

Allelopathic effect of sunflower residues and herbicides on the growth and yield of some oat genotypes and their associated weeds

Rehab Mohammed Hassan¹, Saddam Hussein Abbas¹ and Hameed Abd Khashan AL-Farttoosi²

¹Department of Field Crop, College of Agriculture, Al-Qasim Green University, Babylon, Iraq.

²Department of Field Crop, College of Agriculture, Kerbala University, Kerbala, Iraq

authors: Rehab.mohammed@agre.uoqasim.edu.iq,

mr.abbasbaba@gmail.com , hamed.alfarttosi@uokerbala.edu.iq

Abstract

A field experiment was conducted in Babylon, Iraq, during the 2023–2024. Aimed to evaluate the effectiveness of pesticides and sunflower residues in reducing or controlling the growth of accompaniment weeds and their effect on growth and yield traits and their genetic parameters for oat genotypes. A randomized complete block design was applied in a split-plot arrangement with three replicates. The experiment included three oat genotypes (Carlup, Genzania, Shifa) with five levels of some aspects of integrated management (weedy, hand weeding, Pallas herbicide, sunflower residues, sunflower residues + half the recommended rate of Pallas herbicide). The results showed the superiority of the Carlup genotype in achieving the highest weed control rate after 30, 60, and 90 days, which reached (59.46%, 63.38%, and 62.93%) respectively, compared to the Shifa genotype, which gave the lowest average of (55.27%, 61.04%, and 61.48%) respectively. The Genzania genotype showed superiority in vegetative growth traits, while the Shifa cultivar excelled in yield traits and its components. The weed control methods differed in achieving the highest averages of the studied traits. The treatment of sunflower residues + half the rate of Pallas herbicide achieved the highest weed control percentages after 30, 60, and 90 days, which reached (69.46%, 75.55%, and 77.39%) respectively, and the lowest dry weight of (0.06 g.m^{-2}). As for growth and yield traits, the Pallas herbicide treatment was superior in plant height, flag leaf area, number of panicles, number of grains per panicle, 1000-grain weight, and grain yield. The traits showed high broad-sense heritability values for all traits except for the 1000-grain weight. There was a complex interaction between the genotypes and the environment generated by the different control methods to achieve a balance between crop production and elimination of harmful weeds.

Keywords: Oat genotypes, Pallas OD herbicide, Sunflower residues, Heritability.

Introduction

Oat is a dual-purpose crop grown globally over an area of 8.71 million hectares with a grain production of 22.32 million tons [32]. The high nutritional value of oats, ease of cultivation, and adaptability over a wide range distinguish it from other cereals. Moreover, oats contain high levels of vitamins, unsaturated fats, proteins, and antioxidants, which contribute to their high nutritional value, in addition to the high fiber content in oat grains [20].

Oat suffers from a low average grain yield per unit area, one of the main reasons being the presence of both narrow-leaved and broad-leaved weeds and their direct or indirect competition with the crop. Weeds compete efficiently with the crop for vital growth requirements such as water, light, and nutrients, especially during early growth stages. Weeds disrupt ecological balance by displacing native plant species, negatively affecting human and environmental health,

and depleting natural resources such as water and soil nutrients [7].

One of the most important methods used to control weeds is the use of high-yielding genotypes adapted to environmental conditions. Genetic variation among genotypes is considered a critical factor for selecting high-yielding genotypes adapted to local conditions to expand the cultivation area and increase productivity, in addition to managing other agronomic practices [31].

Heritability is defined as the degree to which inheritance controls a certain trait, and its value increases as the genetic variance increases out of the total variance, which leads to higher expected genetic improvement for the trait [1] for all traits [5]. Some researchers have indicated high values of genetic and phenotypic coefficients of variation and genetic gain for the number of grains per spike trait [15].

