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Morphological characterization and agronomic traits of some lupine genotypes

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ABSTRACT

A two-year study was conducted at Giza Research Station, Agricultural Research Center (ARC), Giza, Egypt during 2020/2021 and 2021/2022 seasons to evaluate the yield potential of twenty five lupine genotypes and identify their morphological traits compared with cultivar Giza 1. Twenty six genotypes (75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9 and Giza 1) were distributed in a randomized complete blocks design in three replications. Sixteen morphological traits were described using UPOV (The International Union for the Protection of New Varieties of Plant) Guidelines. The morphological characterization indicated that the short or medium growth habits of genotypes at the flower bud stage were absent, and very tall genotypes at the green repining stage were not observed. Also, violet, pink, light yellow, and dark yellow flower wings, as well as late or very late maturing genotypes were absent. Moreover, stem anthocyanin coloration and the leaf green color at the flower bud stage, as well as the density of seed ornamentation were observed in all genotypes. The combined analysis of variance showed that lupine genotypes differed significantly for all the studied traits. Meanwhile, seasonal effects and their interactions were not significant for all the studied traits. Genotypes Qous 5 and P 20950 had a higher numbers of branches and pods per plant. Meanwhile, genotypes Qous 3 and Qous 5 had a higher number of seeds per plant and 100-seed weight. GT-biplot analysis revealed that Qous 4, Belbais 9, Family 2, P 20950, Qous 5, Qous 3 and Qous 1 are considered the most desirable genotypes for yield traits. In addition to, cluster (C) that contains nine genotypes (Family 2, Qous 5, Family 4, Edfo, Isna 6, Isna 2, Belbais 9, Qous 4 and Giza 1) surpassed the other genotypes in seed yield per plant. Concerning on high-yielding genotypes per unit area, Qous 3 and Qous 5 can be promising genotypes for selection criteria to increase lupine productivity. On the basis of previous information and relationships identified, genotypes Qous 4, Belbais 9, Family 2 and Qous 5 can be distinguished for lupine development and preparation future breeding programs in Egypt.

Keywords: Lupine genotypes, Morphological characterization , Seed yield, GT-biplot analysis, Cluster analysis

INTRODUCTION

The Egyptian government have been implemented the requirements of the actual convention according to UPOV's regulations and laws. Hence, Egypt has become a member of the International Convention for the Protection of New Varieties of Plants (UPOV) since 2019, according to UPOV (2022). Breeding programs require a specified characterization of some lupine (*Lupinus albus* L.) genotypes to choose suitable selection criteria for producing a high yielding variety. *Lupinus albus* consider a historical food legume that has been spread around the different Mediterranean areas for thousands of years (Cowling *et al*., 1998). It is known that lupines have good adaptation over different region in Egypt. The nutritional quality of the lupines seed can be similar to soybean seeds which contain over 20% fat rich in unsaturated fatty acids as reported by Gulewicz *et al*. (2014). However, there are few breeding efforts on this plant despite genetic variability among several genotypes of lupines (Noffsinger *et al*., 2000). Lupine cultivated area reached about 160 fad in 2020 with an average yield of 6 ardab per fad (Bulletin of Statistical Cost Production and Net Return, 2021). According to Hamman *et al*. (1987), most germplasm of white lupine until about 1986 were old low-yielding landraces in Egypt, although lupine represents a rich protein source for humans and livestock in different regions of the world (Kohajdova *et al*., 2011). A study carried out by Mahfouze *et al*. (2018), recommended six genotypes of lupines that can be useful in white lupine breeding programs. In this context, Khalifa *et al*. (2020) revealed that Giza 2 surpassed Giza 1 for most yield attributes of lupine in the first and second seasons. In another study, Alemu *et al*. (2019) showed that the boregine variety gave the highest number of seeds per pod and seed yield per ha, meanwhile, Bora and Sanabor varieties recorded the greatest number of branches per plant and the tallest plants, respectively. Meanwhile, there was a wide variation among seasons of different lupine genotypes in the number of pods and seeds per plant, as well as seed yield per plant, seed index, and seed yield per unit area (Abo-Hegazy *et al*., 2020).

White lupine germplasm collections were identified not only through agronomic but also morphological traits (Buirchell and Cowling, 1998 and Cowling *et al*., 1998). It is known that the morphological description is considered a precondition for the protection and registration of varieties (UPOV 2002). Practically, Andres et al. (2007) reported that there is a major genetic pool in lupines sp. through different agronomical and morphological traits. Hence, the genotype by trait (GT) biplot, as a graphical application of the GGE biplot technique, was used for exploring multiple trait data in this study. According to Yan and Rajcan, (2002), it gives the conception of the associations among traits across the genotypes. Also, it has been utilized to study trait relations and genotype evaluation in different crops including lupine (Rubio *et al*., 2004). In addition, Arab *et al*. (2014) reported that the biplot showed pod length and maturity date are valuable to identify lupine genotypes. In another study, EL-Harty *et al*. (2016) showed that the Egyptian landraces Fayed 1, and Sohag 2, as well as the cultivar Giza 1 gave the highest seed yield per ha compared with the other genotypes of lupines. They added that pod number, as well as seed yield either per plant or per ha, have been grouped on the positive PC1 axis of the biplot with genotypes Fayed 1, 75B9.10, and Sohag 2. Therefore, the objective of this study was to evaluate the yield potential of twenty-five lupine genotypes and identify their morphological traits compared with cultivar Giza 1.

MATERIALS AND METHODS

A two-year study was carried out at Giza Research Station, Giza government (Lat. 30°00'30" N, Long. 31°12'43" E, 26 m a.s.l), Agricultural Research Center (ARC) during the 2020/2021 and 2021/2022 winter seasons to evaluate the yield potential of twenty five lupine genotypes and identify their morphological traits compared with cultivar Giza 1. The common names and origin of the tested genotypes are shown in Table (1).

Furrow irrigation was the prevalent system in the region. Maize was the preceding summer crop in both seasons. Calcium super phosphate (15.5% P_2O_5) at the rate of 150 kg per fad was applied during soil preparation in the two summer seasons. Thereafter, the lupine genotypes were seeded at density 20 plants per m in one row of the ridge. Lupine seeds were sown on 22nd and 29th November at 2020 and 2021 seasons, respectively. Mineral N fertilizer was added at a rate of 45 kg N per fad (3 equal doses) as ammonium nitrate (33.5% N) before the first, second and third water irrigation, respectively. Normal recommended cultural practices for growing lupines genotypes were used. A randomized complete blocks design with three replications was used. The area of the plot was 10.8 m^2 with each plot consisting of six ridges and each ridge was 3.0 m in length and 0.6 m in width.

The studied traits:

A) Morphological traits:

The identification of the following morphological traits was conducted using the procedures of UPOV (The International Union for the Protection of New Varieties of Plant). The morphological traits were evaluated in Seed Technology Research Department laboratories belonging to Field Crops Research Institute, ARC. These traits namely plant height at three weeks from seedling, plant growth habit at flower bud stage, plant height at beginning of flowering, plant height at green ripening stage, color of flower wings, time of beginning of flowering, stem anthocyanin coloration at flower bud stage, leaf green color at flower bud stage, central leaflet length, central leaflet width, time of green ripening, pod length, color of seed ornamentation, distribution of seed ornamentation, density of seed ornamentation (excluding genotypes with eyebrow only),and 100-seed weight (harvested seed). The decimal code for the growth stage of legume according to Tottman (1987) was also used to standardize the growth stages of varieties during morphological description and identification.

Table 1. The common names and origin of the tested genotypes

Genotypes	Origin	Genotypes	Origin
75 B 15.17	Australia	Sakolta	FCRI, ARC, Egypt
75 B 9.15	Australia	Qena	FCRI, ARC, Egypt
P 20950	Australia	Edfo	FCRI, ARC, Egypt
Family 2	FCRI, ARC, Egypt	Isna 1	FCRI, ARC, Egypt
Family 4	FCRI, ARC, Egypt	Isna 2	FCRI, ARC, Egypt
Family 11	FCRI, ARC, Egypt	Isna 6	FCRI, ARC, Egypt
Family 12	FCRI, ARC, Egypt	Isna 7	FCRI, ARC, Egypt
Local 12	FCRI, ARC, Egypt	Qous 1	FCRI, ARC, Egypt
Local 20	FCRI, ARC, Egypt	Qous 3	FCRI, ARC, Egypt
Line 6	FCRI, ARC, Egypt	Qous 4	FCRI, ARC, Egypt
Line 15	FCRI, ARC, Egypt	Qous 5	FCRI, ARC, Egypt
Line 21	FCRI, ARC, Egypt	Belbais 9	FCRI, ARC, Egypt
X1/90/72	FCRI, ARC, Egypt	Giza 1	Egypt

B) Agronomic traits:

At harvest, ten guarded plants were taken randomly from each plot to estimate the following traits: plant height (cm), first nod height (cm), number of branches per plant, number of pods per plant, number of seeds per plant, seed yield per plant (g), 100-seed weight (g), and seed yield per fad (ardab).

C) Grouping trait and genotypes:

The principal component (PC) analysis was applied on the collected data. The first two PCs were used to generate the biplot; PC1 was used on the horizontal axis, whereas PC2 was used on the vertical axis as described by Yan and Rajcan (2002) to explain the relationship between each pairs of the studied traits. GGE (genotype main effect plus genotype-by-environments interaction) biplot are used to analyze two-way data (Yan and Hunt, 2002). Then, GGE biplot might be modified to the GT biplot analysis and conducted on the 26 genotypes yield-related traits to show the lupine genotypes by trait two-way data. In a genotype-by-trait table, genotypes are entries and traits are testers. All biplots presented in this study were generated using the software GenStat 18th.

