteemed for its commercial utility as vegetable oil, animal feed, cut flower, leafy vegetable, pharmaceuticals, food colorants, textile dye, cosmetics, and biofuel production (Janmohammadi, 2015; Emongor & Emongor, 2023). Safflower oil extracted from seeds is of high quality and is one of the most desirable vegetable oils because it contains the monounsaturated fatty acid oleic and polyunsaturated fatty acids α -linolenic and linoleic which cannot be biosynthesized by the human body hence, making them essential (Piccinin *et al.*, 2019; Nazir *et al.*, 2021). Although safflower is multipurpose and adaptable to various climatic conditions, the crop is underutilized and has

remained minor in terms of area of production (Ekin, 2005; Emongor, 2010). Therefore, to increase the area under safflower production, especially in new areas like Botswana that have not fully adopted this crop, more studies on genotype and environmental interactions are critical. Planting location has been identified as one of the important factors to be considered when selecting stable safflower genotypes. This is because Alivelu *et al.* (2015) found that planting location (environment) significantly affected safflower seed yield and contributed 51 % of the total ($G + E + GEI$) variation, while $G \times E$ interaction contributed 14.9 % of the total sum of squares. Similarly, Hamza and Abdalla (2015) and Hussein *et al.* (2018) demonstrated that safflower genotypes showed varied yield performance when planted at different locations. This highlights the need to select genotypes that are suitable for each location. Moreover, past studies have shown that the yield of safflower is significantly

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affected by the planting season with winter sowing being the most favourable and summer planting being the least favourable (Emongor *et al.*, 2017; Moatshe & Emongor, 2019). Other studies have reported that safflower does better when sown in autumn than in winter (Golzarfar *et al.*, 2012; Sampaio *et al.*, 2018). These discrepancies in past results prompt the need to conduct multi-environment/season and/or multi-location studies as they efficiently select the most stable, adaptable, and high-yielding genotypes. Thus, cultivars selected from one environment might not maintain their high performance in another environment due to the G×E interaction effect (Li *et al.*, 2017). This is because some genotypes are adapted to a broader range of environmental conditions, while others are more limited in their potential distribution and have specific adaptations (Mohammadi *et al.*, 2008). Therefore, this study evaluated safflower genotypes in two different seasons and three locations. This was done to select safflower genotypes that produce stable yields across the study sites of Botswana. Moreover, it has been difficult to select superior genotypes considering all studied traits, therefore, a genotype by yield*trait (GYT) biplot model suggested by Yan and Fréreau-Rei (2018) was employed to evaluate genotypes based on yield*traits combination.

MATERIALS AND METHODS

Experimental Conditions and Plant Materials

The study was conducted under on-farm conditions at three different locations (Sebele, Molepolole, and Ramonaka) in southern Botswana during the summer and winter of 2020/2021. The vegetation of these three sites is characterized as tree savanna and climate is characterized as hot semi-arid. The warmest month of the year in these sites is January and the coolest and driest month is July. These locations experience the most rainfall in summer, which commonly starts in late October and continues to April. Rainfall in this region is limited and highly erratic. Soil sampling was done as per Soil and Plant Analytical Laboratory, Department of Agricultural Research, Botswana, where the soil was sampled from five different spots in each field/farm using a zigzag pattern, and subsamples were mixed to make a composite sample. The soil was air dried and sieved with a 2 mm mesh sieve. Soil analysis was done for pH, EC, CEC, P, K, Ca, Na, Mg, texture, and organic carbon using the standard procedures (Table 1). Calcium nitrate fertilizer was side dressed at a rate of 120 kg/ha two weeks after emergence. The experiment design in each site was a randomized complete block with three replications. The treatments in each site were five safflower genotypes (Gila, Sina, Turkey, PI537636, and Kenya9819). Two plantings were done (winter and summer of the 2020/2021 season). The experimental sites were disc ploughed using a tractor to have a smooth planting bed. Two seeds were sown per hill and three weeks after emergence plants were thinned to one plant per hill. Planting was done at an inter-row spacing of 40 cm and intra-row spacing of 25 cm to maintain a population of 100000 plants/ha as recommended by Moatshe *et al.* (2016). Each sub-plot was 3 x 5 m. Plants were mainly rainfed and supplementary irrigation was only

Table 1: Soil chemical and physical characteristics of the three experimental sites

Soil characteristic	Sebele	Molepolole	Ramonaka
pH (CaCl ₂)	5.38	4.99	5.88
EC (µs/cm)	35.8	73.7	120.4
CEC (meq/100g)	4.0	4.6	14.0
Organic carbon (%)	0.1	0.23	0.30
Textural class	Sandy loam	Sandy clay loam	Clay loam
Sand (%)	78.3	65.6	39.2
Silt (%)	9.7	7.8	31.4
Clay (%)	12	26.6	29.4
Total N (%)	0.03	0.05	0.10
Available P (ppm)	12.08	45.3	52.8
Exchangeable K (cmol/kg)	0.11	0.21	0.29
Exchangeable Ca (cmol/kg)	1.23	2.22	4.42
Exchangeable Mg (cmol/kg)	1.02	2.00	4.1
Exchangeable Na (cmol/kg)	0.30	0.28	0.38

provided in periods of prolonged dry spells where no rainfall was received after 14 days. Weeds were controlled manually by hoeing between the rows and plants.