Chemical herbicides are used to limit the spread of weeds, reduce associated losses, and increase crop yield. One such herbicide is Pallas OD, used to control broadleaf and narrow leaf weeds in wheat and oat fields. It contains the active ingredient pyroxsulam at a concentration of 24 g/L, which inhibits the synthesis of essential amino acids required for cell division, leading to weed death at the 1–5 leaf stage [23]. However, the indiscriminate use of herbicides poses serious problems such as environmental pollution, human health risks, and the development of weed resistance. [18] suggested that allelopathic treatments may be a safer method for weed control compared to herbicides.

On the other hand, many researchers reported that combining herbicides with sunflower residues provides an integrated approach that can enhance crop productivity, maintain ecological balance, and reduce agricultural

costs and negative impacts on farmers and ecosystems [10].

This study aims to enhance understanding of the effects of herbicides and allelopathic crop residues as part of integrated weed management, thereby supporting sustainable productivity of growth and yield traits in oat genotypes while reducing the adverse effects of weeds.

Materials and Methods

A field experiment was conducted in the experimental field of the Department of Field Crops– College of Agriculture– Al-Qasim Green University, Babylon Governorate, Iraq, located at 32.40°N latitude and 44.39°E longitude during the 2023–2024 agricultural season. The experiment followed a randomized complete block design (RCBD) with a split-plot arrangement and three replicates [17].

The experiment included three oat genotypes (Carlup, Genzania, Shifa) arranged in the main plots, while the sub-plots included five levels of some aspects of integrated management (weedy, hand weeding, Pallas herbicide, sunflower residues, sunflower residues + 50% pallas OD).

Sunflower residues were obtained from a field planted the previous year after harvesting the inflorescences. The plants were left to dry naturally, then cut into 5–7 cm pieces, oven-dried until constant weight, ground, and placed in paper bags for use in the experiment at a rate of 1 ton.ha⁻¹, added 15 days before sowing.

The herbicide pallas OD was sprayed at the (2–3 leaf) stage for narrow leaf weeds and (6–8 leaf) stage for broadleaf weeds at a rate of 500 ml.ha⁻¹. Standard soil preparation practices were followed, and the field was divided into 45 experimental units, each of size 1.5 × 1.5 m² with 7 rows spaced 20 cm

apart. The oat genotypes were sown on 18/11/2023 at a seed rate of 120 kg.ha⁻¹.

Phosphorus fertilizer DAP (NP 18:46) was mixed with the soil at a recommended rate of 100 kg.ha⁻¹ [16]. Nitrogen was added in the form of urea at a rate of 200 kg.ha⁻¹ in three equal doses: the first at sowing, the second at the beginning of tillering, and the third at 50% flowering of plants in each experimental unit. Measurements were taken from 1 m² at the center of each experimental unit for weed-related traits as follows:

- Weed control percentage after 30, 60, and 90 days: Calculated using the formula

$$\% \text{Weed control} = [(\text{Weed density in the weedy control} - \text{Weed density in treatment}) / \text{Weed density in the weedy control}] \times 100$$
- Dry weight of weeds (g.m⁻²): Weeds were cut from a 0.5 m² randomly selected area at soil level at harvest, oven-dried at 70°C until constant weight, and the dry weight was calculated [3].

Field traits of oat crop included:

First: Growth traits

- Plant height (cm): Measured for the main stem of ten randomly selected plants from each plot at flowering stage using a measuring tape.
- Number of tillers (tillers.m⁻²): Counted at full maturity from a 0.5 m² area in each plot.
- Flag leaf area: Calculated from the average of ten randomly selected plants at full flowering using the formula:

Flag leaf area = Leaf length × Maximum width × 0.75 [30]

Second: Yield component traits

- Number of panicles (panicles.m⁻²): Counted at harvest from 0.5 m² in each plot.
- Number of grains per panicle (grains.panicle⁻¹): Average of ten panicles

randomly selected from central rows of each plot.

- -1000grain weight (g): 1000 grains were randomly selected and weighed using a precision balance.
- Grain yield (tons.ha⁻¹): Grain yield from the specified area was harvested and converted to tons per hectare.