D) The cluster analysis:

It was performed using a measure of similarity levels and Euclidean distance (Everitt, 1993 and Eisen *et al*., 1998).

Statistical analysis:

Analysis of variance of studied traits of each season was performed. Combined analysis of variance according to Gomez and Gomez (1984) was performed after proving homogeneity of error mean squares across seasons by Levene's test (1960). The least significant differences (L.S.D) were tested with a significance level of 5%.

RESULTS

A) Morphological traits:

A collection of three genotypes from Australia and twenty two lupine genotypes from different regions in Egypt with along check cultivar Giza 1 were evaluated according to the procedures of UPOV (Table 2).

1) Plant height:

a) At three weeks from seedling:

Eighty two of lupine genotypes were medium (75 B 15.17, P 20950, Family 2, Family 11, Family 12, Local 12, Local 20, Line 6, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, and Belbais 9). Meanwhile, eleven percentages of the genotypes were short (75 B 9.15, Line 15, and Line 21). Moreover, seven percentages of the genotypes were tall (Family 4 and Giza 1).

Table 2. Variation of morphological traits for the studied genotypes

Characteristic	Class	Percentage (%)	Lupine genotypes
	Visual assessment by a single observation of a group of plants or parts of plants		
	Plant height		
Plant height at three weeks from seedling	**Short**	11	75 B 9.15, Line 15, and Line 21
	Medium	82	75 B 15.17, P 20950, Family 2, Family 11, Family 12, Local 12, Local 20, Line 6, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, and Belbais 9
	Tall	7	Family 4 and Giza 1
	Very tall	00	---
Plant growth habit at flower bud stage	**Short**	00	---
	Medium	00	---
	Tall	62	75 B 15.17, 75 B 9.15, Local 12, Local 20, Line 6, Line 15, Line 21, Sakolta, Edfo, Isna 2, Isna 6, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1
	Very tall	38	P 20950, Family 2, Family 4, Family 11, Family 12, X1/90/72, Qena, Isna 1, and Isna 7
Plant height at beginning of flowering	**Short**	27	Line 21, Qena, Edfo, Isna 2, Isna 6, Isna 7, and Qous 1
	Medium	61	75 B 15.17, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, X1/90/72, Sakolta, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1
	Tall	8	75 B 9.15 and P 20950
	Very tall	4	Isna 1
Plant height at green ripening stage	**Very short**	15	Local 20, Line 6, Line 15, and Isna 1
	Short	19	Family 4, Qena, Isna 2, Isna 6, and Giza 1
	Medium	54	75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Line 21, X1/90/72, Sakolta, Edfo, Isna 7, Qous 1, and Belbais 9
	Tall	12	Qous 3, Qous 4, and Qous 5
	Very tall	00	---
	Flowering		
Color of flower wings	**White**	15	P 20950, Family 2, Qous 5, and Belbais 9
	Bluish white	73	75 B 15.17, 75 B 9.15, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 21, X1/90/72, Sakolta, Edfo, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 4, and Giza 1
	Blue	12	Line 15, Qena, and Qous 3
	Violet	00	---
	Pink	00	---
	Light yellow	00	---
	Dark yellow	00	---
Time of beginning of flowering	**Very early**	00	---
	Early	38	75 B 9.15, Family 2, Family 4, Local 12, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, and Giza 1
	Medium	62	75 B 15.17, P 20950, Family 11, Family 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 2, Isna 6, and Belbais 9
	Late	00	---
	Very late	00	---
Stem anthocyanin coloration at flower bud stage	**Weak**	4	75 B 15.17
	Medium	4	Family 11
	Strong	81	75 B 9.15, P 20950, Family 2, Family 4, Local 12, Local 20, Line 15, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 2, Isna 6, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1
	Very strong	11	Family 12, Line 6, and Isna 7

Table 2. Continued

Leaves and pods			
Leaf green color at flower bud stage	**Light**	11	X1/90/72, Qena, and Qous 4
	Medium	53	Family 2, Family 11, Family 12, Local 12, Local 20, Line 15, Line 21, Sakolta, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 5, and Belbais 9
	Dark	31	75 B 15.17, 75 B 9.15, P 20950, Family 4, Line 6, Edfo, Qous 3, and Giza 1
Central leaflet length	**Very short**	00	---
	Short	00	---
	Medium	23	Family 2, Family 11, Sakolta, Qena, Edfo, and Isna 6
	Long	77	75 B 15.17, 75 B 9.15, P 20950, Family 4, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Edfo, Isna 1, Isna 2, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1
	Very long	00	---
Central leaflet width	**Very narrow**	11	Sakolta, Qena, and Edfo
	Narrow	81	75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 5, Belbais 9, and Giza 1
	Medium	00	---
	Broad	8	Family 4 and Qous 4
	Very broad	00	---
Time of green ripening	**Very early**	42	75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, and Line 15
	Early	16	X1/90/72, Isna 1, Isna 6, and Giza 1
	Medium	23	Line 21, Qena, Isna 7, Qous 1, Qous 5, and Belbais 9
	Late	19	Sakolta, Edfo, Isna 2, Qous 3, and Qous 4
	Very late	00	---
Pod length	**Short**	00	---
	Medium	65	Family 4, Local 12, Local 20, Line 6, Line 15, X1/90/72, Qena, Edfo, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1
	Long	31	75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Line 21, and Isna 1
	Very long	4	Sakolta
Seed			
Color of seed ornamentation	**Beige light**	8	Family 2 and Qous 4
	Beige	69	75 B 15.17, P 20950, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 7, Qous 1, Qous 3, and Giza 1
	Brown	00	---
	Grey	00	---
	Black	00	---
	Multicolored	23	75 B 9.15, Line 15, Isna 2, Isna 6, Qous 5, and Belbais 9
Distribution of seed ornamentation	**Total**	4	75 B 15.17
	Total with eyebrow	15	75 B 9.15, Edfo, Qous 4, and Giza 1
	Dorsal	00	---
	Ventral	81	P 20950, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Sakolta, Qena, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 5, and Belbais 9
	Eyebrow only	00	---
Density of seed ornamentation (excluding genotypes with eyebrow only)	**Very sparse**	19	75 B 15.17, Family 2, X1/90/72, Isna 7, and Qous 1
	Sparse	35	P20950, Family4, Local 12, Line 6, Line 15, Line 21, Sakolta, Qena, Isna 1
	Medium	19	Edfo, Isna 2, Qous 3, Qous 5, and Belbais 9
	Dense	19	75 B 9.15, Local 20, Isna 6, Qous 4, and Giza 1
	Very dense	8	Family 11 and Family 12
100-seed	**Very low**	00	---
weight (harvested seed)	**Low**	00	---
	Medium	69	75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Line 21, Qena, Edfo, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1
	High	23	Local 12, Local 20, Line 6, Line 15, X1/90/72, and Sakolta
	Very high	8	Family 4 and Line 21

b) Plant growth habit at flower bud stage:

Sixty two percentage of lupine genotypes were tall (75 B 15.17, 75 B 9.15, Local 12, Local 20, Line 6, Line 15, Line 21, Sakolta, Edfo, Isna 2, Isna 6, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1), meanwhile thirty eight of the genotypes were very tall (P 20950, Family 2, Family 4, Family 11, Family 12, X1/90/72, Qena, Isna 1, and Isna 7).

c) At beginning of flowering:

Sixty one percentage of lupine genotypes were medium (75 B 15.17, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, X1/90/72, Sakolta, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1). Meanwhile, twenty seven percentage of the genotypes were short (Line 21, Qena, Edfo, Isna 2, Isna 6, Isna 7, and Qous 1). Moreover, eight percentages of the genotypes were tall (75 B 9.15 and P 20950). Finally, four percentages of the genotypes were very tall (Isna 1).

d) At green repining stage:

Fifty four percentage of lupine genotypes were medium (75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Line 21, X1/90/72, Sakolta, Edfo, Isna 7, Qous 1, and Belbais 9). Meanwhile, nineteen percentages of the genotypes were short (Family 4, Qena, Isna 2, Isna 6, and Giza 1). Moreover, fifteen percentages of the genotypes were very short (Local 20, Line 6, Line 15, and Isna 1). Finally, twelve percentages of the genotypes were tall (Qous 3, Qous 4, and Qous 5).

2) Flowering:

a) Color of flower wings:

Seventy three percentage of lupine genotypes were Bluish white (75 B 15.17, 75 B 9.15, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 21, X1/90/72, Sakolta, Edfo, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 4, and Giza 1). Meanwhile, fifteen percentages of the genotypes were white (P 20950, Family 2, Qous 5, and Belbais 9). Moreover, twelve percentages of the genotypes were blue (Line 15, Qena, and Qous 3).

b) Time of beginning of flowering

Sixty two percentage of lupine genotypes were medium (75 B 15.17, P 20950, Family 11, Family 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 2, Isna 6, and Belbais 9). Meanwhile, thirty eight percentages of the genotypes were early (75 B 9.15, Family 2, Family 4, Local 12, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, and Giza 1).

c) Stem anthocyanin coloration at flower bud stage:

Eighty one percentage of lupine genotypes were strong (75 B 9.15, P 20950, Family 2, Family 4, Local 12, Local 20, Line 15, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 2, Isna 6, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1). Meanwhile, eleven percentages of the genotypes were very strong (Family 12, Line 6, and Isna 7). Moreover, four percentages of the genotypes were medium (Family 11) or weak (75 B 15.17).