Data Collection

Days to emergence were recorded when 80% of the plants in a plot had emerged while days to onset of stem elongation, and flowering were recorded as the number of days from seed sowing. Primary branches per plant (a total number of branches originating from the core stem) were counted at physiological maturity. Plant height was measured from the ground level to the apex of the main stem at physiological maturity. Shoot biomass were determined at 50% flowering by harvesting and oven drying the shoots at 70 °C for 72 hours. The number of capitula per plant was recorded on ten plants randomly selected from the inner rows of each plot at physiological maturity. For seed yield and thousand seed weight, the plants were harvested in an area of 9 m² in the center of each experimental plot. Seeds were threshed and weighed to determine seed yield. One thousand seeds were counted using a seed counter (Contador, Pfeuffer GmbH, Germany) and weighed using a digital balance to determine the 1000-seed weight. Oil content was determined using the soxhlet n-hexane extraction method (Wrolstad *et al.*, 2005). Approximately 15 g of safflower seeds were grounded using Polymix (Analysenmuhle A10 model, Kinematica, Switzerland). Then exactly 5 g of crushed safflower seed was weighed and inserted into a soxhlet extractor connected to a round bottom flask containing 150 mL of n-hexane. The extraction was conducted as the solvent was heated up to a boiling temperature around of 70 °C for six hours. After extraction, the solvent was evaporated using a rotary evaporator. The final weight of the oil was determined by weighing and expressed as a percentage of oil content.

$$\text{Oil content (\%)} = \frac{\text{weight of oil extracted}}{\text{weight of seed sample}} \times 100$$

Oil yield (kg/ha) was calculated by multiplying seed oil content by seed yield.

Data Analysis

The GGE biplots were executed using GGE biplot software version 4.1. Data were analyzed as a 2 x 3 x 5 factorial experiment to study the seasons (2), locations (3), safflower genotypes (5), and their interactions. Measured variables were analysed by three-way analysis of variance (ANOVA) using R-Software version 4.2.2 and the agricolae package version 1.3-5. Treatment means and interaction effects were compared using Fisher's least significant difference (LSD) procedure at a significance level of 5%. To select the most adaptable and high-yielding genotype, seed yield data was graphically analysed using a genotype main effect and genotype environment interaction (GGE) biplot based on the principal component analysis (PCA) of environment data (Yan & Tinker, 2006). The genotype by yield*trait (GYT) biplot was generated by the combination of each trait and grain yield as developed by Yan and Fréreau-Reid (2018). Each trait was multiplied with grain yield. The GGE and GYT biplot analyses were executed on R-Software version 4.2.2 using the METAN package of Olivoto and Lúcio (2020).

RESULTS

Soil and Climate

The soils of the three planting locations varied from textural to their mineral composition with Sebele recording the lowest NPK as compared to the other two locations. Ramonaka which had a clay loam textural soil type recorded the highest chemical properties examined (Table 1). The average temperature for the summer planting season was 24 °C and for winter was 17 °C, but July (mean average temperature of 11.9 °C) was the coldest month and plants grew slowly due to low air temperature and some suffered chilling injury (Figure 1).

Effect of Genotype, Planting Location, Planting Season, and their Interactions on the Phenological Development and Growth of Safflower

Results of the combined analysis of variance for yield-related parameters showed significant differences among the two seasons for all the studied traits (Table 2). Winter planting significantly

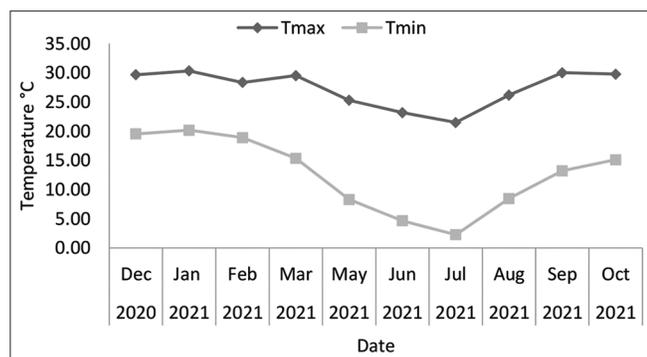


Figure 1: Average monthly temperature for the summer and winter growing season (Data extracted from the Department of Meteorological Services, Village, Gaborone)

prolonged the phenological development of safflower genotypes (number of days to emergence, elongation, and flowering), while summer planting shortened the developmental stages (Figures 2-4). The three-way interaction of season, location, and genotype showed a significant effect on days to elongation and flowering as crops planted at Ramonaka reached elongation and flowering earlier in summer and late in winter as compared to those at Sebele and Molepolole (Figures 3 & 4). Genotypes Sina and PI537636 were consistently the earliest to emerge, elongate, and flower independent of season and location.

Seasonal effect on crops had a highly significant influence on growth parameters studied, even though winter planting had a prolonged development, the final observation on growth (plant height and shoot biomass) showed higher values compared with the summer planted crops (Table 2). The interaction effect on planting season and planting location showed that plants grown in summer accumulated a similar shoot biomass, and plant height across all study locations and genotypes (Figures 5a & b). In contrast, winter planting at Ramonaka resulted in increased accumulation of shoot biomass and plant height than at other locations (Figure 5).