Statistical Analysis

The collected data were analyzed using Genstat and Microsoft Excel software according to the experimental design. Treatment means were compared using the Least Significant Difference (LSD) test at the 0.05 probability level.

Genetic Analysis

Phenotypic variance and its components, as well as broad-sense heritability, were estimated according to the method of [11] using the following equation:

$$h^2_{bs} = \sigma^2_G / \sigma^2_P = \sigma^2_G / (\sigma^2_G + \sigma^2_{GE/e} + \sigma^2_{E/re})$$

Where:

- σ^2_G = Genotypic variance
- σ^2_P = Phenotypic variance
- σ^2_{GE} = Genotype × Environment interaction variance
- σ^2_E = Environmental variance
- e = Number of environments
- r = Number of replications

In addition, expected genetic gain in the next generation was estimated. Whereas, the expected genetic advance estimated: $GA = k \times \sigma_p \times H$, where k = Intensity of selection. as a percentage of the trait mean, and the coefficient of variation was calculated to determine the environmental influence on the trait relative to its mean.

The values of the coefficients of phenotypic and genetic variation estimated:

$$GCV\% = (\sigma_G / \text{general mean}) \times 100$$

PCV%=(σ_p /general mean) \times 100

σ_G and σ_P =standard deviations of genotypic and phenotypic, respectively

Table. Names of broad and narrow leaf weeds scattered in the experiment

English name	Scientific name	Family	Ratio density
Cheese weed	<i>Malva rotundifolia</i> L.	Malvaceae	very abundant
Wild Radish	<i>Raphanus raphanistrum</i> L.	Cruciferae	abundant
Wild beet	<i>Beta vulgaris</i> L.	Chenopodiaceae	abundant
Field Bind weed	<i>Convolvulus arvensis</i> L.	Convolvulaceae	abundant
Barley	<i>Hordeum bulbosum</i> L.	Poaceae	low
Milk thistle	<i>L. Silybum marianum</i>	Compositae	low
Darnal	<i>Lolium temulentum</i> L.	Poaceae	medium
Wild Oat	<i>Avena fatua</i> L.	Poaceae	medium

Results

and

Discussion

First – Weed Traits

1. Weed control percentage after 30 days of spraying:

The results of Table (1) showed significant differences among cultivars in the weed control percentage after 30 days of spraying, where the genotype Carlup recorded the highest control percentage of 59.46%, which did not differ significantly from Genzania (59.04%), compared to the genotype Shifa, which gave the lowest percentage of 55.27%. This is attributed to the genetic differences between genotypes, as the genetic characteristics of a genotype may be more adapted to resist or reduce the impact of weeds compared to other genotypes such as the release of allelopathic chemical substances that suppress surrounding weed growth [4].

From the same table, there was a significant difference among weed control treatments after 30 days, where the treatment of (sunflower residues + 50% of the

recommended rate of Pallas). resulted in the highest weed control percentage (69.46%), which did not significantly differ from Pallas herbicide at 69.37%. Meanwhile, the (hand weeding) treatment showed the highest average of 100.00%, whereas the (sunflower residues) treatment gave the lowest percentage of 50.78% .

The interaction between genotypes and control treatments showed a significant effect on weed control percentage. The combination (Genzania + sunflower residues + 50% Pallas) recorded the highest percentage (74.65%), which did not significantly differ from (Carlup + Pallas) and (Carlup + sunflower residues + 50% Pallas), which gave 73.65% and 72.32%, respectively, compared to the lowest average recorded by (Shifa + sunflower residues) at 49.6% .

The superiority of sunflower residues + 50% Pallas and Pallas herbicide treatments in weed control percentage is due to the efficiency of allelopathic compounds in sunflower residues

and the active ingredient of Pallas in killing the living tissues of weeds, thus clearly

reducing weed density per square meter [19.]