3) Leaves and pods:

a) Leaf green color at flower bud stage:

Fifty three percentage of lupine genotypes were medium (Family 2, Family 11, Family 12, Local 12, Local 20, Line 15, Line 21, Sakolta, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 5, and Belbais 9). Meanwhile, thirty one percentages of the genotypes were dark (75 B 15.17, 75 B 9.15, P 20950, Family 4, Line 6, Edfo, Qous 3, and Giza 1). Moreover, eleven percentages of the genotypes were light (X1/90/72, Qena, and Qous 4).

b) Central leaflet length:

Seventy seven percentage of lupine genotypes were long (75 B 15.17, 75 B 9.15, P 20950, Family 4, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Edfo, Isna 1, Isna 2, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1). Meanwhile, twenty three percentages of the genotypes were medium (Family 2, Family 11, Sakolta, Qena, Edfo, and Isna 6).

c) Central leaflet width:

Eighty one percentage of lupine genotypes were narrow (75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 5, Belbais 9, and Giza 1). Meanwhile, eleven percentages of the genotypes were very narrow (Sakolta, Qena, and Edfo). Moreover, eight percentages of the genotypes were broad (Family 4 and Qous 4).

d) Time of green repining:

Forty two percentage of lupine genotypes were very early (75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, and Line 15). Meanwhile, twenty three percentages of the genotypes were medium (Line 21, Qena, Isna 7, Qous 1, Qous 5, and Belbais 9). Moreover, nineteen percentages of the genotypes were late (Sakolta, Edfo, Isna 2, Qous 3, and Qous 4). Finally, sixteen percentages of the genotypes were early (X1/90/72, Isna 1, Isna 6, and Giza 1).

e) Pod length:

Sixty five percentage of lupine genotypes were medium (Family 4, Local 12, Local 20, Line 6, Line 15, X1/90/72, Qena, Edfo, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1). Meanwhile, thirty one percentages of the genotypes were long (75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Line 21, and Isna 1). Moreover, four percentages of the genotypes were very long (Sakolta).

4) Seed:

a) Color of seed ornamentation:

Sixty nine percentage of lupine genotypes were beige (75 B 15.17, P 20950, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna 7, Qous 1, Qous 3, and Giza 1). Meanwhile, twenty three percentages of the genotypes were multicolored (75 B 9.15, Line 15, Isna 2, Isna 6, Qous 5, and Belbais 9). Moreover, eight percentages of the genotypes were beige light (Family 2 and Qous 4).

b) Distribution of seed ornamentation:

Eighty one percentages of lupine genotypes were ventral (P 20950, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Sakolta, Qena, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 5, and Belbais 9). Meanwhile, fifteen percentages of the genotypes were total eyebrow (75 B 9.15, Edfo, Qous 4, and Giza 1).

c) Density of seed ornamentation:

Thirty five percentages of lupine genotypes were sparse (P 20950, Family 4, Local 12, Line 6, Line 15, Line 21, Sakolta, Qena, and Isna 1). Meanwhile, fifteen percentages of the genotypes were very sparse (75 B 15.17, Family 2, X1/90/72, Isna 7, and Qous 1). Also, fifteen percentages of the genotypes were medium (Edfo, Isna 2, Qous 3, Qous 5, and Belbais 9). Moreover, fifteen percentages of the genotypes were dense (75 B 9.15, Local 20, Isna 6, Qous 4, and Giza 1). Finally, eight percentages of the genotypes were very dense (Family 11 and Family 12).

d) 100-seed weight:

Sixty nine percentages of lupine genotypes were medium (75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 11, Family 12, Line 21, Qena, Edfo, Isna 1, Isna 2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1). Meanwhile, twenty three percentages of the genotypes were high (Local 12, Local 20, Line 6, Line 15, X1/90/72, and Sakolta). Moreover, eight percentages of the genotypes were very high (Family 4 and Line 21).

B) Agronomic traits:

1) ANOVA analysis:

Data of results revealed that the studied genotypes differed significantly for all the traits in each season. The homogeneity of error across the two seasons was checked by use of Levene (1960) test, and then combined across the two seasons to test the significant differences among genotypes (G), seasons (S), and genotype by season interaction (G x S) for all the studied lupine traits. Combined analysis across the two seasons that presented in Table (3) showed that the studied lupine genotypes differed significantly for all the traits (Plant height, plant height from the first node, branches, pods, and seeds numbers per plant, seed yield per plant, 100-seed weight and seed yield per fad). However, all the studied traits were significantly affected by lupine genotypes. Combined data across the two seasons revealed that S and G × S interaction effects were not significant for all the studied traits.

Table 3. Mean squares of combined analysis of variance for some lupine yield traits over two seasons

S.O.V	df	Plant height	First node height	Branches /plant	Pods /plant
Season (S)	1	0.27	3.57	0.01	6.36
Error	2	24.71	60.15	0.23	14.20
Genotypes (G)	25	1091.96**	1090.52**	3.02**	65.32**
S x G	25	25.56	36.121	0.07	18.09
Error	100	112.14	71.236	0.13	19.14

* and **: significant at 5 and 1% probability levels, respectively.

Table 3. Continued

S.O.V	**df**	**Seeds /plant**	**Seed yield /plant**	**100-seed weight**	**Seed yield /fad**
Season (S)	1	0.58	281.35	116.48	0.00
Error	2	99.18	40.20	39.84	0.06
Genotypes (G)	25	942.92**	214.17**	76.11*	23.37**
S x G	25	19.76	13.99	26.85	0.05
Error	100	179.31	39.00	41.44	0.14

* and **: significant at 5 and 1% probability levels, respectively.

2) Mean performance of some yield traits:

a) Plant height (cm):

There were significant differences among the studied genotypes for plant height at harvest (Table 4). Plant height of the studied genotypes ranged from 103.90 to 144.75 cm. The genotypes Qous 4, Qous 5, Qous 3, P 20950, X1/90/72, Line 21, Family 12, 75 B 9.15, Qous 1, Family 2, 75 B 15.17, Sakolta, Family 11, Edfo, and Isna 7 had higher values of plant height (144.75, 144.66, 140.78, 139.66, 139.66, 138.26, 138.18, 136.50, 133.98, 133.00, 132.16, 128.10, 123.91, 123.83, and 122.13 cm, respectively) than the other genotypes. Meanwhile, the converse was true for the genotypes Giza 1 (118.75 cm), Local 12 (114.86 cm), Isna 6 (112.33 cm), Isna 2 (111.45 cm), Family 4 (110.66 cm), Line 15 (108.00), Local 20 (106.43 cm), and line 6 (103.88 cm). It is important to mention that there were no significant differences between Giza 1 and Local 12, Isna 6, Isna 2, Family 4, Line 15, Local 20, or line 6 for this trait.Comparing to the commercial cultivar Giza 1, plant height of genotypes Qous 4, Qous 5, Qous 3, P 20950, X1/90/72, Line 21, Family 12, 75 B 9.15, Qous 1, Family 2, 75 B 15.17, Sakolta, Family 11, Edfo, and Isna 7 were increased by 21.89, 21.81, 18.55, 17.60, 17.60, 16.42, 16.36, 14.94, 12.82, 12.00, 11.29, 7.87, 4.34, 4.27, and 2.84 %, respectively, compared with cultivar Giza 1.

b) First node height (cm):

There were significant differences among the studied genotypes for the first node height (Table 4). Plant height from the first node of the studied genotypes ranged from 33.40 to 74.28 cm. The genotypes Qous 4, Qous 5, Qous 3, P 20950, X1/90/72, Line 21, Family 12, Belbais 9, 75B9.15, Qous 1, Family 2, 75B15.17, and Sakolta had higher values of plant height from first node (74.28, 74.10, 70.33, 69.15, 69.15, 67.71, 67.68, 66.73, 65.93, 63.48, 62.60, 61.66, and 57.66 cm, respectively) than the other genotypes. The genotypes Family 11 and Edfo ranked second for this trait (53.40 and 53.33 cm, respectively). Meanwhile, the converse was true for Isna 7 (51.60 cm), Qena (48.45 cm), Giza 1 (48.33 cm), Local 12 (44.33 cm), Isna 6 (41.71 cm), Isna 2 (40.91 cm), Family 4 (40.18 cm), Line 15 (37.50 cm), Local 20 (35.93 cm), Isna 1 (33.50 cm), and Line 6 (33.40 cm). It is important to mention that there were no significant differences between Giza 1 and Isna 7, Qena, Local 12, Isna 6, Isna 2, Family 4, Line 15, Local 20, Isna 1, or Line 6. Comparing to the commercial cultivar Giza 1, the plant height from first node of genotypes Qous 4, Qous 5, Qous 3, P 20950, X1/90/72, Line 21, Family 12, 75 B 9.15, Qous 1, Family 2, 75 B 15.17, and Sakolta were increased by 53.69, 53.32, 45.52, 43.07, 43.07, 40.09, 40.03, 38.07, 36.41, 31.34, 29.52, 27.58, and 19.30 %, respectively, compared with cultivar Giza 1.

c) Branches / plant (no.):

There were significant differences among the studied genotypes for number of branches per plant (Table 4). Number of branches per plant of the studied genotypes ranged from 1.60 to 4.18. The genotypes Qous 5, Sakolta, Qous 4, Isna 1, Qous 1, P 20950, and Edfo had higher values of number of branches per plant (4.18, 4.06, 4.03, 3.88, 3.60, 3.53, and 3.53 respectively) than the other genotypes. The genotypes Qous 3, Isna 6, Isna 7, Belbais 9, Family 2, 75 B 9.15, Family 12, Family 11, X1/90/72, and Qena ranked second for this trait (3.36, 3.31, 3.30, 3.30, 3.13, 3.11, 3.03, 3.00, 3.00 , and 2.80, respectively). Meanwhile, the converse was true for family 4 (2.33), Local 12 (2.33), Line 21 (2.33), 75 B 15.17 (2.13), Giza 1 (2.06), Local 20 (2.03), Line 6 (2.03), and Line 15 (1.60). It is important to mention that there were no significant differences between Giza 1 and Family 4, Local 12, Line 21, 75 B 15.17, Local 20, Line 6, or Line 15. Comparing to the commercial cultivar Giza 1, the number of branches per plant of genotypes Qous 5, Sakolta, Qous 4, Isna 1, Qous 1, P 20950, and Edfo were increased by 102.91, 97.08, 95.63, 88.34, 74.75, 71.35, and 71.35 %, respectively, compared with cultivar Giza 1.