Effect of Genotype, Planting Location, Planting Season and their Interactions on the Yield and Yield Components of Safflower

Planting season, planting location, and genotype all had a significant effect on the yield and yield components of safflower (Table 3). The number of primary branches was similar across all the studied genotypes. An average of season and location showed that the genotype Kenya9819 exhibited the highest values of seed yield (2265.22 kg/ha) while genotype Gila consistently had the highest oil content independent of season, location (Figures 6c and 8). Safflower planted in Sebele during summer had the highest number of primary branches, seed yield/ha, and capitula number per plant (Figure 6). In winter, safflower planted at Ramonaka produced the highest number of primary branches, seed yield/ha, oil yield, and a number of

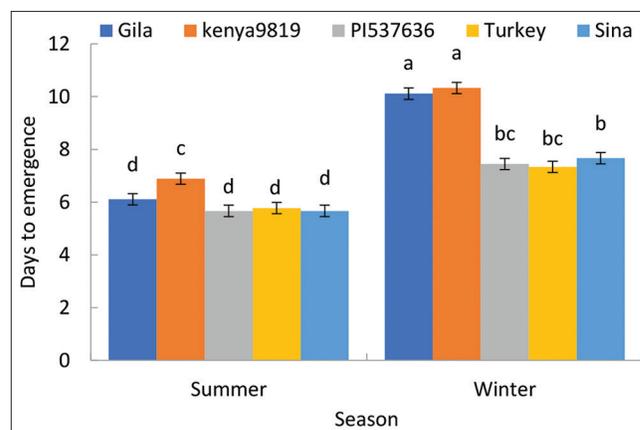


Figure 2: Interaction effect of season genotype on the days to emergence. Means followed by dissimilar letters are significant at $P \leq 0.05$ according to Fisher LSD. Error bars represents standard error of LSMEAN

Table 2: ANOVA summary table for the phenological stages of safflower

Treatment effects	Days to emergence	Days to Elongation	Days to flowering	Plant height	Shoot biomass
Season	347.4***	7078.9***	17595.9***	247.3***	178.7***
Location	12.2***	2.6ns	71.0***	32.4***	29.0***
Genotype	42.5***	16.9***	32.56***	46.0***	1.3ns
Season x location	66.0***	72.1***	187.6***	35.5***	19.5***
Season x genotype	13.1***	0.9ns	1.58ns	9.6***	1.9ns
Location x genotype	1.0ns	1.3ns	1.92ns	1.0ns	2.0ns
Season x location x genotype	1.8ns	2.8**	2.46*	1.8ns	2.9**

*:P≤0.05; **:P≤0.01; ***:P≤0.001. ns=not significant. Values in the columns represent the F-values

Table 3: ANOVA summary table for the yield, yield components, and oil content of safflower

Treatments	No of primary branches	No of capitula/plant	1000-seed weight	Seed yield/ha	Oil content	Oil yield
Season	9.2**	7.5**	95.3***	18.4***	119.6***	30.1***
Location	23.2***	26.7***	17.0***	11.2***	48.3***	7.8***
Genotype	1.45ns	3.4*	105.9***	0.91ns	143.3***	2.0ns
Season x location	24.5***	27.2***	39.0***	30.97***	60.7***	38.5***
Season x genotype	2.2ns	2.4ns	4.4**	0.70ns	2.1ns	0.9ns
Location x genotype	0.22ns	1.0ns	3.2**	0.96ns	3.3**	0.97ns
Season x location x genotype	1.2ns	0.8ns	2.4*	0.8ns	3.0**	0.6ns

*:P≤0.05; **:P≤0.01; ***:P≤0.001. ns=not significant. Values in the columns represent the F-values

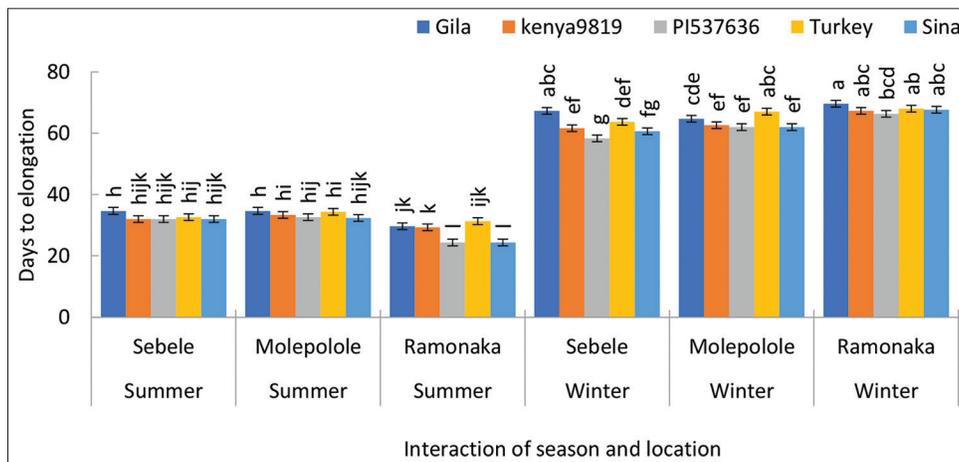


Figure 3: Interaction effect of season × location × genotype days to elongation. Means followed by dissimilar letters are significant at P ≤ 0.05 according to Fisher LSD. Error bars represents standard error of LSMEAN