Table 1: Effect of genotypes, control treatments and their interaction on the percentage of control after 30 days of control date

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	0.00	100.00	73.65	51.31	72.32	59.46
Genzania	0.00	100.00	69.81	51.37	74.65	59.04
Shiffa	0.00	100.00	65.29	49.67	61.41	55.27
Mean	0.00	100.00	69.37	50.78	69.46	
L.S.D 5% V = 2.62 L.S.D 5% M= 2.21 L.S.D V*M=4.12						

.2 Weed control percentage after 60 days of spraying:

The results of Table (2) showed the superiority of Carlup in achieving the highest weed control percentage of

,%63.38 which did not differ significantly from Genzania (63.36%) compared to Shifa, which recorded the lowest percentage at 61.04% .

The same table also indicated a significant effect of control treatments, where both

(sunflower residues + 50% Pallas) and (Pallas herbicide) recorded the highest averages of 75.55% and 75.16%, respectively, compared to (sunflower residues) with the lowest value of 62.25% .

The interaction between genotypes and control treatments showed the combination (Genzania + sunflower residues + 50% Pallas) achieved the highest weed control percentage of 80.08%, compared to the combination (Shifa + sunflower residues) which recorded the lowest percentage of 60.39%.

Table 2: Effect of genotypes, control treatments and their interaction on the percentage of control after 60 days of control date.

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	0.00	100.00	76.83	64.95	75.14	63.38
Genzania	0.00	100.00	75.29	61.42	80.08	63.36
Shifa	0.00	100.00	73.37	60.39	71.43	61.04
Mean	0.00	100.00	75.16	62.25	75.55	
L.S.D V= 0.61 L.S.D M= 1.61 L.S.D V*M=2.68						

.3Weed control percentage after 90 days of spraying:

The results of Table (3) showed significant differences among genotypes with Genzania recording the highest average weed control percentage of 63.47% compared to Shifa, which recorded the lowest average of 61.48% . The same table showed a significant effect of control treatments, where (sunflower residues + 50% Pallas) gave the highest average of

77.39%, compared to (sunflower residues) which gave the lowest average of 64.22% .

As for the interaction between genotypes and control treatments, the combination (Genzania + sunflower residues + 50% Pallas) showed the highest average weed control percentage of 80.91%, compared to (Genzania + sunflower residues) which gave the lowest value of 63.01% .

Table 3: Effect of genotypes, control treatments and their interaction on the percentage of control after 90 days of control date.

Genotype s (V)	Control Methods (M)					Mea n
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	0.00	100.00	71.18	65.20	78.26	62.93
Genzania	0.00	100.00	73.43	63.01	80.91	63.47
Shifa	0.00	100.00	69.95	64.44	73.01	61.48
Mean	0.00	100.00	71.52	64.22	77.39	
L.S.D V= 1.54 L.S.D M= 1.59 L.S.D V*M=2.85						

The results of Tables (1, 2, and 3) confirm the integrated role of weed suppression factors, as the genotype contributes through its competitive ability to reduce light access for weeds and thus suppress their growth. Meanwhile, the herbicide action combined with the allelopathic chemical compounds in sunflower residues inhibits weed germination and growth due to their physiological effects on the plant. This leads to a reduction in weed density per unit area and thus increases weed control percentage [26] [23].

.4Weed dry weight (g.m^{-2})

The results in Table (4) indicate that the genotype Shifa gave the lowest dry weight of weeds at 8.13 g.m^{-2} compared to Carlup, which recorded the highest dry weight at 9.08

g.m^{-2} . This is attributed to differences among oat cultivars in their ability to compete with weeds due to variation in morphological and physiological traits, which play a key role in weed competitiveness. These traits include growth rate, plant height, leaf density, and root system. For instance, genotypes with fast growth and large leaf area can shade weeds quickly, reducing their ability to obtain the light necessary for growth [12].