d) Pods / plant (no.):

Moreover, there are significant differences among the studied genotypes for the number of pods per plant (Table 4). The number of pods per plant of the studied genotypes ranged from 13.00 to 26.53. The genotypes Qous 5, Family 2, Isna 7, Qous 4, Isna 6, P 20950, Isna 2, Qous 3, Qous 1, Giza 1, Family 11, Local 20, family 4, and X1/90/72 had higher values of number of pods per plant (26.53, 24.13, 21.63, 21.61, 21.10, 21.00, 20.61, 19.13, 18.60, 18.50, 17.85, 17.53, 17.31, and 17.31, respectively) than the other genotypes. Meanwhile, the converse was true for 75 B 9.15 (16.86), Isna 1 (16.15), Belbais 9 (16.11), Sakolta (16.00), 75 B 15.17 (16.00), Edfo (15.33), Line 6 (15.33), Family 12 (14.80), Line 15 (14.53), Qena (14.33), Line 21 (14.00), and Local 12 (13.00).

e) Seeds / plant (no.):

Significant differences were observed among the studied genotypes (Table 4). The number of seeds per plant of the studied genotypes ranged from 35.18 to 76.83. The genotypes Family 4, Isna 2, Belbais 9, Qous 4, P 2095, Isna 7, Qous 3, Family 2, Isna 1, Qous 1, Edfo, Isna 6, Giza 1, Qous 5, and Local 12 had higher values of number of seeds per plant (76.83, 71.26, 69.75, 66.83, 63.75, 63.58, 62.13, 60.91, 60.76, 59.56, 58.33, 57.43, 56.45, 56.11, and 49.16, respectively) than the other genotypes.

Table 4. Combined mean performance of some yield traits for lupine genotypes across two seasons

Seasons (S)	Plant height (cm)	First node height (cm)	Branches /plant (no.)	Pods /plant (no.)	Seeds /plant (no.)	Seed yield /plant (g)	100-seed weight (g)	Seed yield (ardab/fad)
1stseason	125.57	54.96	3.015	18.10	52.76	25.99	35.83	6.43
2ndseason	125.66	55.27	3.000	17.69	52.88	23.31	34.11	6.44
LSD	NS	NS	NS	NS	NS	NS	NS	NS
Genotypes (G)								
75 B 15.17	132.16	61.66	2.13	16.00	36.50	19.83	28.01	5.78
75 B 9.15	136.50	65.93	3.11	16.86	40.13	19.00	34.18	7.84
P 20950	139.66	69.15	3.53	21.00	63.75	22.21	34.48	6.93
Family 2	133.00	62.60	3.13	24.13	60.91	36.53	35.20	6.56
Family 4	110.66	40.18	2.33	17.31	76.83	33.00	41.35	7.57
Family 11	123.91	53.40	3.00	17.85	39.33	20.00	34.11	8.70
Family 12	138.18	67.68	3.03	14.80	43.30	18.28	35.43	7.10
Local 12	114.86	44.33	2.33	13.00	49.16	27.86	37.71	8.65
Local 20	106.43	35.93	2.03	17.53	47.33	23.33	39.80	6.47
Line 6	103.88	33.40	2.03	15.33	41.20	18.91	39.93	9.46
Line 15	108.00	37.50	1.60	14.53	45.25	25.78	36.45	7.47
Line 21	138.26	67.71	2.33	14.00	38.53	17.91	42.26	8.33
X1/90/72	139.66	69.15	3.00	17.31	36.26	16.43	37.83	8.50
Sakolta	128.10	57.66	4.06	16.00	37.58	20.58	38.93	7.89
Qena	118.91	48.45	2.80	14.33	35.18	15.83	31.00	5.71
Edfo	123.83	53.33	3.53	15.33	58.33	29.96	32.23	3.50
Isna 1	103.90	33.50	3.88	16.15	60.76	19.38	34.26	2.09
Isna 2	111.45	40.91	3.13	20.61	71.26	28.81	30.31	2.35
Isna 6	112.33	41.71	3.31	21.10	57.43	29.18	32.33	5.83
Isna 7	122.13	51.60	3.30	21.63	63.58	23.83	32.43	3.52
Qous 1	133.98	63.48	3.60	18.60	59.56	28.00	35.83	6.88
Qous 3	140.78	70.33	3.36	19.13	62.13	21.85	34.00	7.84
Qous 4	144.75	74.28	4.03	21.61	66.83	32.55	31.30	5.83
Qous 5	144.66	74.10	4.18	26.53	56.11	33.83	35.50	7.15
Belbais 9	137.33	66.73	3.30	16.11	69.75	27.23	33.21	4.92
Giza 1	118.75	48.33	2.06	18.50	56.45	30.80	31.21	4.48
L.S.D. 0.05	23.14	18.44	0.78	9.56	29.26	13.65	14.07	0.81

NS: non-significant

Meanwhile, the converse was true for the genotypes Local 20 (47.33), Line 15 (45.25), Family 12 (43.30), Line 6 (41.20), 75 B 9.15 (40.13), Family 11 (39.33), Line 21 (38.53), Sakolta (37.58), 75 B 15.17(36.50), X1/90/72 (36.26), and Qena (35.18).

f) Seed yield / plant (g):

There were significant differences among the studied genotypes for seed yield per plant (Table 4). Seed yield per plant of the studied genotypes ranged from 15.83 to 36.53 g. The genotypes Family 2, Qous 5, Family 4, Qous 4, Giza 1, Edfo, Isna 6, Isna 2, Qous 1, Local 12, Belbais 9, Line 15, Isna 7, and Local 20 had heavier seed yield per plant (36.53, 33.83, 33.00, 32.55, 30.80, 29.96, 29.18, 28.81, 28.00, 27.86, 27.23, 25.78, 23.83, 23.33 g, respectively) than the other genotypes. The converse was true for the genotypes P 20950 (22.21 g), Qous 3 (21.85 g), Sakolta (20.58

g), Family 11 (20.00 g), 75 B 15.17 (19.83 g), Isna 1 (19.38g), 75 B 9.15 (19.00 g), Line 6 (18.91 g), Family 12 (18.28 g), Line 21 (17.91 g), X1/90/72 (16.43 g), and Qena (15.83 g).

g) 100-seed weight (g):

Significant differences were noticed among the studied genotypes for 100-seed weight (Table 4). Weight of 100-seed of the studied genotypes ranged from 28.01 to 42.26. The genotypes Line 21, Family 4, Line 6, Local 20, Sakolta, X1/90/72, Local 12, Line 15, Qous 1, Qous 5, Family 12, Family 2, P 20950, Isna 1, 75 B 9.15, Qous 3, Belbais 9, Isna 7, Isna 6, Edfo, Qous 4, Giza 1, and Isna 2 had heavier 100-seed weight (42.26, 41.35, 39.93, 39.80, 38.93, 37.83, 37.71, 36.45, 35.83, 35.50, 35.43, 35.20, 34.48, 34.26, 34.18, 34.00, 33.21, 32.43, 32.33, 32.23, 31.30, 31.21, and 30.31 g, respectively) than genotype 75 B 15.17(28.01 g).

h) Seed yield / fad (ardab):

There were significant differences among the studied genotypes for seed yield per fad (Table 4). Seed yield of the studied genotypes ranged from 2.09 to 9.46 ardab per fad. The genotypes Line 6, Family 11, and Local 12 had higher seed yield per fad (9.46, 8.70, and 8.65 ardab, respectively) than the other genotypes. The genotypes X1/90/72, Line 21, Sakolta, 75 B 9.15, and Qous 3 ranked second (8.50, 8.33, 7.89, 7.84, 7.84 ardab, respectively), followed by Family 4 (7.57 ardab/fad), Line 15 (7.47 ardab/fad), Qous 5 (7.15 ardab/fad), and family 12 (7.10 ardab/fad). Meanwhile, the genotypes Isna 2 and Isna 1 had lower seed yield per fad (2.35, 2.09 ardab, respectively) than the others.

3) The interaction between lupine genotypes and seasons:

The interaction between lupine genotypes and seasons did not affect significantly all the studied traits (Table 5).