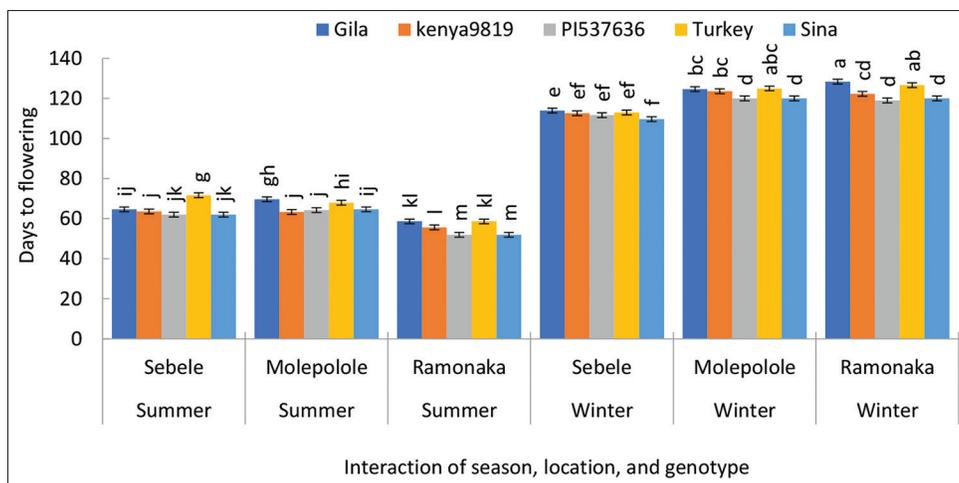


Figure 4: Interaction effect of season × location × genotype on the days to flowering. Means followed by dissimilar letters are significant at P ≤ 0.05 according to Fisher LSD. Error bars represents standard error of LSMEAN

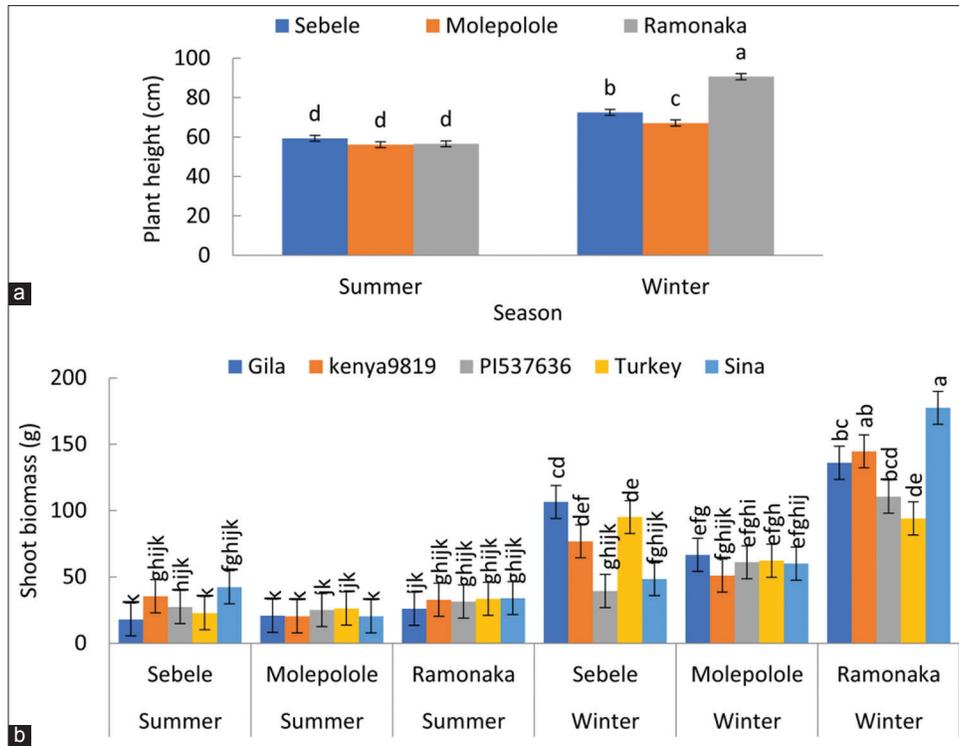


Figure 5: Interaction effect of (a) season × location on plant height and (b) season × location × genotype on the shoot biomass. Means followed by dissimilar letters are significant at $P \leq 0.05$ according to Fisher LSD. Error bars represents standard error of LSMEAN