Table (4) also shows a significant effect of weed control treatments, with all treatments causing a significant reduction in weed dry weight. However, the treatment of (sunflower residues + 50% Pallas) was superior with the lowest dry weight value of 4.06 g.m^{-2} , while the (weedy) treatment recorded the highest value of 26.80 g.m^{-2} .

The interaction between study factors also had a significant effect on weed dry weight, where the combination (Genzania + sunflower residues + 50% Pallas) gave the lowest value of 3.36 g.m^{-2} , compared to (Genzania + weedy), which gave the highest value of 29.25 g.m^{-2} .

The reduction in weed dry weight in the herbicide and residue treatments, whether individually or in combination, is attributed to their role in inhibiting photosynthesis and energy production [1]. Additionally, flavonoids in sunflower residues affect the rate

of photophosphorylation and electron carriers by inhibiting the enzyme phosphor ribulo kinase (PRK), which leads to a reduction in sugar concentration and, consequently, in weed dry weight. These compounds also inhibit enzymes responsible for ATP production, reducing energy needed for weed growth, and inhibit NADP-MDH enzyme, leading to reduced NADPH production and carbon fixation, and thus, a reduction in weed dry weight [27].

Table 4: Effect of genotypes, control treatments and their interaction on weed dry weight(g/m²).

Genotype s (V)	Control Methods (M)					Mea n
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	26.61	0.00	6.77	7.76	4.28	9.08
Genzania	29.25	0.00	5.11	7.22	3.36	8.99
Shifa	24.53	0.00	5.41	6.19	4.53	8.13
Mean	26.80	0.00	5.76	7.06	4.06	
L.S.D V= 0.18 L.S.D M=0.29 L.S.D V*M=0.50						

Second – Growth Traits

Plant Height (cm):

The results of Table (5) showed significant differences among genotypes in plant height, where the genotype Genzania was superior with the highest average of 118.53 cm compared to Carlup, which recorded the lowest height of 105.62 cm. This may be attributed to genetic differences among genotypes in their genetic makeup, which affected their response and nutrient utilization, thus increasing the rate of internode division and elongation, leading to increased plant height. These results are consistent with those of [2].

The same table showed that the (hand weeding) treatment recorded the highest

average plant height of 123.35 cm, followed by (Pallas herbicide) with 120.23 cm, compared to (sunflower residues) which gave the lowest average of 101.18 cm. The decrease in plant height in the (sunflower residues) treatment is attributed to the presence of phenolic acids released from the residues, which act as inhibitory compounds at high concentrations, suppressing cell division and elongation, thus reducing vegetative growth [29].

The interaction effect was also significant, with the combination (Genzania + Pallas) recording the highest height of 126.57 cm, compared to (Carlup + sunflower residues) which gave the lowest value of 94.06 cm.

Table 5: Effect of genotypes, control treatments and their interaction on plant height (cm.)

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	111.41	116.06	112.30	94.06	94.26	105.62
Genzania	122.69	129.11	126.57	106.87	107.41	118.53
Shifa	118.81	124.87	121.83	102.60	104.38	114.50
Mean	117.64	123.35	120.23	101.18	102.02	
L.S.D V= 0.87 L.S.D M= 0.78 L.S.D V*M=1.43						

Number of Tillers (tillers.m⁻²):

Table (6) shows significant differences among genotypes for the number of tillers. Genzania recorded the highest average (404.33 tillers.m⁻²), while Carlup recorded the lowest (350.80 tillers.m⁻²). This may be due to the genetic potential of genotypes to produce more tillers [9].

The table also shows a significant effect of control methods, where (hand weeding) gave the highest average of 409.45 tillers.m⁻², compared to the other treatments (weedy, Pallas, sunflower residues, sunflower residues

+ 50% Pallas), which gave averages of (388.22, 377.11, 359.44, and 351.78 tillers.m⁻²) respectively. The superiority of the hand weeding treatment is due to the absence of competition with weeds and lack of chemical or allelopathic stress, which allowed plants to maintain higher tiller production [19].