Table 5. The interaction between seasonal effects and lupine genotypes

Lupine genotypes	Plant height (cm)		First node height (cm)		Branches/plant (no.)		Pods /plant (no.)	
	1st season	2nd season	1st season	2nd season	1st season	2nd season	1st season	2nd season
75 B 15.17	131.00	133.33	65.33	58.00	2.13	2.13	17.33	14.66
75 B 9.15	132.36	140.63	67.66	64.20	3.06	3.16	18.00	15.73
P 20950	141.33	138.00	75.56	62.73	3.46	3.60	22.33	19.66
Family 2	131.00	135.00	62.16	63.03	3.40	2.86	28.20	20.06
Family 4	112.66	108.66	40.30	40.06	2.30	2.36	18.70	15.93
Family 11	125.53	122.30	50.53	56.26	3.13	2.86	20.40	15.30
Family 12	136.30	140.06	69.26	66.10	3.16	2.90	16.46	13.13
Local 12	118.33	111.40	44.33	44.33	2.30	2.36	14.00	12.00
Local 20	105.66	107.20	31.90	39.96	2.03	2.03	15.76	19.30
Line 6	102.46	105.30	31.86	34.93	1.93	2.13	13.33	17.33
Line 15	109.33	106.66	34.83	40.16	1.63	1.56	14.00	15.06
Line 21	136.10	140.43	70.00	65.43	2.30	2.36	13.66	14.33
X1/90/72	141.33	138.00	68.10	70.20	2.90	3.10	15.36	19.26
Sakolta	131.33	124.86	56.33	59.00	3.86	4.26	14.00	18.00
Qena	118.43	119.40	44.66	52.23	2.80	2.80	15.00	13.66
Edfo	124.50	123.16	52.33	54.33	3.63	3.43	15.33	15.33
Isna 1	100.13	107.66	32.00	35.00	3.76	4.00	17.23	15.06
Isna 2	111.66	111.23	43.46	38.36	3.23	3.03	18.70	22.53
Isna 6	111.00	113.66	42.80	40.63	3.40	3.23	19.80	22.40
Isna 7	122.03	122.23	48.86	54.33	3.10	3.50	19.60	23.66
Qous 1	136.33	131.63	63.66	63.30	3.66	3.53	17.23	19.96
Qous 3	139.23	142.33	69.33	71.33	3.36	3.36	19.93	18.33
Qous 4	143.13	146.36	72.83	75.73	4.20	3.86	20.56	22.66
Qous 5	146.33	143.00	73.53	74.66	4.23	4.13	26.16	26.90
Belbais 9	136.33	138.33	70.13	63.33	3.33	3.26	17.86	14.36
Giza 1	121.16	116.33	47.33	49.33	2.03	2.10	21.60	15.40
L.S.D. 0.05	NS		NS		NS		NS	

NS: non-significant

Table 5. Continued

Lupine genotypes	Seeds/plant (no.)		Seed yield /plant (g)		100-seed weight (g)		Seed yield (ardab /fad)	
	1st season	2nd season	1st season	2nd season	1st season	2nd season	1st season	2nd season
75 B 15.17	37.26	35.73	18.33	21.33	25.33	30.70	5.85	5.72
75 B 9.15	37.93	42.33	19.66	18.33	31.36	37.00	7.86	7.83
P 20950	63.00	64.500	23.10	21.33	38.23	30.73	6.89	6.97
Family 2	59.83	62.00	41.06	32.00	35.86	34.53	6.63	6.48
Family 4	74.00	79.66	34.00	32.00	46.83	35.86	7.44	7.70
Family 11	39.66	39.00	22.00	18.00	38.53	29.70	8.82	8.57
Family 12	41.33	45.26	17.00	19.56	36.20	34.66	7.19	7.01
Local 12	47.56	50.76	28.23	27.50	39.73	35.70	8.55	8.75
Local 20	45.00	49.66	24.00	22.66	43.86	35.73	6.41	6.53
Line 6	44.46	37.93	20.83	17.00	40.86	39.00	9.38	9.53
Line 15	45.86	44.63	27.56	24.00	37.13	35.76	7.33	7.61
Line 21	35.73	41.33	19.90	15.93	44.53	40.00	8.32	8.33
X1/90/72	36.10	36.43	19.53	13.33	38.00	37.66	8.56	8.43
Sakolta	37.16	38.00	22.10	19.06	41.26	36.60	7.91	7.86
Qena	35.40	34.96	17.70	13.96	33.00	29.00	5.59	5.83
Edfo	58.00	58.66	32.50	27.43	32.50	31.96	3.49	3.50
Isna 1	62.20	59.33	20.80	17.96	34.76	33.76	2.20	1.97
Isna 2	71.73	70.80	28.90	28.73	31.30	29.33	2.45	2.24
Isna 6	58.10	56.76	27.93	30.43	33.00	31.66	6.08	5.57
Isna 7	64.66	62.50	27.06	20.60	32.20	32.66	3.46	3.58
Qous 1	62.33	56.80	29.00	27.00	36.33	35.33	6.84	6.92
Qous 3	61.93	62.33	20.80	22.90	31.33	36.66	7.81	7.87
Qous 4	68.30	65.36	34.43	30.66	29.66	32.93	5.76	5.90
Qous 5	56.83	55.40	37.66	30.00	35.46	35.53	7.03	7.28
Belbais 9	67.16	72.33	29.10	25.36	34.50	31.93	4.89	4.95
Giza 1	60.33	52.56	32.66	28.93	30.00	32.43	4.53	4.42
L.S.D. 0.05	NS		NS		NS		NS	

NS: non-significant

C) Grouping trait and genotypes:

1) Trait relationships:

Principal components (PC) analysis was performed to summarize the interrelationships among the all phenotypic plant and seed traits with other yield components in lupine. Loading of different trends of trait associations were illustrated in Figure (1), considering the sign of horizontal PC1 as the direction of correlation among the examined traits. So, it is noted that allocated traits in the left side of the horizontal axis as B, D, F, G, I, J, K, L, M, P and W (B: seed distribution of ornamentation, D: 100-seed weight (visual assessment), F: plant growth habit at flower bud stage, G: plant height at beginning of flowering, I: color of flower wings, J: time of beginning of flowering, K: leaf green color at flower bud stage, L: stem anthocyanin coloration at flower bud stage, M: central leaflet length, P: pod length, W: 100-seed weight) indicated the negative correlations with other traits in the right side. Regarding the coloration strength, loadings divided the mentioned traits into similar correlated groups among the graph surface. Accordingly, traits of T (number of pods/plant) and U (number of seeds/plant) were the closest or more correlated to V (seed yield/plant) followed by E (plant length at three weeks from seedling) and N (central leaflet width) indicating their importance as selection criteria for lupine yield development. Meanwhile W (100-seed weight) recorded negative correlations with V (seed yield/plant), T (number of pods/plant), and U (number of seeds/plant). However, traits of H (plant height at green ripening stage), O (time of green ripening), Q (plant height at harvest), and R (first node height) were the nearest and close to S (number of branches per plant) trait, pointing to selection for some or all these traits may be help in production the more profuse branches.

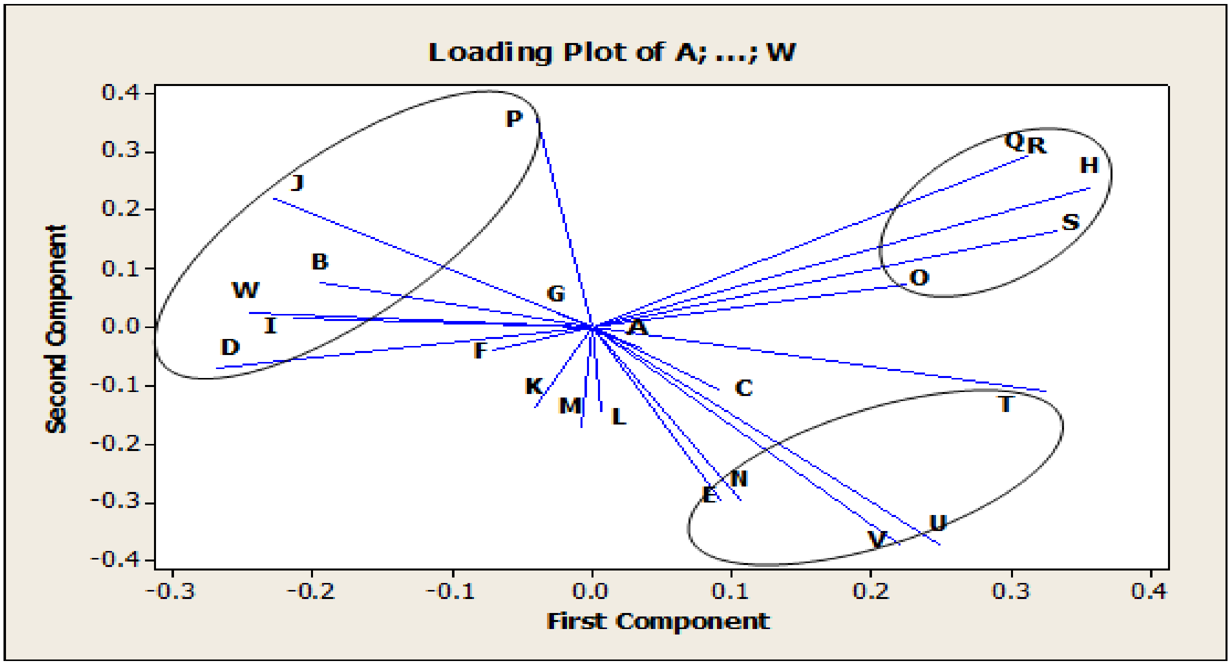

Fig. 1. Loading graph of the first two principal components (PC) to explain interrelationships among the studied traits
A: color of seed ornamentation, B:distribution of seed ornamentation, C:density of seed ornamentation (excluding genotypes with eyebrow only), D:100-seed weight (visual assessment), E:plant length at three weeks from seedling, F: plant growth habit at flower bud stage, G:plant height at beginning of flowering, H:plant height at green ripening stage, I:color of flower wings, J:time of beginning of flowering, K:leaf green color at flower bud stage, L:stem anthocyanin coloration at flower bud stage, M:central leaflet length, N:central leaflet width, O:time of green ripening, P:pod length, Q:plant height at harvest, R:plant height from first node , S:number of branches/plant, T:number of pods/plant, U:number of seeds/plant, V:seed yield/plant and W:100-seed weight.