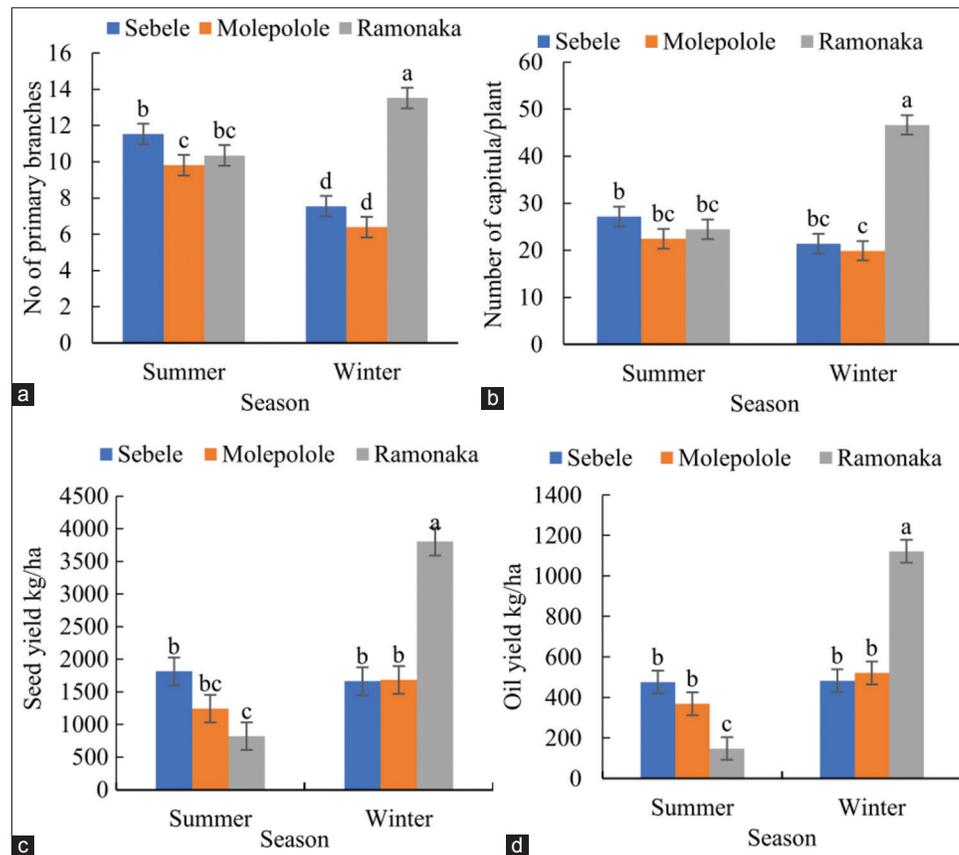


Figure 6: Interaction of planting season × location on the a) number of primary branches/plant, b) number of capitula/plant, c) seed yield kg/ha, and d) oil yield kg/ha. Means followed by dissimilar letters are significant at $P \leq 0.05$ according to Fisher LSD. Error bars represents standard error of LSMEAN

capitula/plant (Figure 6). The season by location (LxS) revealed a highly significant interaction for all the traits (Table 3). The influence of location on genotype (LxG) showed no effect on all the studied traits except for 1000-seed weight, oil content and oil yield and this suggested that the genotypes were stable across the studied locations (Figures 7 & 8). The interaction between season by location by genotype (SxLxG) had no influence on all yield-related parameters except for the 1000-seed weight and oil content (Table 3).

Genotype by Environment Interaction of Safflower Seed Yield

The G×E interactions for seed yield kg/ha were determined through the combined seasons GGE biplot analysis. In this study, a test environment refers to year and location combination. The biplots examined 94.17% of the total variation (PC1 and PC2) of the environment-centered G×E table. The arrowed line is the average environment coordinate (AEC) abscissa points to higher mean yield across environments. The genotypes located on the right of the line cutting the axis, representing the mean seed yield according to the mean center of coordinates, yielded higher seed yield than the mean. While the genotypes on the left yielded lower seed yield than the average. The results showed

that Kenya9819 and Turkey were the highest-yielding genotypes while Sina, PI537636, and Gila were poor yielding genotypes (Figures 9a & b) as shown by their projections onto the average environment coordination (AEA) axis. The genotypes Sina and Gila had greater instability as they had the longest vector of the genotypes on either side of AEA (Figures 9a & b). While the genotypes Kenya9819 and Turkey had greater yield stability followed by PI537636 though low yielding (Figures 9a & b). According to Yan and Tinker (2006), a polygon is drawn on genotypes that are farthest from the biplot origin so that all other genotypes are confined within the polygon. The equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex. The which-won-where polygon view revealed that the test environments (Sebele and Molepolole) fell within one sector of the four sectors (Figure 9b). Genotypes Gila and PI537636 each fell within a sector that did not have any environment. On the other hand, genotypes Kenya9819 and Turkey fell within a sector that had two environments (Sebele and Molepolole) suggesting that these genotypes were high yielding at those locations although Kenya9819 was the winner genotype because it fell at the vertex of that sector (Figure 9b). Genotype Sina fell within a sector that had Ramonaka suggesting that it was a winner genotype at Ramonaka (Figure 9b). The length of the location (environment)

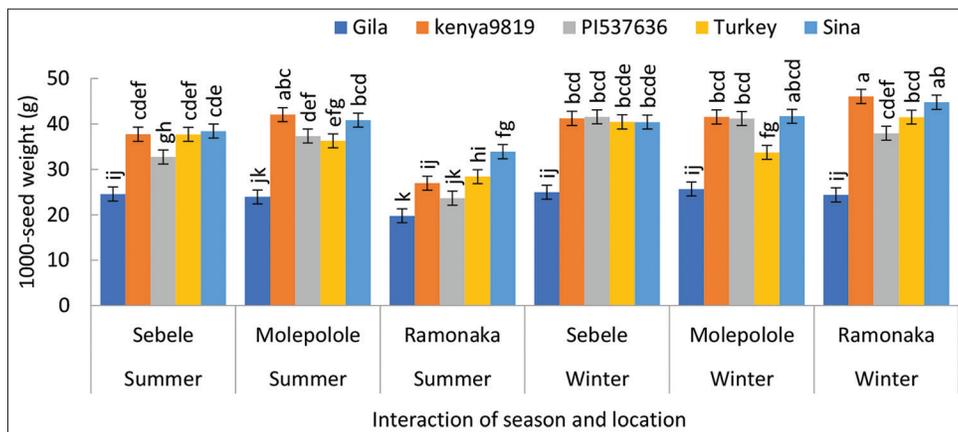


Figure 7: Interaction effect of season × location × genotype on 1000-seed weight. Means followed by dissimilar letters are significant at $P \leq 0.05$ according to Fisher LSD. Error bars represents standard error of LSMEAN