The interaction between genotypes and control methods was significant. The combination (Genzania + hand weeding) recorded the highest average (441.00 tillers.m⁻²), while (Carlup + sunflower residues + 50% Pallas) gave the lowest (316.67 tillers.m⁻²).

Table 6: Effect of genotypes, control treatments and their interaction on Numbers of tillers/m².

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	360.33	385.67	356.67	334.67	316.67	350.80
Genzania	417.67	441.00	399.67	381.33	382.00	404.33
Shifa	386.67	401.67	375.00	362.33	356.67	376.47
Mean	388.22	409.45	377.11	359.44	351.78	
L.S.D V=3.65 L.S.D M= 5.36 L.S.D V*M=9.18						

Flag Leaf Area (cm²):

The results in Table (7) show that the genotype Shifa recorded the highest average flag leaf area (31.140 cm²), compared to Genzania and Carlup, which were not significantly different (27.997 and 27.390 cm²,

respectively). This superiority is attributed to genetic differences and the ability of genotypes to utilize absorbed light efficiently [8].

The table also shows significant differences among control treatments. (Hand weeding) gave the highest leaf area (34.270 cm²),

followed by (Pallas) with 31.782 cm², while (sunflower residues + 50% Pallas) gave the lowest (25.579 cm²). This may be due to hormonal changes affected by allelopathic compounds that influence leaf development [28].

The interaction was also significant, where (Shifa + Pallas) recorded the highest value (33.543 cm²), compared to (Carlup + sunflower residues) which recorded the lowest (22.746 cm²).

Table7: Effect of genotypes, control treatments and their interaction on leaf area(cm2.)

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	24.567	33.753	31.423	22.746	24.460	27.390
Genzania	25.593	32.083	30.383	26.207	25.717	27.997
Shifa	28.870	36.973	33.543	29.703	26.613	31.140
Mean	26.343	34.270	31.783	26.219	25.597	
L.S.D V= 0.445		L.S.D M= 0.466		L.S.D V*M= 0.831		

Third – Yield Component Traits

Number of panicles (panicles.m⁻²):

The results in Table (8) indicate significant differences among genotypes control treatments, and their interactions in the number of spikes. The genotype Genzania recorded the highest average (365.13 spikes.m⁻²), while Carlup recorded the lowest (305.13 spikes.m⁻²). This is likely due to the cultivar's ability to produce more tillers, as cultivars with higher tillering capacity often produce more spikes per unit area [22].

The highest number of spikes was observed in the (hand weeding) and (Pallas) treatments, which gave 382.00 and 350.11 spikes.m⁻²,

respectively, while the lowest value was recorded in (sunflower residues + 50% Pallas) at 315.89 spikes.m⁻². This is due to the effectiveness of Pallas in increasing weed control (Tables 1, 2, 3) and reducing weed dry weight (Table 4), allowing crop plants to grow without stress and compete efficiently, enhancing photosynthesis and biological activity, thus increasing spike number [25].

As for interactions, the highest number of spikes was recorded in (Genzania + Pallas) with 379.00 spikes.m⁻², while the lowest was in (Carlup + sunflower residues + 50% Pallas) with 287.00 spikes.m⁻².

Table 8: Effect of genotypes, control treatments and their interaction on Numbers of panicles /m2.

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	274.33	350.00	312.67	301.67	287.00	305.13
Genzania	342.00	417.00	379.00	357.67	330.00	365.13
Shifa	332.00	379.00	358.67	349.33	330.67	349.93
Mean	316.11	382.00	350.11	336.22	315.89	
L.S.D V= 2.55		L.S.D M= 4.41		L.S.D V*M= 7.47		

Number of Grains per panicle:

Table (9) shows a significant effect of genotype on the number of grains per spike. Carlup recorded the highest average (47.80 grains), which did not differ significantly from Shifa (47.44 grains), while Genzania gave the lowest average (44.66 grains). This trait is largely controlled by genetic factors [21]. Control treatments also had a significant

effect, where (Pallas) treatment gave the highest average (49.28 grains), compared to (weedy), which gave the lowest (41.21 grains). The interaction was also significant: (Shifa + Pallas) gave the highest value (51.39 grains), while (Genzania + weedy) recorded the lowest (41.17 grains).