2) Biplot graph:

In this investigation, the application of GGE-biplot method of experimental data was sufficient to explain the whole variation of genotypes (Yan and Hunt, 2002).

a) Biplot graph to find the phenotypic markers characteristics

This graph of GT biplot in Figure (2) showed that a vector is drawn from the biplot origin to each marker traits to visualize the relationships among the studied related traits (Yan and Tinker, 2005); describing the interaction between the genotype and the traits. A genotype may be a gain of group traits that considered as breeding aims (Yan, 2014). In this experiment, the genotypes were described by multiple traits among evaluation levels, that it may be used as phenotypic markers traits in discriminating the examined genotypes. Polygon view of the which -wins-where in GT-biplot (Figure2) were constructed based on mean values of the different levels of traits (I, II, III and IV).Lines from center point of graph to many sectors. The genotypes and criteria locating in the same sector of the graph are closely related (Yan and Tinker, 2006; Kendal *et al*., 2016 and Kendal, 2019). The codes from Line 1 to Line 25 were used for evaluating white lupines genotypes as compared with the commercial cultivar Giza 1 (Figure 2). These codes are (Line 1 "75 B 15.17", Line 2 "75 B 9.15", Line 3 "P 20950", Line 4 "Family 2", Line 5 "Family 4", Line 6 "Family 11", Line 7 "Family 12", Line 8 "Local 12", Line 9 "Local 20", Line 10 "Line 6", Line 11 "Line 15", Line 12 "Line 21", Line 13 "X1/90/72", Line 14 "Sakolta", Line 15 "Qena", Line 16 "Edfo", Line 17 "Isna 1", Line 18 "Isna2", Line 19 "Isna 6", Line 20 "Isna 7", Line 21 "Qous 1", Line 22 "Qous 3", Line 23 "Qous 4", Line 24 "Qous 5", and Line 25 "Belbais 9").

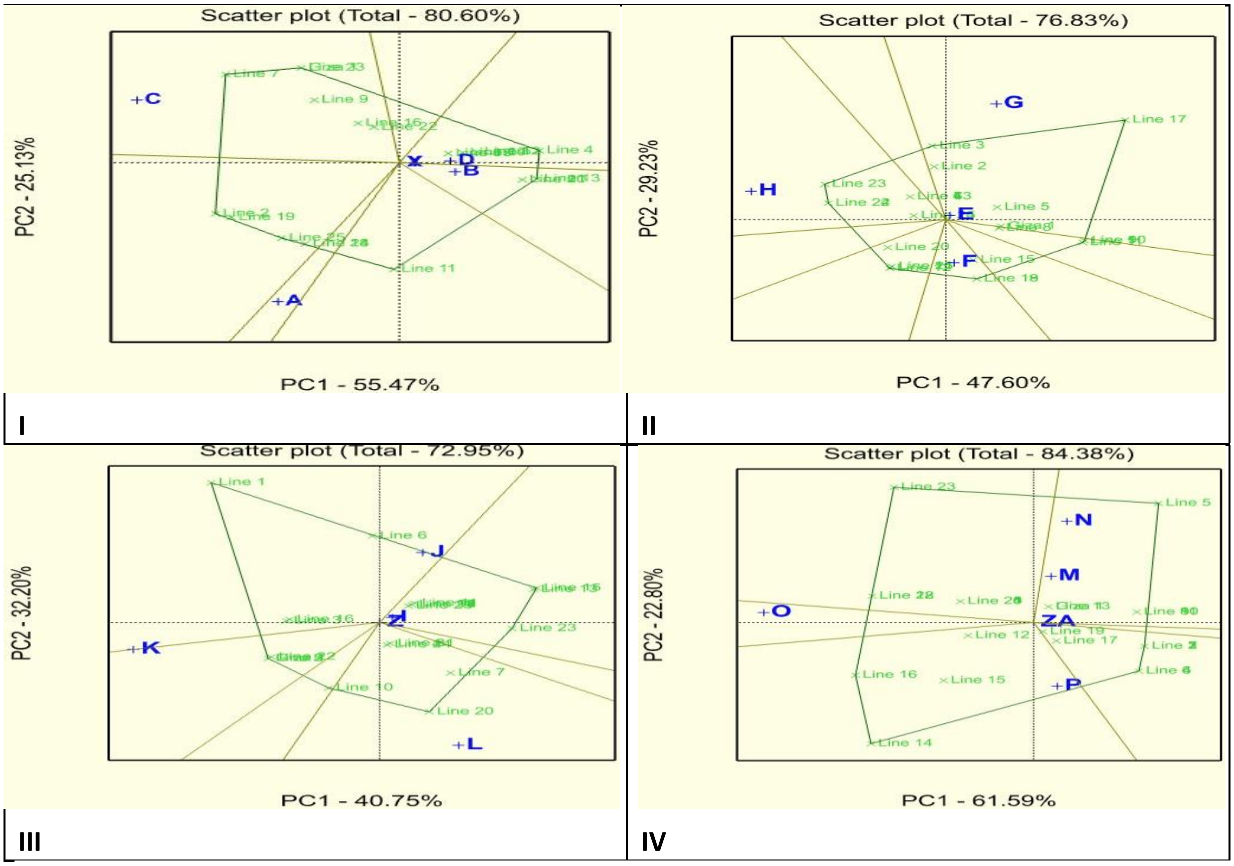

Fig. 2. Polygon view of the morphological traits, describing white lupine genotypes comparison on the basis of GT-biplot. (I) seed criteria; (II) plant height criteria; (III) flower criteria and (IV) leaflet and plant growth criteria.

Line1 – Line25 are codes for evaluated white lupine genotypes with Giza1 variety. A: color of seed ornamentation, B: distribution of seed ornamentation, C: density of seed ornamentation (excluding genotypes with eyebrow only), D: 100-seed weight (visual assessment), E: plant height at three weeks from seedling, F: plant growth habit at flower bud stage, G: plant height at beginning of flowering, H: plant height at green ripening stage, I: color of flower wings, J: time of beginning of flowering, K: leaf green color at flower bud stage, L: stem anthocyanin coloration at flower bud stage, M: central leaflet length, N: central leaflet width, O: time of green ripening, P: pod length, X: seed bitter principle, Y: seed ornamentation, Z: flower color of tip of carina and AZ: plant growth type.

In Figure (2 I) of seed criteria, GT-biplot of the mean performance of the data explained 80.60% of the total variation. The first and two principal components (PC1 and PC2) explained 55.47 and 25.13%, respectively. Many genotypes as Family 2, X1/90/72, Isna 7, Qous 1, Sakolta, and Line 21 and the B and D traits fall in the same right sector of the graph, indicating to closely positive related. Then, B: distribution of seed ornamentation and raising D: 100-seed weight (visual assessment) may be used to distinguish these genotypes under vegetative growth. Meanwhile, traits of X and Y were spread near the central point, they had not any discriminating criteria. Regarding the Figure (2 II), genotypes Isna 1, Local 20, Line 6, P 20950 and 75 B 9.15 could be distinguished by increase G trait (plant height at beginning of flowering). Meanwhile, the decrease in H trait (plant height at green ripening stage) considered as feature in genotypes of Qous 4, Family 2, and Qous 3. Accordingly, the genotypes 75 B 15.17 and Family 11 (Figure 2 III) may be discriminated by increase J (time of beginning of flowering) trait and Isna 7 by high L (stem anthocyanin coloration at flower bud stage). Lupine genotypes Family 4 and Qous 3 had low K (leaf green color at flower bud stage). However, two traits of (I: color of flower wings and Z: flower color of tip of carina) were spread near the central origin. In Figure (2 IV), genotypes Family 4, Local 20, Line 6 and Line 15 may be discriminated by increase two traits M: central leaflet length and N: central leaflet width. Meanwhile, Family 4 had low K (leaf green color at flower bud stage). However, AZ (plant growth type) that plotted near the central origin had not any distinction features.

b) Ideal genotypes of GT-biplot:

The genotype-by-trait (GT) graph in Figure (3) illustrated ranked genotypes along the average tester coordinate (ATC) line that passes through the biplot origin and the average trait with the arrow pointing to higher mean (small circle which is located on the line.

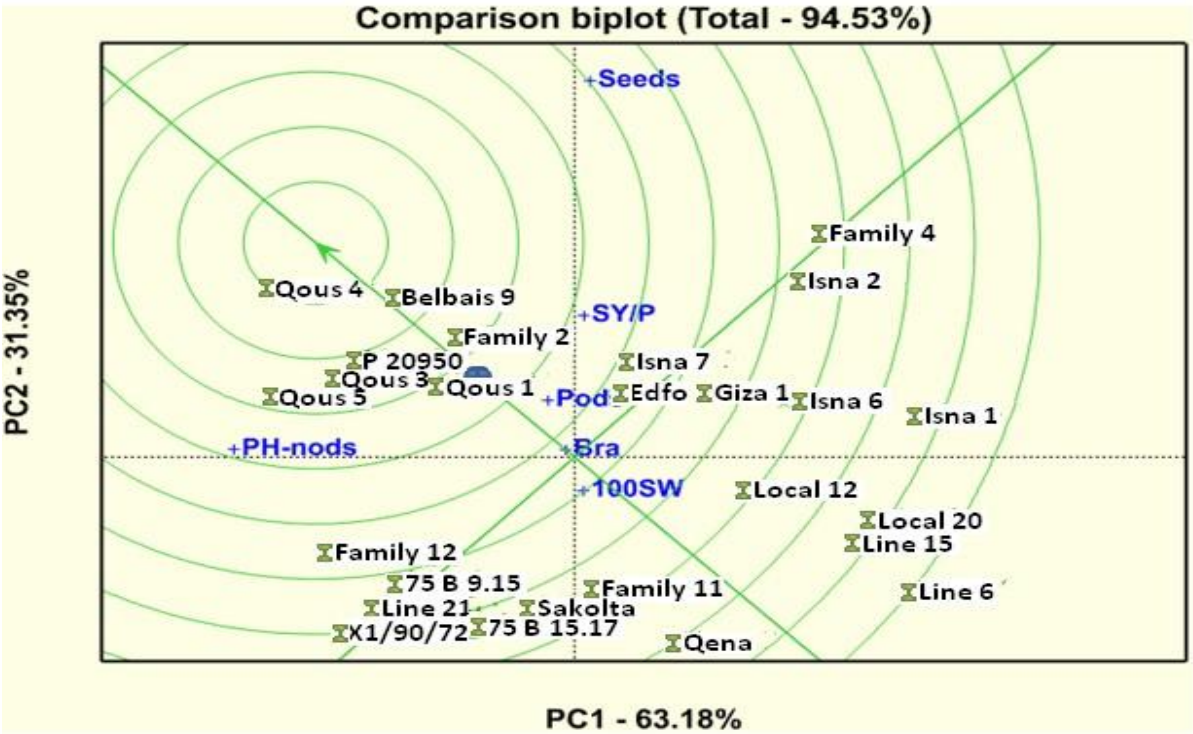

Fig. 3. Ideal genotypes of GT-biplot, showing the ranking of twenty-six lupine genotypes for various examined traits