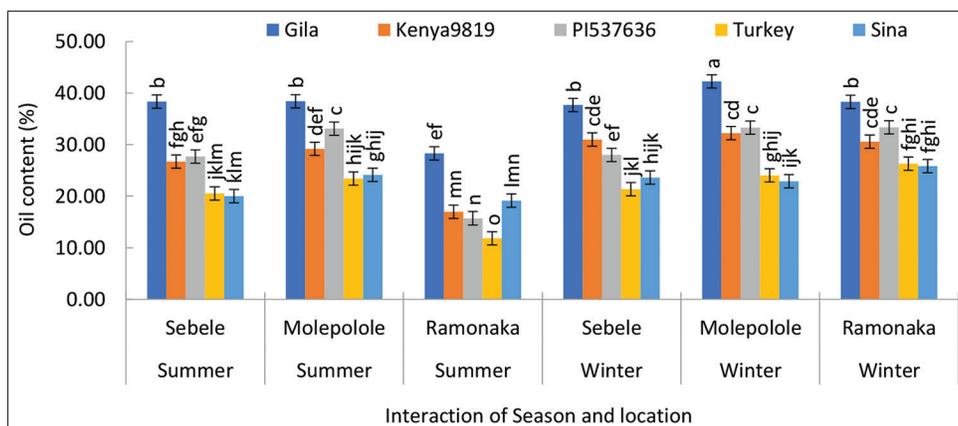


Figure 8: Interaction effect of season × location × genotype on the oil content. Means followed by dissimilar letters are significant at $P \leq 0.05$ according to Fisher LSD. Error bars represents standard error of LSMEAN

vector from the biplot origin, shows the discriminative ability of the location. Figure 10a shows that Ramonaka and Sebele had the longest vector from the biplot origin hence the most discriminative. Molepolole had the shortest vector closer to the biplot origin hence least discriminative. The representativeness of location is determined by the closeness of its angle with AEC, with smaller angle between location vector and the AEC indicating that the test location is more representative of other test environments (Yan & Tinker, 2006). The representativeness analysis revealed that Sebele had a smallest angle with the AEA, hence, it is more representative of the other test environments followed by Ramonaka while Molepolole was the least representative (Figure 10b).

The yield*trait biplot was based on the fact that yield is the most important trait while all other target traits are only important when combined with high yield (Yan & Frégeau-Reid, 2018). In the GYT biplot below (Figures 11a & b) yield was not included because it was already integrated into each of the yield-trait combinations. This biplot presents data from

three locations replicated in winter and summer. The cosine of the angle between the vectors of two traits approximates the Pearson correlation between them. Therefore, an angle below 90° denotes a positive correlation, an angle above 90° denotes a negative correlation, and an angle of 90° denotes zero correlation. Figure 11a depicts that most of the studied yield-trait combinations correlated positively with each other as shown by the acute angle between the vectors. Yield*oil content was positively correlated with yield*all phenological traits, yield*capitula diameter, yield*capitula weight, and yield*oil yield while it negatively correlated with the rest of the traits (Figure 11a).

Further, an acute angle denotes that the genotype is above-average for the trait while an obtuse angle denotes that the genotype is below-average for the trait; and a right angle denotes that the genotype is average for the trait (Yan & Frégeau-Reid, 2018). Figure 11a shows that genotype Kenya9819 had an acute angle with all the studied yield*traits indicating that it is above average for all traits. As for genotype Turkey an acute

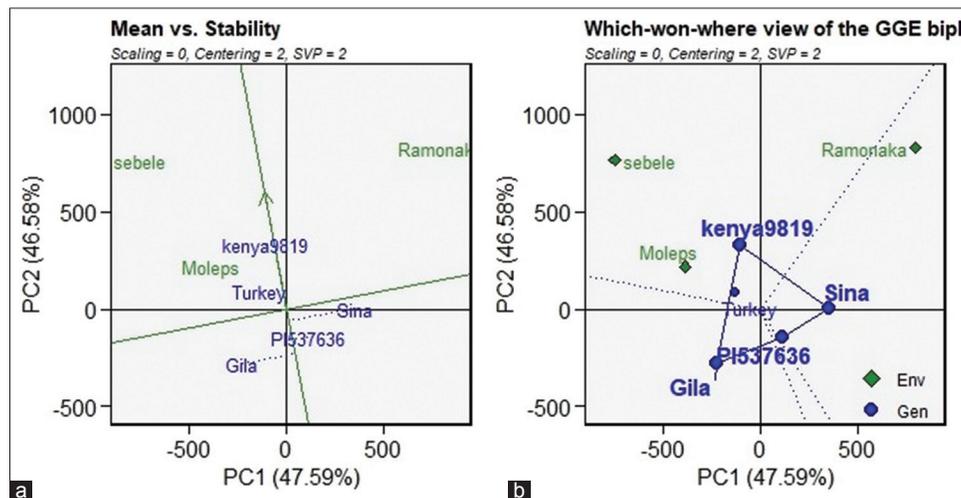


Figure 9: The vector view of GGE biplot showing the a) mean vs stability and b) which-won-where view of the GGE biplot