Table9: Effect of genotypes, control treatments and their interaction on grains par panicle.

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	43.14	55.72	50.32	46.19	43.61	47.80
Genzania	41.17	49.22	46.13	43.06	43.74	44.66
Shifa	41.21	56.99	51.39	44.83	42.78	47.44
Mean	41.84	53.98	49.28	44.69	43.38	
L.S.D V= 0.63	L.S.D M= 0.75		L.S.D V*M=1.31			

Weight of 1000 grains (g):

Table (10) confirms a significant effect of genotypes, treatments, and their interaction on 1000-grain weight. Carlup was superior with an average of 31.82 g, while Genzania recorded the lowest average (28.55 g). This reflects the cultivar's efficiency in utilizing

photosynthates and nutrient accumulation in the grains [14].

The (Pallas) treatment gave the highest average (31.62 g), while the (weedy) treatment gave the lowest (28.29 g), due to reduced competition with weeds [19]. The highest interaction value was in (Carlup + Pallas) with 33.13 g, while (Genzania + weedy) gave the lowest (26.48 g).

Table10: Effect of genotypes, control treatments and their interaction on weight of 1000 grains(g).

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	30.26	33.92	33.13	31.17	30.63	31.82
Genzania	26.48	31.54	29.56	28.64	26.50	28.55
Shifa	28.14	34.43	32.16	30.37	30.91	31.20
Mean	28.29	33.30	31.62	30.06	29.35	
L.S.D V= 0.22	L.S.D M= 0.38		L.S.D V*M=0.64			

Grain Yield (ton.ha^{-1}):

Table (11) shows a significant effect of genotypes on grain yield, with Shifa outperforming the others with an average of $5.267 \text{ ton.ha}^{-1}$, despite not being superior in individual yield components. This is attributed to a balanced combination of components and efficient remobilization of nutrients to the grain during maturity [13].

Pallas treatment gave the highest average ($5.436 \text{ ton.ha}^{-1}$), while the (weedy) treatment

gave the lowest ($3.720 \text{ ton.ha}^{-1}$), likely due to the herbicide's role in controlling weeds (Tables 1–4) and enhancing spike number, grain number, and 1000-grain weight (Tables 8–10).

The interaction was also significant, with (Shifa + Pallas) giving the highest yield ($5.928 \text{ ton.ha}^{-1}$), and (Carlup + weedy) the lowest ($3.582 \text{ ton.ha}^{-1}$).

Table11: Effect of genotypes, control treatments and their interaction on Seed yield (ton ha^{-1}).

Genotype s (V)	Control Methods (M)					Mean
	Weedy	Weedy free	Pallas OD	Sunflower Residues	50%Pallas+ sunflower residues	
Carlup	3.582	6.615	5.211	4.343	3.834	4.717
Genzania	3.728	6.473	5.169	4.411	3.827	4.722
Shifa	3.849	7.436	5.928	4.755	4.368	5.267
Mean	3.720	6.841	5.436	4.503	4.010	
L.S.D V= 0.073		L.S.D M= 0.107		L.S.D V*M=0.183		

Fourth – Genetic, Environmental, and Phenotypic Variance, Broad-Sense Heritability and Genetic Advance

1. Growth Traits

The results shown in Table (12) indicate that genetic, environmental, and phenotypic variances were significant for all traits. The values of genetic variance for plant height, number of tillers, and flag leaf area were (43.542, 716.702, and 6.481) respectively, while the corresponding environmental variances were (0.270, 0.467, and 2.472), and phenotypic variances were (43.812, 717.169, and 8.953) respectively.