PH-nods: Plant height from first node, Bra: No. of branches, Pod: No. of pods, Seeds: No. of seeds, SY/P: Seed yield /plant and 100-SW: 100-Seed weight.

3) Cluster analysis:

Cluster analysis considered as an efficient procedure for extracting the structured relationships among genotypes to provides a hierarchical classification of them (Polignano *et al*., 1989). Hierarchical cluster dendrogram of the estimated lupine genotypes based on yield traits for clustering the investigated 26 genotypes obtained was illustrated in Table (6) and Figure (4). Cluster analysis showed the interrelationships of the genotypes, grouping those (genotypes) into three main clusters (A, B and C). Each of the main clusters was divided into sub clusters concluded similar genotypes. Regarding first cluster, nine genotypes (9) were grouped in the same cluster (A) that had the lowest seed yield, recording 20.02g/plant as a grand mean for this cluster. However, second cluster (B) consisted of eight (8) genotypes that had the medium seed yield value (22.35 g/plant). Concerning of third cluster (C) with the nine genotypes (9) that scored highest seed yield (31.32 g/plant).

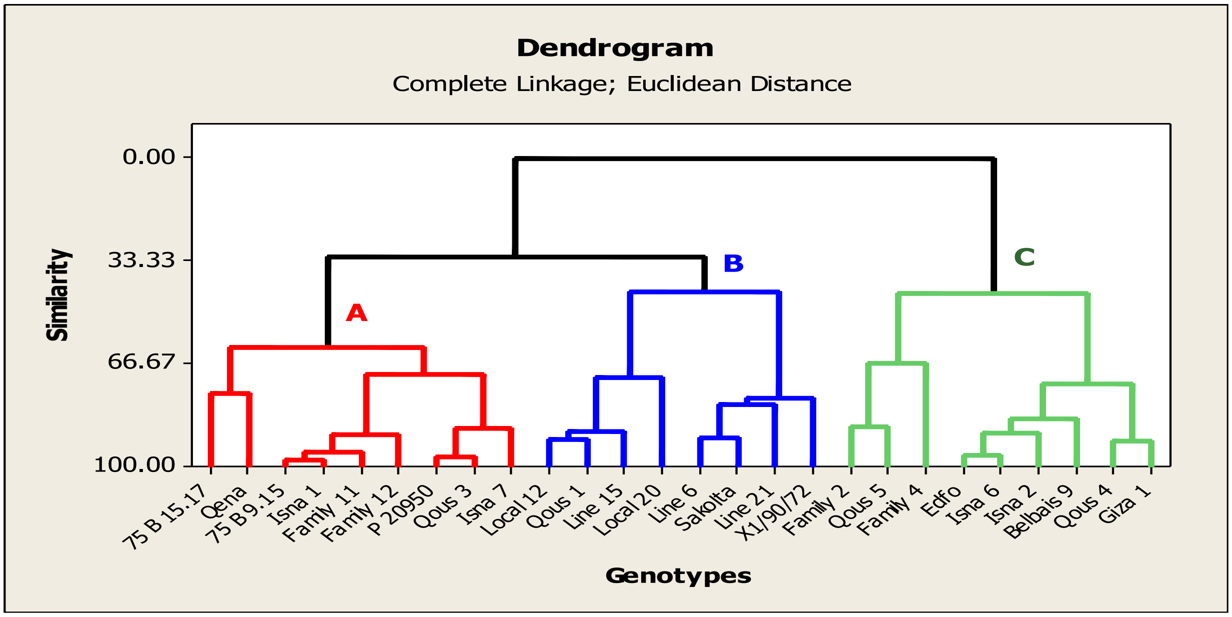

Figure 4. Dendrogram of cluster analysis showing the relationship among lupine genotypes based on yield traits

Table 6. Level of different clusters for soybean studied traits under pests' infestation

Cluster No.	Similarity	No. of genotypes	Included genotypes	Cluster yield grand mean (g)
Cluster A	61.53	9 genotypes (1, 15, 2, 17, 6, 7, 3, 22 and 20)	75 B 15.17, Qena, 75 B 9.15, Isna 1, Family 11, Family 12, P 20950, Qous 3 and Isna 7.	20.02
Cluster B	43.36	8 genotypes (8, 21, 11, 9, 10, 14, 12 and 13)	Local 12, Qous 1, Line 15, Local 20, Line 6, Sakolta, Line 21 and X1/90/72.	22.35
Cluster C	44.10	9 genotypes (4, 24, 5, 16, 19, 18, 25, 23 and 26)	Family 2, Qous 5, Family 4, Edfo, Isna 6, Isna 2, Belbais 9, Qous 4 and Giza 1	31.32

DISCUSSION

A) Morphological traits:

With regard to plant height, plant growth habit at flower bud stage, and flowering, it is worth noting that late or very late maturing genotypes were absent very tall genotypes at three weeks from seedling were absent. These results are in harmony with Arab *et al*. (2014) who found that two from thirty-seven accessions recorded high values of plant height at the vegetative stage. It is important to mention that short or medium growth habit of genotypes at flower bud stage were absent. Meanwhile, previous studies investigated that nine accessions had short plant height at beginning of flowering (Arab *et al*., 2014).Moreover, very tall genotypes at green repining stage were absent. From the other point, violet, pink, light yellow or dark yellow flower wings were absent. These results are in agreement with those obtained by Arab *et al*. (2014) who revealed that the color of wings in most accessions was bluish white. It is worth noting that late or very late maturing genotypes were absent. Meanwhile, previous studies found that the intensity of anthocyanine coloration was absent in one accession (Arab *et al*., 2014).

With regard to leaves, pods, and seed, thirteen accessions have been characterized by an intensity of green color as light in the leaf from thirty-seven accessions (Arab *et al*., 2014). The results shows that very short, short or very long central leaflet genotypes were absent. Eight accessions have been characterized by short-length central leaflets from thirty-seven accessions (Arab *et al*., 2014).In the same trend, the results reveal that medium or very broad central leaflet genotypes were absent. Nine accessions have been characterized by narrow-length central leaflets from thirty-seven accessions (Arab *et al*., 2014). Meanwhile, very late green repining genotypes were absent. These results are in harmony with Arab *et al*. (2014) who found that seven accessions identified as an early group from thirty-seven accessions. On the other hand, the results shows that short pod of genotypes were absent. These results are in agreement with Arab *et al*. (2014) who reported that four accessions were short in their pod length from thirty-seven accessions. It is important to mention that seed ornamentation can reflect the implied genetics and in turn, be beneficial in breeding programs (Haridasan and Mukherjee, 1988). It was detected in three accessions from thirty seven accessions (Arab *et al*., 2014). Also, the results indicate that brown, grey or black seed ornamentation of genotypes was absent. Moreover, the results reveal that dorsal or eyebrow seed ornamentation of genotypes was absent. Furthermore, the low or very low 100-seed weight of genotypes was absent. Similar results are obtained by Arab *et al*. (2014) who revealed that twenty-seven accessions gave a higher 100-seed weight than the others.

B) Agronomic traits:

1) ANOVA analysis:

The results indicate that expected genetic gain from selection for these traits could be fast in this genetic material. There are the narrower environmental fluctuation, which might have resulted in insignificant seasonal effects on the performance of yield and some of the essential components. Generally, a consistent response is observed between genotypes and seasons for all the studied traits, indicating that genotypes can be selected with limited evaluations under the conditions of the experiment. These results reveal that there was high experimental precision, providing reliability for selecting superior genotypes under the experimental conditions.

2) Mean performance of some yield traits:

With regard to plant height, the results are probably due to the differences in plant hormones that translated from the genetic makeup of the studied genotypes. These results reveal that the plant height is much under the control of the genetic background of lupines genotypes which had a specific elongating effect on plants. The results are in accordance with Ashrei *et al*. (2018) who reported that lupine genotypes Fakous 3, Ismailia 3, Beni salh, Beni Suef 1, Aswan 1, and Butter Cup were taller than cultivar Giza 1.

With respect to plant height from the first node, the results can be attributed to the differences in the genetic makeup of these genotypes which translated into differences in their internodes. With regard to the number of branches per plant, these results may be due to the differences in the genetic makeup of these genotypes which translated into differences in their growth habits. In this concern, Ashrei *et al*. (2018) and Alemu *et al*. (2019) found that some lupine genotypes have differed in their branches number.