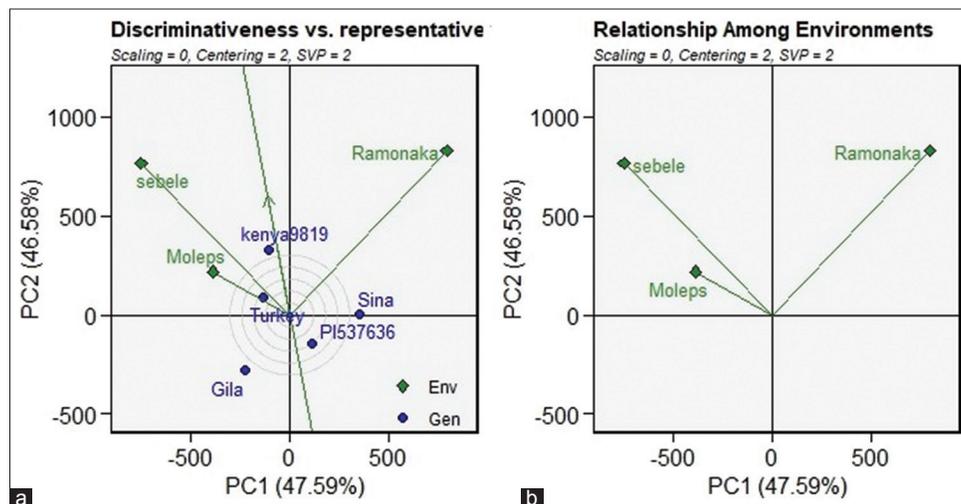


Figure 10: The vector view of GGE biplot showing the a) discriminative versus representativeness and b) relationship among test environments

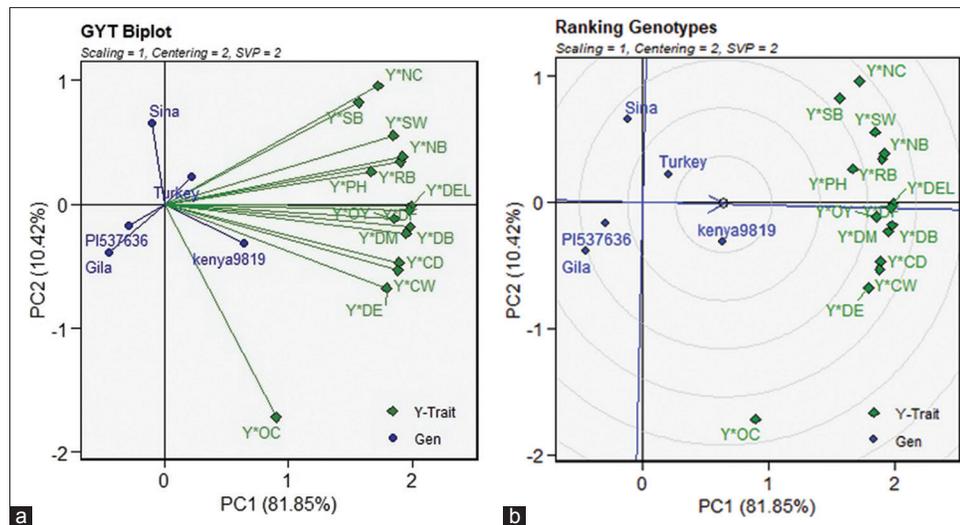


Figure 11: The tester coordination view of the (a) yield*trait (GYT) biplot showing correlations among yield-trait combinations and (b) ranking of genotypes. Seed yield kg/ha (Y), 1000-seed weight (SW), oil content (OC), oil yield (OY), number of primary branches/plant (NB), number of capitula/plant (NC), capitula diameter (CD), capitula weight (CW), plant height (PH), shoot biomass (SB), root biomass (RB), days to emergence (DE), days to elongation (DEL), days to branching (DB), days to flowering (DF), and days to maturity (DM)

angle was observed in relation to all the yield*traits except for yield*oil content indicating that it is above average for most of the studied traits (Figure 11a). Inversely, genotypes Gila and PI537636 had an obtuse angle with all yield*trait combinations indicating that they were below-average for all traits except for yield*oil content which was above-average (Figure 11a). An ideal genotype was denoted by a small circle with an arrow pointing to it and had both the highest mean yield*trait combination and is overall superior. Therefore, when ranking genotypes in terms of overall superiority based on the yield*trait combinations, genotype Kenya9819 was found to be an ideal genotype followed by Turkey then Sina and PI537636 while genotype Gila was the least desirable (Figure 11b).

DISCUSSION

Environmental variations played a significant role in the growth and development of safflower genotypes. Winter planting of safflower delayed seedling emergence while summer planting sped the process. Torabi *et al.* (2015) found that there was a significant and negative correlation between days to emergence and temperature in safflower with 22 °C being optimal. The temperatures for the winter and summer safflower planting in the current study averaged 17.33 °C and 23.97 °C, respectively. The winter temperature averages in the current study were below the optimal germination temperatures as reported by Torabi *et al.* (2015). A similar genotypic variation in response to a number of days to emergence has been reported (Moatshe & Emongor, 2019).

The interaction of planting location and season showed that safflower planted during winter at Molepolole and Sebele reached the elongation stage earlier (July) than those at Ramonaka (August). Since July was the coldest month, they incurred chilling injuries. However, plants at Ramonaka during winter were able to tolerate chilling injuries because they

were still at the rosette stage during the coldest period (July). According to Koc (2019), a longer rosette habit provides an advantage of avoiding winter chilling injury, thereby preventing plants from being damaged by low temperatures in winter. In summer, plants flowered earlier compared to winter. The seasonal differences in the flowering time of safflower in the current study were partly caused by variations in temperature, photoperiod, and the anatomy of genotypes. Torabi *et al.* (2020) reported that the flowering period in safflower was quickened by high temperatures and longer days. According to Daba *et al.* (2016), flowering time was delayed when plants were exposed to short day lengths during the photoperiod-sensitive phase.