The phenotypic and genotypic coefficients of variation for plant height were (5.864%, 5.846%), for number of tillers (7.100%, 7.097%), and for flag leaf area (10.573%, 8.996%). These values suggest minimal

differences between genotypic and phenotypic coefficients of variation for plant height and tiller number, indicating low environmental influence and strong genetic expression.

However, flag leaf area showed a moderate difference between the two coefficients, indicating a moderate environmental effect.

Broad-sense heritability was very high for plant height and number of tillers (99.384% and 99.935%, respectively), indicating strong genetic control with minimal environmental influence. The expected genetic advance for these traits suggests noticeable improvement in future generations.

Flag leaf area showed moderate heritability (72.391%), implying significant genetic contribution but also some environmental influence. Its expected genetic advance was lower than for the other two traits, suggesting

that reducing environmental effects could improve selection efficiency [1.]

2. Yield and Yield Components

The results in Table (12) also showed higher genetic variance compared to environmental variance for number of spikes, grains per spike, and grain yield: (972.947, 8.402, and 0.099), respectively. Corresponding environmental variances were (6.160, 4.556, and 0.004), indicating that genetic control is the primary factor in determining these traits and most of the phenotypic variation is due to genetics with limited environmental effects. These traits are ideal for improvement through breeding programs [6]. In contrast, 1000-grain weight appeared to be equally influenced by genetic and environmental factors, with genetic variance of 1.891 and environmental variance of 2.877. Improving this trait would require intensive, well-planned selection programs with supportive environmental management. Broad-sense heritability was high for number of spikes and grain yield

(99.371% and 95.911%), moderate for number of grains per spike (64.840%), and relatively low for 1000-grain weight (39.660%). The differences between genotypic and phenotypic coefficients of variation for number of spikes and grain yield were small (9.171% vs. 9.200%, and 6.329% vs. 6.546%, respectively), suggesting weak environmental influence. A moderate difference was found for number of grains per spike (6.329% vs. 7.859%), while 1000-grain weight showed a large gap (4.592% vs. 7.292%), indicating a stronger environmental effect. The expected genetic advance values ranged from low to high. The highest was for number of spikes (64.053), and the lowest for 1000-grain weight (1.784) [24.]

It concluded that the high genetic variances and broad-sense heritability for most traits provide good opportunities for breeders to use these traits as selection indicators, especially in early generations.

Table 12: Genetic, environmental, and phenotypic variances, coefficients of variation, broad-sense heritability, and expected genetic advance for the studied traits

Parameters	Traits						
	Plant Height (cm)	No. Tillers (m ²)	Flag Leaf Area (cm ²)	No. Spikes (m ²)	Grains per Spike	1000-grain Weight (g)	Grain Yield (ton.ha ⁻¹)
VE	0.270	0.467	2.472	6.160	4.556	2.877	0.004
VG	43.542	716.702	6.481	972.947	8.402	1.891	0.099
VP	43.812	717.169	8.953	979.107	12.959	4.768	0.103
H²_{bs}	99.384	99.935	72.391	99.371	64.840	39.660	95.911
GA	13.551	55.131	4.462	64.053	4.808	1.784	0.634
GA%	12.004	14.615	15.767	18.831	10.497	5.957	12.933
CVG%	5.846	7.097	8.996	9.171	6.329	4.592	6.411
CVP%	5.864	7.100	10.573	9.200	7.859	7.292	6.546
mean	112.882	377.200	28.299	340.133	45.802	29.946	4.902

Where: $\sigma^2 G$ is genetic variance, $\sigma^2 E$ is environmental and $\sigma^2 p$ is phenotypic variances, h^2_{bs} is Heritability broad sense, GA is genetic advance, GA% is genetic advance of mean and C.V% is coefficient variance .

Conclusions

It can be concluded that the use of herbicides and sunflower residues effectively contributed to reducing the density of weeds associated with the oat crop, which positively reflected on improving plant growth and increasing

yield. These treatments also influenced some genetic parameters related to high productivity, which supports their role as an integrated approach in weed control and in enhancing agricultural productivity .

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