With respect to the number of pods per plant, it can be attributed to the differences in the genetic makeup of these genotypes which translated into differences in their morphological traits that reflected different rates of photosynthetic process in the plant during the growth and development stages. This observation indicates the substantial role of morphological traits as a parallel mechanism for enhancing agronomic traits under genetic differences of lupines. So, it may be possible that Qous 5, Family 2, Isna 7, Qous 4, Isna 6, P 20950, Isna 2, Qous 3, Qous 1, Giza 1, Family 11, Local 20, family 4, and X1/90/72 had some morphological and agronomic characteristics which can be utilizing available agricultural resources and convert to crop biomass during growth and development stages than the others. Similar results are obtained by EL-Harty *et al*. (2016) and Abo-Hegazy *et al*. (2020).

With regard to the number of seeds per plant, the results are probably due to the difference in the genetical constituent of the studied genotypes that translated into the differences in the length and size of the pod. The pod can be considered a temporary sink and the photosynthates were translocated to seeds during their development. Similar results are obtained by Ashrei *et al*. (2018) who revealed that the best lupines genotypes for this trait were Algeerb 2, Badrashein, and El-Aiat as compared with others.

With respect to seed yield per plant, it can be attributed to the genetic makeup of these genotypes being different in the translocation of photosynthates metabolites to the seed during the growth and development stages. In other studies, Ashrei *et al*. (2018) and Khalifa *et al*. (2020) showed that plants of some lupines genotypes have differed in their seed yields.

With regard to 100-seed weight, it can be attributed to the differences in the genetic makeup of these genotypes that differentiated into changes in the photosynthates translocation rates through morphological plant organs to seed during seed filling stage. These results are in accordance with Ashrei *et al*. (2018) who found that the genotype Sohag was superior to the other genotypes for 100-seed weight.

With respect to the seed yield per fad, these results are probably due to the integration between the yield potential of each genotype with its plant density. The results are in agreement with those obtained by EL-Harty *et al*. (2016).

3) The interaction between lupine genotypes and seasons:

With regard to the interaction between lupine genotypes and seasons, these results reveal that the differences among genotypes were stable from one year to another, and these interactions can be valuable in the breeding programs of lupine in the future.

C) Grouping trait and genotypes:

1) Trait relationships:

From previous results, it could be predicted with plants that had most profuse branches. Also, it recommended that the important traits overall were number of pods/plant and number of seeds/plant. Whereupon, breeders could be realized high income of lupine yield by interest and selection to more pods and seeds in the field, contrasting to 100-seed weight that would not be among the selected yield components in lupine. These results are in harmony with those obtained by Atnaf *et al*. (2017).

2) Biplot graph:

GGE-biplot graph was used to compare genotypes on the basis of the multiple seed yield-related traits to identify the ideal genotypes in the lupine as shown in Figure (3). Another application of GGE-biplot was GT-biplot (genotype and traits) that revealed the relationship among the genotypes and traits (Yan, 2014), describing each specific trait marker for the studied genotypes as shown in Figure (2).

a) Biplot graph to find the phenotypic markers characteristics

The results showed the importance of GT-biplot in discriminating different genotypes among crops.

b) Ideal genotypes of GT-biplot:

This graph (Figure 3) showed a vector view of GT-biplot revealing the ranking of twenty-six (25 genotypes + only one commercial cultivar) genotypes of based on their ideal mean performance over measured yield traits. The GT-biplot sowed that Qous 4 located as a closest to the center of the concentric circles was the ideal genotype (best) across the selected yield traits. Accordingly, the other followed ideal genotypes were Belbais 9, Family 2, P 20950, Qous 5, Qous 3 and Qous 1 that obtained the nearer to the ideal genotypes and fall in the nearest of the central circle. Similarly, Hefny (2013) and Rubio *et al*. (2004) used this method to explain the importance of GT-biplot in ranking and identifying the best genotypes based on the mean performance over the multiple traits.

3) Cluster analysis:

It was cleared that, genotypes in cluster (C) that contain (Family 2, Qous 5, Family 4, Edfo, Isna 6, Isna 2, Belbais 9, Qous 4 and Giza 1) were more related to check genotype (Giza 1) and was considered as the best yield performance. Then, the presence of considerable genetic diversity among the studied lupine genotypes could be useful in selecting promising genotypes (cluster C) on the basis of their phenotypic expression to use them in breeding programs to improve the important traits as seed yield.

CONCLUSION

It can be concluded that morphological traits are used as effectively alongside agronomic traits to contrast all the genotypes held within a collection for selecting high-yielding genotypes of lupines. GT-biplot can be an effective tool to reveal the important relationships among the studied traits of lupine genotypes. Identifying the best lupine genotypes over the multiple traits can be achieved by using GT-biplot analysis. The lupine genotypes Qous 3 and Qous 5 can be considered genetic sources of agronomic traits to support breeding efforts. Twelve lupine genotypes (Line 6, Family 11, Local 12, X1/90/72, Line 21, Sakolta, 75 B 9.15, Qous 3, Family 4, Line 15, Qous 5, and Family 12) surpassed Giza 1 and the other genotypes in seed yield per fad. In addition to, cluster (C) that contains nine genotypes (Family 2, Qous 5, Family 4, Edfo, Isna 6, Isna 2, Belbais 9, Qous 4 and Giza 1) which included Giza 1 (check genotype) was scored the highest seed yield. However, Family 2, Qous 5, Family 4 and Qous 4 genotypes surpassed the yield of Giza1 (check). Then, Family 4 and Qous 5 recorded the best genotypes with the highest seed yield per plant or fad.

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التوصيف المورفولوجي والصفات المحصولية لبعض التراكيب الوراثية للترمس

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أجريت دراسة لمدة عامين في محطة البحوث الزراعية بالجيزة ، مركز البحوث الزراعية ، جيزة، مصر خلال موسمي الزراعيين ٢٠٢٠/٢٠٢١م و ٢٠٢١/٢٠٢٢م لتقييم القدرة المحصولية لخمسة وعشرين تركيبا وراثيا للترمس وتحديد صفاتها المورفولوجية مقارنة بالصنف التجارى Giza 1 . تم زراعة ستة وعشرون تركيبا وراثيا للترمس هى (75 B 15.17, 75 B 9.15, P 20950, Family 2, Family 4, Family 11, Family 12, Local 12, Local 20, Line 6, Line 15, Line 21, X1/90/72, Sakolta, Qena, Edfo, Isna 1, Isna2, Isna 6, Isna 7, Qous 1, Qous 3, Qous 4, Qous 5, Belbais 9, and Giza 1)، وقد تم زراعتها في تصميم القطاعات العشوائية الكاملة في ثلاثة مكررات. تم إستخدام ستة عشر توصيفيا مورفولوجيا طبقا لإرشادات UPOV (الاتحاد الدولي لحماية الأصناف النباتية الجديدة). أشار التوصيف المورفولوجى إلى عدم وجود تراكيب وراثية للترمس قصيرة أو متوسط النمو عند مرحلة تكشف الأزهار وكذلك لم تتواجد تراكيب وراثية طويلة جدا عند فترة النضج الأخضر. كما لم تتواجد تراكيب وراثية للترمس أزهارها ذات أجنحة بنفسجية أو وردية أو صفراء فاتحة أو صفراء داكنة أو ذات نضج متأخر أو متأخر جدا. كذلك وجد أن جميع التراكيب الوراثية للترمس تمتاز بتلون الساق بصبغة الأنثوسيانين وكذلك اللون الأخضر للأوراق عند مرحلة تكشف الأزهار وكثافة زخرفة البذور. أظهر تحليل التباين المشترك أن التراكيب الوراثية المدروسة للترمس تختلف اختلافًا معنويا ً لجميع الصفات تحت الدراسة. بينما لم تعطى التأثيرات الموسمية وكذلك تفاعلاتها مع التراكيب الوراثية اى تاثير معنوى على اى من الصفات المدروسة. وقد أعطى التركيبين الوراثيين للترمس (Qous 5 و P 20950) أعلى عدد قرون ومحصول بذور للنبات. بينما أعطى التركيبين الوراثيين للترمس (Qous 3 و Qous 5) أعلى عدد بذور للنبات ووزن المائة بذرة. أشار تحليل ثنائى الاتجاه GT-biplot أن التراكيب الوراثية للترمس (Qous 4 و Belbais 9 و Family 2 و P 20950 و Qous 5 و Qous 3 و Qous 1) تعتبر أفضل التراكيب الوراثية المرغوبة لصفات المحصول. بالإضافة إلى أن نتائج التحليل العنقودى قد اظهرت المجموعة (ج) التي تحتوي على تسعة تراكيب وراثية (Family 2, Qous 5, Family 4, Edfo, Isna 6, Isna 2, Belbais 9, Qous 4 and Giza 1) تفوقت على الطرز الوراثية الأخرى في محصول بذور النبات. بالنظر الى التراكيب الوراثية العالية المحصول بالنسبة لوحدة المساحة، فان التركيبين الوراثيين Qous 3 and Qous 5 يعتبرا تركيبين وراثيين مبشرين لمعايير الانتخاب لزيادة إنتاجية الترمس. على أساس المعلومات والعلاقات السابقة التي تم مناقشتها ، يمكن التوصية التراكيب الوراثية Qous 4, Belbais 9, Family 2 and Qous 5 لتحسين انتاجية الترمس باستخدامها خلال إعداد برامج التربية المستقبلية في مصر.

الكلمات المفتاحية: التراكيب الوراثية للترمس، التوصيف المورفولوجى، محصول البذور، تحليل ثنائى الإتجاه GT-biplot، التحليل العنقودى Cluster