There was a significant season by location by genotype interaction for shoot biomass at flowering. This implied that the plant growth was substantially influenced by the genotype by environment interaction effect. Planting season on the other hand had a significant effect on the vegetative growth of safflower as observed by Moatshe *et al.* (2016). Naseri (2011) reported that the greater plant height of winter planted safflower was due to low temperatures and better moisture regimes which resulted in vegetative growth being slower and longer.

The results of this study showed a significant genotypic variation among the genotypes for yield and yield components. Gila had the lowest 1000-seed weight across all the environments; its seeds were distinctively brownish in color with a very thin hull while other genotypes had white seeds with a thick hull. The presence of genetic variability in yield components of the genotypes in the current study suggested the need to select the most promising ones for increased yield. Genotypic variations in yield and yield components of safflower have been reported (Beyavvas *et al.*, 2011; Ahmad *et al.*, 2016; Moatshe *et al.*, 2016; Emongor *et al.*, 2017). The results of current study found a significant genotypic variation in seed yield/ha with genotype Kenya9819 showing the highest seed yield due to 1000-seed weight. This

agrees with the findings reported elsewhere (Ahmad *et al.*, 2016; Koc, 2021). Oil content was substantially higher in winter than summer. Emongor and Emongor (2023) highlighted that reduced oil content in summer-grown safflower is attributed to contracted phenological stages. Furthermore, the fact that genotype Gila was able to produce high oil content irrespective of the location and season showed that this genotype is very adaptable as compared to other genotypes concerning this trait. Mosupiemang *et al.* (2022) found that the genotype Gila had the highest oleosin gene expression and a smaller oil body diameter which are characteristics of a high oil-producing genotype. Oil yield followed a similar trend with oil content and seed yield/ha because oil yield is a product of oil content and seed yield/ha. Therefore, oil yield was influenced by all factors that influenced seed yield/ha and oil content.

Safflower is traditionally a spring sown crop, but spring or winter sowing is possible in regions with mild winters (Johnson *et al.*, 2012). The current study has identified winter planting as the ideal season for increased yield and yield components in Botswana. Similar findings were obtained by Moatshe *et al.* (2016) and Emongor *et al.* (2017). This is because winter planting favors the production of more biomass due to the longer growth period of safflower. According to Chehade *et al.* (2022) and Koutroubas *et al.* (2004), when more dry matter is produced by the time of flowering, it leads to its translocation into the seed during the grain filling period and hence greater seed yield. The findings of the current study demonstrated that planting safflower in different locations played a significant role in the yield and yield components of safflower. Similarly, Hamza and Abdalla (2015) found that locations had a significant effect on the yield traits of safflower. They postulated that variations among locations such as soil differences may affect yield traits. The interaction of season and location significantly affected the yield and yield components in the current study. For instance, winter planted safflower at Ramonaka produced the highest seed yield because of higher growth and a number of capitula, while summer planted safflower at Ramonaka had significantly lower seed yield. This might be due to the excessive rainfall which was experienced at the site during the grain filling stage in summer. Furthermore, Ramonaka soils were clay loam which is more susceptible to waterlogging (Table 1). According to GRDC (2010), excessive rain during flowering can reduce yield by inhibiting pollination, and discoloring seed, promoting diseases either or causing ripe seeds to sprout in the heads.

The GGE biplots identified Kenya9819 as the highest-yielding and Gila as the poor-yielding genotypes. Furthermore, stability analysis showed that Sina and Gila had greater yield instability while Kenya9819, Turkey, and PI537636 had greater yield stability. This suggested that the relative performance of Kenya9819, Turkey, and PI537636 was consistent across the environments. Sebele had high representativeness and discriminative ability hence considered an ideal location for selecting genotypes adapted to the whole region.

The results of the biplot revealed that most of the studied yield-trait combinations positively correlated with each other mostly because they have the yield component. Similar findings

were reported in literature (Karahana & Akgün, 2020; Kendal, 2020; Gholizadeh *et al.*, 2023). Overall, genotypes Turkey and Kenya9819 were ranked as superior because they had above-average yield*trait combinations. This is in accordance with the hypothesis by Yan and Frégeau-Reid (2018) which states that the superiority of a genotype should be judged by its levels of combining yield with other desired traits, instead of its levels in individual traits. This is because the selection of genotypes based on the seed yield only without considering other traits of interest may be misleading (Takele *et al.*, 2022). In contrast, genotype Gila ranked last in terms of overall superiority. This means that this genotype cannot be used as multi-trait genotype rather it can be used for breeding of specific individual traits like oil content. The GYT method has not been appraised in safflower genotype selection but it can be a novel approach for selecting genotypes not only based on one trait but a combination of yield with other traits. Thus, in selection of desirable genotypes, the combined effects of yield-trait are highly significant than the effects of individual traits (Kendal, 2020).

CONCLUSION

Generally, in winter the phenological stages were prolonged as compared with summer. This resulted in increased plant growth yield, yield components, and oil content depending on the genotype and location. The major source of variation among the seasons was temperature and day length. The biplots identified Kenya9819 and Gila as the highest-yielding and poor-yielding genotypes respectively. Stability analysis showed that Kenya9819, Turkey, and PI537636 had greater yield stability while Gila and Sina were the least stable. Sebele was the most representative and discriminative of all test environments hence, the ideal environment for selecting genotypes adaptable in all three locations. The yield*trait combination biplot showed that genotypes Kenya9819 and Turkey had above average values of yield*trait combinations followed by Sina, while PI537636 and Gila had below-average values. Hence, genotypes Kenya9819 is recommended to be planted in the southern region of Botswana because of its overall superiority.

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